CONTIG4950	16836505_c2_9	5745	19848	435	145	YKR026C	469	1.2(10)-44	Saccharomyces cerevisiae	[ui:ykr026c] [pn:translation initiation factor eif2b, 34 kd, alpha subunit:translation initiation factor eif-2b alpha subunit:eif-2b gdp-gtp exchange factor:guanine nucleotide exchange factor subunit gcn3:gcd complex subunit gcn3:trans
CONTIG5254	24113537_c3_24	5746	19849	528	176	YKR084C	455	3.6(10)-43	Saccharomyces cerevisiae	[ui:ykr084c] [pn:translation elongation factor eef-1 alpha chain homolog:elongation factor 1 alpha-like protein] [gn:hbs1-ykr404] [gtcfc:10.7] [keggfc:14.2] [sgdfc:5.2.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5254	4375703_c3_23	5747	19850	711	237	YKR084C	154	2.1(10)-9	Saccharomyces cerevisiae	[ui:ykr084c] [pn:translation elongation factor eef-1 alpha chain homolog:elongation factor 1 alpha-like protein] [gn:hbs1-ykr404] [gtcfc:10.7] [keggfc:14.2] [sgdfc:5.2.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5254	4100936_c3_22	5748	19851	423	141	YKR084C	115	5.2(10)-6	Saccharomyces cerevisiae	[ui:ykr084c] [pn:translation elongation factor eef-1 alpha chain homolog:elongation factor 1 alpha-like protein] [gn:hbs1-ykr404] [gtcfc:10.7] [keggfc:14.2] [sgdfc:5.2.0:9.2.0] [db:gtc-saccharomyces cerevisiae]

CONTIG989	56_f1_1	5749	19852	597	199	YKR084C	176	1.5(10)-12	Saccharomyces cerevisiae	[ui:ykr084c] [pn:translation elongation factor eef-1 alpha chain homolog:elongation factor 1 alpha-like protein] [gn:hbs1:ykr404] [gtcfc:10.7] [keggfc:14.2] [sgdfc:5.2.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3453	1562_c1_6	5750	19853	1317	439	YLR249W	1265	5.2(10)-129	Saccharomyces cerevisiae	[ui:ylr249w] [pn:translation elongation factor eef3:elongation factor 3:ef-3] [gn:yef3:tef3:efc1:l9672] [gtcfc:10.7] [keggfc:14.2] [sgdfc:5.2.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3994	132962_c3_10	5751	19854	564	188	YLR249W	690	1.5(10)-67	Saccharomyces cerevisiae	[ui:ylr249w] [pn:translation elongation factor eef3:elongation factor 3:ef-3] [gn:yef3:tef3:efc1:l9672] [gtcfc:10.7] [keggfc:14.2] [sgdfc:5.2.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3994	1288135_c3_9	5752	19855	234	78	YLR249W	138	3.6(10)-8	Saccharomyces cerevisiae	[ui:ylr249w] [pn:translation elongation factor eef3:elongation factor 3:ef-3] [gn:yef3:tef3:efc1:l9672] [gtcfc:10.7] [keggfc:14.2] [sgdfc:5.2.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4952	25636466_f2_2	5753	19856	1782	594	YLR289W	1866	1.1(10)-192	Saccharomyces cerevisiae	[ui:ylr289w] [pn:strong similarity to e. coli elongation factor-type gtp-binding protein lepa:gtp-binding protein:gtpase] [gn:gufl] [gtcfc:10.7] [keggfc:14.2] [sgdfc:5.2.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5506	21969677_f3_6	5754	19857	1128	376	YLR291C	902	1.6(10)-90	Saccharomyces cerevisiae	[ui:ylr291c] [pn:translation initiation factor eif2b, 43 kda subunit:translation initiation factor eif-2b gamma subunit:eif-2b gdp-gtp exchange factor:guanine nucleotide exchange factor subunit gcd7:gcd complex subunit gcd7] [gn:gcd7:l]
CONTIG5782	36504568_c3_24	5755	19858	906	302	YMR146C	858	7.2(10)-86	Saccharomyces cerevisiae	[ui:ymr146c] [pn:translation initiation factor eif3, p39 subunit:translation initiation factor eif-3 p39 subunit] [gn:tif34:ymr9375] [gtcfc:10.7] [keggfc:14.2] [sgdfc:5.2.0.9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5466	4566_c3_16	5756	19859	507	169	YMR260C	542	2.2(10)-52	Saccharomyces cerevisiae	[ui:ymr260c] [pn:translation initiation factor eif1a:eukaryotic initiation factor 1a:eif-1a:eif-4c] [gn:tif11:ym8156] [gtcfc:10.7] [keggfc:14.2] [sgdfc:5.2.0.9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4683	16281457_c3_5	5757	19860	1890	630	YMR309C	1048	5.2(10)-106	Saccharomyces cerevisiae	[ui:ymr309c] [pn:associated with 40s ribosomal subunit:nuclear transport protein nip1] [gn:nip1:ym9924] [gtcfc:10.4:10.7:10.1:12.6] [keggfc:14.2] [sgdfc:5.2.0.9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG959	6325_f2_2	5758	19861	351	117	YNL244C	404	9.1(10)-38	Saccharomyces cerevisiae	[ui:ynl244c] [pn:translation initiation factor 3:eif3:protein translation factor sui1] [gn:sui1:rfi1:n0905] [gtcfc:10.7] [keggfc:14.2] [sgdfc:5.2.0.9.2.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4356	10969075_f1_1	5759	19862	1965	655	YNL163C	919	1.8(10)-110	Saccharomyces cerevisiae	[ui:ynl163c] [pn:translation elongation factor eef4:hypothetical 124.5 kd protein in sko1-rpl44a intergenic region] [gn:n1718] [gtcfc:10.7] [keggfc:14.2] [sgdfc:5.2.0] [db:gtc-saccharomyces cerevisiae]
b1x18355.x	14554563_c3_3	5760	19863	483	161	YNL163C	502	4.9(10)-47	Saccharomyces cerevisiae	[ui:ynl163c] [pn:translation elongation factor eef4:hypothetical 124.5 kd protein in sko1-rpl44a intergenic region] [gn:n1718] [gtcfc:10.7] [keggfc:14.2] [sgdfc:5.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1921	33375286_f1_1	5761	19864	246	82	YNL062C	165	1.5(10)-11	Saccharomyces cerevisiae	[ui:ynl062c] [pn:translation initiation factor eif3 rna-binding subunit:gcd10 protein] [gn:gcd10:n2422] [gtcfc:10.7] [keggfc:14.2] [sgdfc:5.2.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3550	35283312_f2_1	5762	19865	948	316	YNL062C	616	3.2(10)-60	Saccharomyces cerevisiae	[ui:ynl062c] [pn:translation initiation factor eif3 rna-binding subunit:gcd10 protein] [gn:gcd10:n2422] [gtcfc:10.7] [keggfc:14.2] [sgdfc:5.2.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1531	31808333_f3_2	5763	19866	984	328	YNL014W	1377	7.2(10)-141	Saccharomyces cerevisiae	[ui:ynl014w] [pn:translation elongation factor eef3 homolog:putative elongation elongation factor 3 homolog:ef-3] [gn:n2846] [gtcfc:10.7:12.6] [keggfc:14.2] [sgdfc:5.2.0:7.9.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3994	14628192_c2_7	5764	19867	354	118	YNL014W	429	2.8(10)-39	Saccharomyces cerevisiae	[ui:ynl014w] [pn:translation elongation factor eef3 homolog:putative elongation factor 3 homolog:ef-3] [gn:n28846] [gtcfc:10.7:12.6] [keggfc:14.2] [sgdfc:5.2.0:7.9.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3078	5312510_c2_6	5765	19868	1122	374	YOL139C	120	2.0(10)-5	Saccharomyces cerevisiae	[ui:yol139c] [pn:translation initiation factor eif4e:eukaryotic initiation factor 4e:eif-4e:mrna cap-binding protein] [gn:tif45:cdc33] [gtcfc:10.7] [keggfc:14.2] [sgdfc:5.2.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4733	25476625_f2_4	5766	19869	669	223	YOL139C	583	9.9(10)-57	Saccharomyces cerevisiae	[ui:yol139c] [pn:translation initiation factor eif4e:eukaryotic initiation factor 4e:eif-4e:mrna cap-binding protein] [gn:tif45:cdc33] [gtcfc:10.7] [keggfc:14.2] [sgdfc:5.2.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
b3x16009.y	14095287_f1_1	5767	19870	270	90	YOL139C	230	2.5(10)-19	Saccharomyces cerevisiae	[ui:yol139c] [pn:translation initiation factor eif4e:eukaryotic initiation factor 4e:eif-4e:mrna cap-binding protein] [gn:tif45:cdc33] [gtcfc:10.7] [keggfc:14.2] [sgdfc:5.2.0:9.2.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2719	35803130_f3_2	5768	19871	855	285	YOR260W	303	1.5(10)-38	Saccharomyces cerevisiae	[ui:yor260w] [pn:translation initiation factor eif2bgamma subunit:translation initiation factor eif-2b gamma subunit:eif-2b gdp-gtp exchange factor:guanine nucleotide exchange factor subunit gcd1:gcd complex subunit gcd1] [gn:gcd1:tra3]
CONTIG3491	26604767_f2_5	5769	19872	459	153	YOR260W	172	1.1(10)-15	Saccharomyces cerevisiae	[ui:yor260w] [pn:translation initiation factor eif2bgamma subunit:translation initiation factor eif-2b gamma subunit:eif-2b gdp-gtp exchange factor:guanine nucleotide exchange factor subunit gcd1:gcd complex subunit gcd1] [gn:gcd1:tra3]
CONTIG3568	19943775_f3_1	5770	19873	546	182	YOR276W	161	5.2(10)-12	Saccharomyces cerevisiae	[ui:yor276w] [pn:mrna cap-binding protein:eif4f, 20k subunit:cap associated protein] [gn:caf20:cap20] [sgdfc:5.2.0.9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4524	10156507_c2_6	5771	19874	927	309	YOR361C	402	1.3(10)-54	Saccharomyces cerevisiae	[ui:yor361c] [pn:translation initiation factor eif3 subunit:cell cycle regulation and translation initiation protein] [gn:prt1:cdc63] [gtcfc:10.7:12.8] [keggfc:14.2] [sgdfc:3.8.0:5.2.0:9.2.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3920	25478412_f2_1	5772	19875	858	286	YPL237W	693	2.2(10)-68	Saccharomyces cerevisiae	[ui:ypl237w] [pn:translation initiation factor eif2 beta subunit:translational initiation factor 2 beta subunit:eif-2-beta] [gn:sui3] [gtcfc:10.7] [keggfc:14.2] [sgdfc:5.2.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5642	23915932_f2_3	5773	19876	3591	1197	YPL226W	3359	0	Saccharomyces cerevisiae	[ui:ypl226w] [pn:similarity to translation elongation factor eef3] [gtcfc:10.7:12.6] [keggfc:14.2] [sgdfc:5.2.0:7.9.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4304	23478550_c3_9	5774	19877	585	195	YPL048W	310	8.4(10)-28	Saccharomyces cerevisiae	[ui:ypl048w] [pn:translation elongation factor eef1 alpha chain:elongation factor 1-gamma 1:ef-1-gamma 1] [gn:tef3:cam1] [gtcfc:10.7] [keggfc:14.2] [sgdfc:5.2.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4304	4297162_c2_8	5775	19878	234	78	YPL048W	186	5.5(10)-14	Saccharomyces cerevisiae	[ui:ypl048w] [pn:translation elongation factor eef1 alpha chain:elongation factor 1-gamma 1:ef-1-gamma 1] [gtcfc:10.7] [keggfc:14.2] [sgdfc:5.2.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4885	7308137_c1_9	5776	19879	1170	390	YPL048W	713	1.0(10)-96	Saccharomyces cerevisiae	[ui:ypl048w] [pn:translation elongation factor eef1 alpha chain:elongation factor 1-gamma 1:ef-1-gamma 1] [gn:tef3:cam1] [gtcfc:10.7] [keggfc:14.2] [sgdfc:5.2.0:9.2.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2323	4303191_f2_1	5777	19880	1089	363	YPR041W	537	4.5(10)-84	Saccharomyces cerevisiae	[ui:ypr041w] [pn:translation initiation factor eif5:eukaryotic initiation factor 5:eif-5] [gn:tif5:yp3085] [gtcfc:10.7] [keggfc:14.2] [sgdfc:5.2.0-9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3182	29376640_f2_2	5778	19881	756	252	YPR041W	303	4.2(10)-41	Saccharomyces cerevisiae	[ui:ypr041w] [pn:translation initiation factor eif5:eukaryotic initiation factor 5:eif-5] [gn:tif5:yp3085] [gtcfc:10.7] [keggfc:14.2] [sgdfc:5.2.0-9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1758	5207026_f3_3	5779	19882	948	316	YPR163C	344	2.1(10)-31	Saccharomyces cerevisiae	[ui:ypr163c] [pn:translation initiation factor tif3/stm1:translation initiation factor tif3/stm1:eif-4b] [gn:tif3:stm1:p9325] [gtcfc:10.7] [keggfc:14.2] [sgdfc:5.2.0-9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3827	24697182_f3_3	5780	19883	867	289	YFR009W	893	1.3(10)-89	Saccharomyces cerevisiae	[ui:yf009w] [pn:positive effector of gcn2p:protein] [gn:gcn20] [gtcfc:10.7:12.6] [keggfc:14.2] [sgdfc:5.3.0:7.9.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3827	6843955_f3_4	5781	19884	1026	342	YFR009W	1247	4.2(10)-127	Saccharomyces cerevisiae	[ui:yf009w] [pn:positive effector of gcn2p:protein] [gn:gcn20] [gtcfc:10.7:12.6] [keggfc:14.2] [sgdfc:5.3.0:7.9.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2245	5913393_f1_1	5782	19885	897	299	YGL195W	597	1.8(10)-56	Saccharomyces cerevisiae	[ui:ygl195w] [pn:translational activator:translational activator gcn1] [gn:gcn1:g1318] [gtcfc:10.7] [keggfc:14.2] [sgdfc:5.3.0:9.2.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4938	24787825_f1_3	5783	19886	1338	446	YGL195W	193	1.0(10)-23	Saccharomyces cerevisiae	[ui:ygl195w] [pn:translational activator:translational activator gcn1] [gn:gcn1:gl318] [gtcfc:10.7] [keggfc:14.2] [sgdfc:5.3.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5175	15663535_c2_9	5784	19887	3177	1059	YGL195W	1442	1.3(10)-235	Saccharomyces cerevisiae	[ui:ygl195w] [pn:translational activator:translational activator gcn1] [gn:gcn1:gl318] [gtcfc:10.7] [keggfc:14.2] [sgdfc:5.3.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
b9x13s54.x	23955187_f2_1	5785	19888	363	121	YGL195W	172	2.0(10)-14	Saccharomyces cerevisiae	[ui:ygl195w] [pn:translational activator:translational activator gcn1] [gn:gcn1:gl318] [gtcfc:10.7] [keggfc:14.2] [sgdfc:5.3.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2020	10976532_f1_1	5786	19889	900	300	YJL125C	655	2.2(10)-64	Saccharomyces cerevisiae	[ui:yjl125c] [pn:translational repressor of gcn4·gcd14 protein] [gn:gcd14:j0710] [gtcfc:10.7] [keggfc:14.2] [sgdfc:5.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3643	782750_f3_2	5787	19890	549	183	YMR028W	151	3.8(10)-14	Saccharomyces cerevisiae	[ui:ymr028w] [pn:component of the tor signaling pathway] [gn:tap42] [gtcfc:12.13] [keggfc:14.2]
CONTIG2486	22926268_f2_2	5788	19891	981	327	YNL139C	114	0.0015	Saccharomyces cerevisiae	[ui:ynl139c] [pn:regulatory protein:rlr1 protein] [gn:rlr1:n1209:n1835] [gtcfc:10.7] [keggfc:14.2] [sgdfc:5.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3826	4489075_c3_4	5789	19892	1431	477	YNL139C	234	4.5(10)-16	Saccharomyces cerevisiae	[ui:ynl139c] [pn:regulatory protein:rlr1 protein] [gn:rlr1:n1209:n1835] [gtcfc:10.7] [keggfc:14.2] [sgdfc:5.3.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2848	964062_f1_1	5790	19893	555	185	YGR147C	151	1.5(10)-10	Saccharomyces cerevisiae	[ui:ygr147c] [pn:n-acetyltransferase for n-terminal methionine:n-terminal acetyltransferase 2:amino-terminal, alpha-amino, acetyltransferase 2] [gn:nat2:g6630] [gtcfc:10.7:14.1] [ec:2.3.1.88] [sgdfc:5.5.0:6.3.0:9.2.0] [d
CONTIG5076	1206562_c1_7	5791	19894	465	155	YHR189W	184	1.8(10)-14	Saccharomyces cerevisiae	[ui:yhr189w] [pn:similarity to peptidyl-trna hydrolases:putative peptidyl-trna hydrolase:pth] [gtcfc:10.7] [ec:3.1.1.29] [keggfc:14.1] [sgdfc:5.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1050	24303779_c1_2	5792	19895	621	207	YHR189W	243	1.1(10)-20	Saccharomyces cerevisiae	[ui:yhr189w] [pn:similarity to peptidyl-trna hydrolases:putative peptidyl-trna hydrolase:pth] [gtcfc:10.7] [ec:3.1.1.29] [keggfc:14.1] [sgdfc:5.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3262	4942012_c2_6	5793	19896	1119	373	YMR005W	234	5.7(10)-34	Saccharomyces cerevisiae	[ui:ymr005w] [pn:required for protein synthesis:mpt1 protein] [gn:mpt1:ym8270] [gtcfc:10.7] [keggfc:14.2] [sgdfc:5.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3952	1426093l_c3_7	5794	19897	1650	550	YNL209W	2231	2.2(10)-231	Saccharomyces cerevisiae	[ui:ynl209w] [pn:heat shock protein of hsp70 family, cytosolic:heat shock protein ssb2] [gn:ssb2:n1333] [gtcfc:12.7] [keggfc:14.2] [sgdfc:5.5.0:9.2.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5378	20319182_c2_15	5795	19898	543	181	YBR164C	708	5.5(10)-70	Saccharomyces cerevisiae	[ui:ybr164c] [pn:adp-ribosylation factor:adp-ribosylation factor-like protein 1] [gn:arl1:arf3:ybr1216] [gtcfc:10.7:12.10] [keggfc:14.2] [sgdfc:6.3.0:8.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5109	4103506_f1_1	5796	19899	720	240	YDL212W	314	3.2(10)-28	Saccharomyces cerevisiae	[ui:ydl212w] [pn:endoplasmic reticulum membrane protein:secretory component protein] [gn:shr3] [gtcfc:10.7:11.1:12.16] [keggfc:14.2] [sgdfc:6.2.0:6.3.0:9.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5715	24022191_c1_10	5797	19900	801	267	YDR098C	676	1.3(10)-66	Saccharomyces cerevisiae	[ui:ydr098c] [pn:similarity to legionella glutaredoxin-like protein] [gtcfc:10.7] [keggfc:14.2] [sgdfc:6.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5792	20120390_f2_9	5798	19901	2463	821	YDR495C	103	0.11	Saccharomyces cerevisiae	[ui:ydr495c] [pn:vacuolar sorting protein:vacuolar protein sorting-associated protein vps3] [gn:vps3:d9719] [gtcfc:10.7:11.1:12.16] [keggfc:14.2] [sgdfc:6.2.0:6.3.0:6.4.0:9.10.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4598	14879155_f1_1	5799	19902	579	193	YEL012W	462	$6.5(10)-44$	Saccharomyces cerevisiae	[ui:yel012w] [pn:ubiquitin-conjugating enzyme:ubiquitin-conjugating enzyme e2-24 kd:ubiquitin-protein ligase:ubiquitin carrier protein] [gn:ubc8] [gtcfc:10.7] [ec:6.3.2.19] [keggfc:14.1] [sgdfc:6.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5659	11719175_f3_11	5800	19903	1395	465	YER005W	1212	$2.2(10)-123$	Saccharomyces cerevisiae	[ui:yer005w] [pn:similarity to gda1p:hypothetical 71.9 kd protein in pmi40-pac2 intergenic region] [gtcfc:10.7] [keggfc:14.2] [sgdfc:6.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5659	4882788_f3_12	5801	19904	801	267	YER005W	121	$8.5(10)-5$	Saccharomyces cerevisiae	[ui:yer005w] [pn:similarity to gda1p:hypothetical 71.9 kd protein in pmi40-pac2 intergenic region] [gtcfc:10.7] [keggfc:14.2] [sgdfc:6.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG225	32032160_c3_2	5802	19905	327	109	YGL203C	103	0.00012	Saccharomyces cerevisiae	[ui:ygl203c] [pn:carboxypeptidase:ysc-alpha:carboxypeptidase precursor:carboxypeptidase d] [gn:kex1] [gtcfc:10.7.12.16] [ec:3.4.16.6] [keggfc:14.1] [sgdfc:6.3.0:9.4.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5562	22456555_c1_8	5803	19906	1578	526	YGL203C	971	7.5(10)-98	Saccharomyces cerevisiae	[ui:ygl203c] [pn:carboxypeptidase:ysc-alpha:carboxypeptidase precursor:carboxypeptidase d] [gn:kex1] [gtcfc:10.7:12.16] [ec:3.4.16.6] [keggfc:14.1] [sgdfc:6.3.0:9.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5531	4354803_c3_34	5804	19907	570	190	YGR133W	276	3.3(10)-24	Saccharomyces cerevisiae	[ui:ygr133w] [pn:ubiquitin-conjugating enzyme:ubiquitin-conjugating enzyme e2-2l kd:ubiquitin- protein ligase:ubiquitin carrier protein] [gn:pas2:ubc10] [gtcfc:10.7:12.16.12.6] [ec:6.3.2.19] [keggfc:14.1] [sgdfc:6.3.0:6.4.0:9.8.0] [db
CONTIG4597	19584530_f1_1	5805	19908	378	126	YGR209C	126	2.6(10)-8	Saccharomyces cerevisiae	[ui:ygr209c] [pn:thioredoxin ii:thioredoxin i:tr-i] [gn:trx2:trx1:g7746] [gtcfc:10.7:12.12.12.8] [keggfc:14.2] [sgdfc:3.8.0:6.3.0:11.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5028	10979805_f3_6	5806	19909	990	330	YGR209C	194	3.2(10)-15	Saccharomyces cerevisiae	[ui:gr209c] [pn:thioredoxin ii:thioredoxin i:tr-i] [gn:trx2:trx1:g7746] [gtcfc:10.7:12.12.12.8] [keggfc:14.2] [sgdfc:3.8.0:6.3.0:11.3.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5804	22689062_f1_11	5807	19910	1473	491	YJR117W	1227	5.7(10)-125	Saccharomyces cerevisiae	[ui:yjr117w] [pn:zinc metallo-protease:hypothetical 52.3 kd protein in nnf1-atp2 intergenic region] [gn:ste24:j2032] [gtcfc:10.11:12.9] [keggfc:14.2] [sgdfc:3.3.0:6.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2164	1300_c2_3	5808	19911	330	110	YLR043C	332	3.8(10)-30	Saccharomyces cerevisiae	[ui:ylr043c] [pn:thioredoxin ii:thioredoxin ii:tr-ii] [gn:trx1:trx2] [gtcfc:10.7:12.12:12.8] [keggfc:14.2] [sgdfc:3.8.0:6.3.0:11.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3792	6095437_c1_10	5809	19912	627	209	YLR066W	403	1.2(10)-37	Saccharomyces cerevisiae	[ui:ylr066w] [pn:similarity to signal peptidase] [gtcfc:11.1] [keggfc:14.2] [sgdfc:6.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1309	31645177_c2_4	5810	19913	1179	393	YLR121C	144	5.2(10)-7	Saccharomyces cerevisiae	[ui:ylr121c] [pn:strong similarity to aspartyl proteases] [gtcfc:10.11:5.2] [keggfc:14.2] [sgdfc:6.3.0] [db:gtc-saccharomyces cerevisiae]
b2x10323.y	7219712_f3_1	5811	19914	477	159	YLR244C	616	3.2(10)-60	Saccharomyces cerevisiae	[ui:ylr244c] [pn:methionine aminopeptidase, isoform 1:methionine aminopeptidase 1 precursor:metap 1:peptidase m 1:map] [gn:map1:i9672] [gtcfc:10.7:14.1] [ec:3.4.11.18] [keggfc:14.1] [sgdfc:6.3.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2489	11907537_f1_3	5812	19915	465	155	YLR389C	143	1.0(10)-8	Saccharomyces cerevisiae	[ui:ylr389c] [pn:protease involved in a-factor processing] [gn:ste23] [gtcfc:10.11:12.9] [keggfc:14.2] [sgdfc:6.3.0:6.3.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5476	21523515_f3_7	5813	19916	1077	359	YLR389C	790	1.1(10)-78	Saccharomyces cerevisiae	[ui:ylr389c] [pn:protease involved in a-factor processing] [gn:ste23] [gtcfc:10.11:12.9] [keggfc:14.2] [sgdfc:3.3.0:6.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5476	33396075_f2_5	5814	19917	2469	823	YLR389C	1272	9.5(10)-130	Saccharomyces cerevisiae	[ui:ylr389c] [pn:protease involved in a-factor processing] [gn:ste23] [gtcfc:10.11:12.9] [keggfc:14.2] [sgdfc:3.3.0:6.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG882	4509775_f1_1	5815	19918	819	273	YLR389C	313	6.7(10)-27	Saccharomyces cerevisiae	[ui:ylr389c] [pn:protease involved in a-factor processing] [gn:ste23] [gtcfc:10.11:12.9] [keggfc:14.2] [sgdfc:3.3.0:6.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5196	13671877_f1_2	5816	19919	573	191	YML055W	189	5.5(10)-15	Saccharomyces cerevisiae	[ui:ym1055w] [pn:signal peptidase 18 kd subunit] [gn:spc2] [gtcfc:11.1:10.7:12.16] [keggfc:14.2] [sgdfc:6.3.0:9.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3894	14063427_c2_7	5817	19920	1125	375	YMR152W	305	2.8(10)-27	Saccharomyces cerevisiae	[ui:ymr152w] [pn:mitochondrial inner membrane protease:hypothetical 41.6 kd protein in imp1-hjl1 intergenic region:rf1095] [gn:ym9375] [gtcfc:10.11:12.16] [keggfc:14.2] [sgdfc:6.3.0] [db:gtc-saccharomyces cerevisiae]

CONTIG										
CONTIG5708	23469680_f1_9	5818	19921	1089	363	YMR152W	248	6.7(10)-20	Saccharomyces cerevisiae	[ui:ymr152w] [pn:mitochondrial inner membrane protease:hypothetical 41.6 kd protein in imp1-hjl1 intergenic region:rf1095] [gn:ym9375] [gtcfc:10.11:12.16] [keggfc:14.2] [sgdfc:6.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4441	995300_c3_5	5819	19922	840	280	YNL238W	650	7.9(10)-64	Saccharomyces cerevisiae	[ui:ynl238w] [pn:endoproteinase of late golgi compartment:kexin precursor:kex2 protease:proteinase yscf] [gn:kex2:qds1:n1122] [gtcfc:10.11:12.16:12.9] [ec:3.4.21.61] [keggfc:14.1] [sgdfc:3.3.0:6.3.0:9.4.0] [db:gtc-saccharomyces cerevi
CONTIG5003	506693_f1_1	5820	19923	1191	397	YOR219C	226	8.9(10)-16	Saccharomyces cerevisiae	[ui:yor219c] [pn:type iv dipeptidyl aminopeptidase:dipeptidyl aminopeptidase a:dpap a:ysciv] [gn:ste13:ycil:yor50-9] [gtcfc:10.7:12.16:12.9] [ec:3.4.14.-] [sgdfc:3.3.0:6.3.0:9.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5003	24238387_f2_4	5821	19924	1581	527	YOR219C	958	1.8(10)-96	Saccharomyces cerevisiae	[ui:yor219c] [pn:type iv dipeptidyl aminopeptidase:dipeptidyl aminopeptidase a:dpap a:ysciv] [gn:ste13:ycil:yor50-9] [gtcfc:10.7:12.16:12.9] [keggfc:14.1] [sgdfc:3.3.0:6.3.0:9.4.0] [db:gtc-saccharomyces cerevisiae]

b2x12432.y	980002_c3_10	5822	19925	459	153	YPL051W	161	5.2(10)-12	Saccharomyces cerevisiae	[ui:ypl051w] [pn:strong similarity to adp-ribosylation factors] [gtcfc:10.7:12.10] [keggfc:14.2] [sgdfc:6.3.0:8.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3269	16485902_c3_2	5823	19926	1122	374	YPL050C	1025	1.3(10)-103	Saccharomyces cerevisiae	[ui:ypl050c] [pn:required for complex n-glycosylation:protein] [gn:mnn9] [gtcfc:10.7:12.16] [keggfc:14.2] [sgdfc:6.3.0-9.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5127	33477192_c3_10	5824	19927	465	155	YPR131C	394	1.1(10)-36	Saccharomyces cerevisiae	[ui:ypr131c] [pn:similarity to n-acetyltransferases] [gtcfc:10.7] [keggfc:14.2] [sgdfc:6.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4781	23945177_c2_4	5825	19928	1926	642	YAL002W	254	7.5(10)-36	Saccharomyces cerevisiae	[ui:yal002w] [pn:vacuolar sorting protein, 134 kd:vacuolar protein sorting-associated protein vps8] [gn:vps8:fun15] [gtcfc:10.7:11.1:12.13] [keggfc:14.2] [sgdfc:6.2.0:8.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4781	26368752_c2_3	5826	19929	804	268	YAL002W	188	2.6(10)-12	Saccharomyces cerevisiae	[ui:yal002w] [pn:vacuolar sorting protein, 134 kd:vacuolar protein sorting-associated protein vps8] [gn:vps8:fun15] [gtcfc:10.7:11.1:12.13] [keggfc:14.2] [sgdfc:6.2.0:8.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5445	1194062_c1_9	5827	19930	1035	345	YBL017C	802	9.0(10)-79	Saccharomyces cerevisiae	[ui:ybl017c] [pn:vacuolar protein sorting/targeting protein:vacuolar protein sorting/targeting protein pep1 precursor:vacuolar carboxypeptidase sorting receptor vps10:carboxypeptidase y receptor] [gn:pep1:vps10:ybl0302:ybl03] [gtcfc:10]
CONTIG5445	15648387_c1_8	5828	19931	306	102	YBL017C	183	9.5(10)-13	Saccharomyces cerevisiae	[ui:ybl017c] [pn:vacuolar protein sorting/targeting protein:vacuolar protein sorting/targeting protein pep1 precursor:vacuolar carboxypeptidase sorting receptor vps10:carboxypeptidase y receptor] [gn:pep1:vps10:ybl0302:ybl03] [gtcfc:10]
CONTIG5445	19735877_c3_14	5829	19932	1089	363	YBL017C	466	7.0(10)-43	Saccharomyces cerevisiae	[ui:ybl017c] [pn:vacuolar protein sorting/targeting protein:vacuolar protein sorting/targeting protein pep1 precursor:vacuolar carboxypeptidase sorting receptor vps10:carboxypeptidase y receptor] [gn:pep1:vps10:ybl0302:ybl03] [gtcfc:10]

CONTIG3639	2835062_f2_2	5830	19933	738	246	YBR171W	341	4.4(10)-31	Saccharomyces cerevisiae	[ui:ybr171w] [pn:er protein-translocation complex subunit:translocation protein sec66:hss1 protein] [gn:sec66:hss1:sec71:ybr1232] [gtcfc:10.7:11.1:12.16:12.6] [sgdfc:14.2] [sgdfc:6.2.0:7.11.0:8.8.0:9.4.0] [db:gtc-saccharomyces cerevi
CONTIG5674	897627_f3_10	5831	19934	1509	503	YBR283C	870	3.7(10)-87	Saccharomyces cerevisiae	[ui:ybr283c] [pn:strong similarity to sec61p:hypothetical 53.3 kd protein in mrpl37-ape3 intergenic region] [gn:ybr2020] [gtcfc:10.7:11.1:12.6] [keggfc:14.2] [sgdfc:6.2.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3000	24022761_c2_5	5832	19935	975	325	YBR288C	180	1.1(10)-23	Saccharomyces cerevisiae	[ui:ybr288c] [pn:clathrin-associated protein complex, medium subunit:adaptin medium chain homolog apm3] [gn:apm3:yks6:ybr2035] [gtcfc:10.7:11.1:12.10:12.16] [keggfc:14.2] [sgdfc:6.2.0:8.3.0:9.9.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3000	1067626_c2_4	5833	19936	615	205	YBR288C	103	0.0028	Saccharomyces cerevisiae	[ui:ybr288c] [pn:clathrin-associated protein complex, medium subunit:adaptin medium chain homolog apm3] [gn:apm3:yks6:ybr2035] [gtcfc:10.7:11.1:12.10:12.16] [keggfc:14.2] [sgdfc:6.2.0:8.3.0:9.9.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5426	23546918_f2_4	5834	19937	630	210	YDR005C	205	4.0(10)-16	Saccharomyces cerevisiae	[ui:ydr005c] [pn:required for sorting of mod5p:maf1 protein] [gn:maf1:yd8119] [gtcfc:10.7:11.1] [keggfc:14.2] [sgdfc:6.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG685	33707807_c1_1	5835	19938	495	165	YDR005C	207	2.3(10)-16	Saccharomyces cerevisiae	[ui:ydr005c] [pn:required for sorting of mod5p:maf1 protein] [gn:maf1:yd8119] [gtcfc:10.7:11.1] [keggfc:14.2] [sgdfc:6.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1218	23828127_c3_7	5836	19939	405	135	YDR244W	303	2.7(10)-26	Saccharomyces cerevisiae	[ui:ydr244w] [pn:putative peroxisomal targeting signal receptor:peroxisomal targeting signal receptor:peroxisomal protein pas10:peroxin 5] [gn:pas10:pex5:yd8419] [gtcfc:11.3:12.6:12.12] [keggfc:14.2] [sgdfc:6.2.0:8.4.0:9.8.0] [db:gtc-
CONTIG441	1988968_c3_7	5837	19940	867	289	YDR244W	402	3.0(10)-37	Saccharomyces cerevisiae	[ui:ydr244w] [pn:putative peroxisomal targeting signal receptor:peroxisomal targeting signal receptor:peroxisomal protein pas10:peroxin 5] [gn:pas10:pex5:yd8419] [gtcfc:11.3:12.6:12.12] [keggfc:14.2] [sgdfc:6.2.0:8.4.0:9.8.0] [db:gtc-

CONTIG	Clone					Gene			Organism	Description
CONTIG3841	19703135_f3_4	5838	19941	747	249	YDR323C	209	1.1(10)-27	Saccharomyces cerevisiae	[ui:ydr323c] [pn:vacuolar segregation protein:vac1 protein] [gn:vac1:pep7:vps19] [gtcfc:10.7:11.1:12.13:12.16] [keggfc:14.2] [sgdfc:6.2.0:8.5.0:9.10.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4931	2128317_c1_10	5839	19942	219	73	YDR323C	154	2.6(10)-10	Saccharomyces cerevisiae	[ui:ydr323c] [pn:vacuolar segregation protein:vac1 protein] [gn:vac1:pep7:vps19] [gtcfc:10.7:11.1:12.13:12.16] [keggfc:14.2] [sgdfc:6.2.0:8.5.0:9.10.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2910	19722192_c3_2	5840	19943	1179	393	YDR414C	152	2.7(10)-8	Saccharomyces cerevisiae	[ui:ydr414c] [pn:required for retention of luminal er proteins:erd1 protein] [gn:erd1:d9461] [gtcfc:10.7:11.1:12.16] [keggfc:14.2] [sgdfc:6.2.0:9.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3698	21892017_f1_1	5841	19944	1401	467	YER101C	194	1.3(10)-12	Saccharomyces cerevisiae	[ui:yer101c] [pn:strong similarity to ast1p:protein] [gn:ast2] [gtcfc:10.7:11.1.1] [keggfc:14.2] [sgdfc:6.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2448	14725067_c2_3	5842	19945	1620	540	YGL206C	1665	2.2(10)-171	Saccharomyces cerevisiae	[ui:ygl206c] [pn:clathrin heavy chain] [gn:chc1] [gtcfc:10.7:11.1:12.6] [keggfc:14.2] [sgdfc:6.2.0:8.7.0:9.2.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2931	78182_c3_3	5843	19946	1176	392	YGL206C	1386	8.0(10)-142	Saccharomyces cerevisiae	[ui:ygl206c] [pn:clathrin heavy chain] [gn:chc1] [gtcfc:10.7:11.1:12.6] [sgdfc:6.2.0:8.7.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3596	24697182_c1_6	5844	19947	825	275	YGL206C	732	3.2(10)-71	Saccharomyces cerevisiae	[ui:ygl206c] [pn:clathrin heavy chain] [gn:chc1] [gtcfc:10.7:11.1:12.6] [sgdfc:6.2.0:8.7.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG390	5079805_f2_1	5845	19948	1143	381	YGL206C	1280	1.3(10)-130	Saccharomyces cerevisiae	[ui:ygl206c] [pn:clathrin heavy chain] [gn:chc1] [gtcfc:10.7:11.1:12.6] [sgdfc:6.2.0:8.7.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4107	6720900_f2_1	5846	19949	522	174	YGL095C	240	1.7(10)-19	Saccharomyces cerevisiae	[ui:ygl095c] [pn:vacuolar protein sorting-associated protein:vacuolar protein sorting-associated protein vps45] [gn:vps45:stt10] [gtcfc:10.7:11.1:12:13:12.8] [keggfc:14.2] [sgdfc:3.2.0:6.2.0:8.5.0:10.2.7] [db:gtc-saccharomyces cerevis
CONTIG3468	4084567_f2_2	5847	19950	246	82	YHR110W	121	1.3(10)-7	Saccharomyces cerevisiae	[ui:yhr110w] [pn:similarity to human gp2512 protein:hypothetical 24.2 kd protein in cdc12-orc6 intergenic region precursor] [gtcfc:10.7:11.1] [keggfc:14.2] [sgdfc:6.2.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3468	25788438_f1_1	5848	19951	435	145	YHR110W	393	1.3(10)-36	Saccharomyces cerevisiae	[ui:yhr110w] [pn:similarity to human gp2512 protein:hypothetical 24.2 kd protein in cdc12-orc6 intergenic region precursor] [gtcfc:10.7:11.1] [keggfc:14.2] [sgdfc:6.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5445	4863437_c3_15	5849	19952	186	62	YIL173W	95	0.0022	Saccharomyces cerevisiae	[ui:yil173w] [pn:putative membrane glycoprotein in suc2 5"region precursor] [gtcfc:10.7:11.1] [keggfc:14.2] [sgdfc:6.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5445	11929700_c1_7	5850	19953	858	286	YIL173W	154	6.0(10)-8	Saccharomyces cerevisiae	[ui:yil173w] [pn:putative membrane glycoprotein in suc2 5"region precursor] [gtcfc:10.7:11.1] [keggfc:14.2] [sgdfc:6.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5445	2926675_c1_5	5851	19954	759	253	YIL173W	154	3.7(10)-8	Saccharomyces cerevisiae	[ui:yil173w] [pn:strong similarity to pep1p:putative membrane glycoprotein in suc2 5"region precursor] [gtcfc:10.7:11.1] [keggfc:14.2] [sgdfc:6.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1678	195442_f1_1	5852	19955	804	268	YJL154C	122	0.00013	Saccharomyces cerevisiae	[ui:yjl154c] [pn:protein-sorting protein, vacuolar:vacuolar protein sorting-associated protein vps35] [gn:vps35:j0580] [gtcfc:10.7:11.1:12.16] [keggfc:14.2] [sgdfc:6.2.0:9.10.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4984	25391251_c1_8	5853	19956	780	260	YJL154C	388	3.2(10)-51	Saccharomyces cerevisiae	[ui:yjl154c] [pn:protein-sorting protein, vacuolar:vacuolar protein sorting-associated protein vps35] [gn:vps35:j0580] [gtcfc:10.7:11.1:11.2.16] [keggfc:14.2] [sgdfc:6.2.0:9.10.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5545	4016642_f3_11	5854	19957	1053	351	YJL053W	655	2.2(10)-64	Saccharomyces cerevisiae	[ui:yjl053w] [pn:vacuolar protein sorting/targeting protein:vacuolar protein sorting/targeting protein pep1] [gn:pep8:j1152] [gtcfc:10.7:11.1:11.2.16] [keggfc:14.2] [sgdfc:6.2.0:9.10.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5218	4140825_f2_6	5855	19958	633	211	YKL196C	794	4.2(10)-79	Saccharomyces cerevisiae	[ui:ykl196c] [pn:similarity to sec22p:hypothetical 22.7 kd protein in pas1-mst1 intergenic region] [gtcfc:10.7:11.1:11.2.10:12.16] [keggfc:14.2] [sgdfc:6.2.0:8.3.0:9.9.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5301	4884442_f1_2	5856	19959	930	310	YKL154W	179	1.3(10)-26	Saccharomyces cerevisiae	[ui:ykl154w] [pn:similarity to mouse signal recognition particle receptor beta subunit:putative signal recognition particle receptor beta subunit:sr-beta] [gn:ykl609] [gtcfc:12.13:11.3] [keggfc:14.2] [sgdfc:6.2.0] [db:gtc-saccharomyce

CONTIG5282	1382235_f2_2	5857	19960	1299	433	YKR001C	1437	3.2(10)-147	Saccharomyces cerevisiae	[ui:ykr001c] [pn:member of the dynamin family of gtpases:vacuolar sorting protein 1] [gn:vps1:spo15:lam1] [gtcfc:10.7:11.1:12.16] [keggfc:14.2] [sgdfc:6.2.0-9.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5357	10578562_c2_20	5858	19961	570	190	YKR001C	600	1.6(10)-58	Saccharomyces cerevisiae	[ui:ykr001c] [pn:member of the dynamin family of gtpases:vacuolar sorting protein 1] [gn:vps1:spo15:lam1] [gtcfc:10.7:11.1:12.16] [keggfc:14.2] [sgdfc:6.2.0-9.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG463	20359635_f3_1	5859	19962	717	239	YKR014C	453	5.9(10)-43	Saccharomyces cerevisiae	[ui:ykr014c] [pn:gtp-binding protein of the rab family:gtp-binding protein ypt52] [gn:ypt52:yk112] [gtcfc:10.7:11.1:12.13:12.6] [keggfc:14.2] [sgdfc:6.2.0:8.5.0:8.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5732	15887_f3_22	5860	19963	615	205	YKR014C	307	1.7(10)-27	Saccharomyces cerevisiae	[ui:ykr014c] [pn:gtp-binding protein of the rab family:gtp-binding protein ypt52] [gn:ypt52:yk112] [gtcfc:10.7:11.1:12.13:12.6] [keggfc:14.2] [sgdfc:6.2.0:8.5.0:8.7.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2042	24398317_f1_1	5861	19964	486	162	YLR148W	224	2.0(10)-17	Saccharomyces cerevisiae	[ui:ylr148w] [pn:vacuolar membrane protein:vacuolar membrane protein pep3] [gn:pep3:vps18:i9634] [gtcfc:10.7:11.1:12.16] [keggfc:14.2] [sgdfc:6.2.0:9.10.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5010	23913202_f2_1	5862	19965	2436	812	YLR148W	346	5.0(10)-28	Saccharomyces cerevisiae	[ui:ylr148w] [pn:vacuolar membrane protein:vacuolar membrane protein pep3] [gn:pep3:vps18:i9634] [gtcfc:10.7:11.1:12.16] [keggfc:14.2] [sgdfc:6.2.0:9.10.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5505	6830381_c2_13	5863	19966	1983	661	YLR148W	270	2.0(10)-25	Saccharomyces cerevisiae	[ui:ylr148w] [pn:vacuolar membrane protein:vacuolar membrane protein pep3] [gn:pep3:vps18:i9634] [gtcfc:10.7:11.1:12.16] [keggfc:14.2] [sgdfc:6.2.0:9.10.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5291	4454500_f2_5	5864	19967	1125	375	YLR191W	478	3.0(10)-50	Saccharomyces cerevisiae	[ui:ylr191w] [pn:peroxisomal protein involved in protein import:peroxisomal membrane protein pas20:peroxin 13] [gn:pas20:pex13:i9470] [gtcfc:10.7:11.1:12.2:12.6] [keggfc:14.2] [sgdfc:6.2.0:8.4.0:9.8.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5196	22304062_f1_1	5865	19968	291	97	YLR292C	106	5.0(10)-6	Saccharomyces cerevisiae	[ui:ylr292c] [pn:er protein-translocation complex subunit:translocation protein sec72:p23] [gn:sec72:sec67:sim2:i8003] [gtcfc:10.7:11.1:11.1:12.16:12.6] [keggfc:14.2] [sgdfc:6.2.0:7.11.0:8.8.0:9.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5432	1181442_f1_6	5866	19969	507	169	YLR378C	328	1.1(10)-29	Saccharomyces cerevisiae	[ui:ylr378c] [pn:er protein-translocation complex subunit:protein transport protein sec61 alpha subunit] [gn:sec61:i3502] [gtcfc:12.6:11.1:12.16:10.7] [sgdfc:6.2.0:7.11.0:8.8.0:9.4.0:17.0.0] [db:gtc-saccharomyces cerevis
CONTIG5450	644526_f3_6	5867	19970	975	325	YLR378C	1002	3.8(10)-101	Saccharomyces cerevisiae	[ui:ylr378c] [pn:er protein-translocation complex subunit:protein transport protein sec61 alpha subunit] [gn:sec61:i3502] [gtcfc:12.6:11.1.1:12.16:10.7] [keggfc:14.2] [sgdfc:6.2.0:7.11.0:8.8.0:9.4.0:17.0.0] [db:gtc-saccharomyces cerevis

CONTIG5669	953257_c2_25	5868	19971	2118	706	YLR396C	294	1.8(10)-24	Saccharomyces cerevisiae	[ui:ylr396c] [pn:vacuolar sorting protein:slp1 protein:vacuolar protein sorting protein 33] [gn:slp1:vps33:vam5:l8084] [gtcfc:10.7:11.1:12.10:12.16] [keggfc:14.2] [sgdfc:6.2.0:8.3.0:9.10.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2831	192137_f3_2	5869	19972	600	200	YML097C	247	1.3(10)-20	Saccharomyces cerevisiae	[ui:yml097c] [pn:vacuolar sorting protein:vacuolar protein sorting-associated protein vps9] [gn:vps9:vpl9] [gtcfc:10.7:11.1:12.10:12.13] [keggfc:14.2] [sgdfc:6.2.0:8.3.0:8.5.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2831	11728500_f2_1	5870	19973	1017	339	YML097C	312	1.2(10)-31	Saccharomyces cerevisiae	[ui:yml097c] [pn:vacuolar sorting protein:vacuolar protein sorting-associated protein vps9] [gn:vps9:vpl9] [gtcfc:10.7:11.1:12.10:12.13] [keggfc:14.2] [sgdfc:6.2.0:8.3.0:8.5.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1858	25491258_f3_1	5871	19974	495	165	YMR004W	276	1.3(10)-23	Saccharomyces cerevisiae	[ui:ymr004w] [pn:required for vacuolar protein sorting:mvp1 protein] [gn:mvp1:ym8270] [gtcfc:10.7:11.1:12.13:12.16] [keggfc:14.2] [sgdfc:6.2.0:8.5.0:9.4.0] [db:gtc-saccharomyces cerevisiae]

CONTIG1858	25398561_f3_2	5872	19975	543	181	YMR004W	206	6.0(10)-16	Saccharomyces cerevisiae	[ui:ymr004w] [pn:required for vacuolar protein sorting:mvp1 protein] [gn:mvp1:ym8270] [gtcfc:10.7:11.1:12.13:12.16] [sgdfc:6.2.0:8.5.0:9.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3564	819682_f1_1	5873	19976	1434	478	YMR091C	378	7.9(10)-50	Saccharomyces cerevisiae	[ui:ymr091c] [pn:nuclear protein localization factor:npl6 protein] [gn:npl6:ym9582] [gtcfc:10.7:11.1] [keggfc:14.2] [sgdfc:6.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4357	25578887_c1_4	5874	19977	993	331	YMR214W	464	1.3(10)-55	Saccharomyces cerevisiae	[ui:ymr214w] [pn:similarity to to e.coli dnaj:scj1 protein] [gn:scj1:ym8261] [gtcfc:10.7:11.1:12.16] [keggfc:14.2] [sgdfc:6.2.0:9.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2466	4298260_f3_6	5875	19978	189	63	YNR006W	105	6.4(10)-5	Saccharomyces cerevisiae	[ui:ynr006w] [pn:vacuolar protein sorting-associated protein:vacuolar protein sorting-associated protein vps27] [gn:vps27:grd11:n2038] [gtcfc:10.7:11.1:12.10:12.13:12.16] [keggfc:14.2] [sgdfc:6.2.0:8.5.0:9.9.0] [db:gtc-saccharomyces c

CONTIG5346	2458276_f1_1	5876	19979	2241	747	YNR006W	358	1.3(10)-42	Saccharomyces cerevisiae	[ui:ynr006w] [pn:vacuolar protein sorting-associated protein:vacuolar protein sorting-associated protein vps27] [gn:vps27:grd11:n2038] [gtcfc:10.7:11.1:12.10:12.13:12.16] [keggfc:14.2] [sgdfc:6.2.0:8.5.0:9.0] [db-gtc-saccharomyces c
CONTIG200	5906442_f3_2	5877	19980	468	156	YOL122C	238	3.1(10)-23	Saccharomyces cerevisiae	[ui:yol122c] [pn:manganese transporter:transporter protein smf1/esp1] [gn:smf1:esp1] [gtcfc:12.6:10.7:11.1] [sgdfc:1.8.1:6.2.0:7.2.1:8.7.0:9.1.0] [db-gtc-saccharomyces cerevisiae]
CONTIG1547	5344466_c3_4	5878	19981	654	218	YOL122C	422	1.1(10)-39	Saccharomyces cerevisiae	[ui:yol122c] [pn:manganese transporter:transporter protein smf1/esp1] [gn:smf1:esp1] [gtcfc:12.6:10.7:11.1] [keggfc:14.2] [sgdfc:1.8.1:6.2.0:7.2.1:8.7.0:9.1.0] [db-gtc-saccharomyces cerevisiae]
CONTIG2632	4103127_c1_5	5879	19982	1521	507	YOL122C	728	6.0(10)-118	Saccharomyces cerevisiae	[ui:yol122c] [pn:manganese transporter:transporter protein smf1/esp1] [gn:smf1:esp1] [gtcfc:12.6:10.7:11.1] [keggfc:14.2] [sgdfc:1.8.1:6.2.0:7.2.1:8.7.0:9.1.0] [db-gtc-saccharomyces cerevisiae]

CONTIG1162	1956388_f1_1	5880	19983	837	279	YOL062C	230	2.7(10)-36	Saccharomyces cerevisiae	[ui:yol062c] [pn:clathrin-associate protein yap54] [gn:apm4] [gtcfc:10.7:11.1:12.10:12.16] [sgdfc:6.2.0:8.3.0:9.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5658	12898438_f1_1	5881	19984	369	123	YOL062C	255	2.5(10)-21	Saccharomyces cerevisiae	[ui:yol062c] [pn:clathrin-associate protein yap54] [gn:apm4] [gtcfc:10.7:11.1:12.10:12.16] [keggfc:14.2] [sgdfc:6.2.0:8.3.0:9.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1497	23439632_c1_4	5882	19985	531	177	YOR016C	158	1.1(10)-11	Saccharomyces cerevisiae	[ui:yor016c] [pn:similarity to hamster cop-coated vesicle membrane protein] [gtcfc:10.7:11.1] [keggfc:14.2] [sgdfc:6.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1324	9852253_f3_3	5883	19986	444	148	YOR036W	127	7.2(10)-8	Saccharomyces cerevisiae	[ui:yor036w] [pn:syntaxin:t-snare:pep12 protein] [gn:pep12:vps6:vpt13:or26] [gtcfc:10.7:11.1:12.13:12.16] [keggfc:14.2] [sgdfc:6.2.0:8.5.0:9.10.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5649	236258_c3_20	5884	19987	927	309	YOR036W	206	8.8(10)-17	Saccharomyces cerevisiae	[ui:yor036w] [pn:syntaxin:t-snare:pep12 protein] [gn:pep12:vps6:vpt13:or26] [gtcfc:10.7:11.1:12.13:12.16] [keggfc:14.2] [sgdfc:6.2.0:8.5.0:9.10.0] [db:gtc-saccharomyces cerevisiae]

b2x18145.y	24862567_f3_1	5885	19988	471	157	YOR036W	142	1.5(10)-9	Saccharomyces cerevisiae	[ui:yor036w] [pn:syntaxin:t-snare:pep12 protein] [gn:pep12:vps6:vpt13:or26] [gtcfc:10.7:11.1:12.13:12.16] [keggfc:14.2] [sgdfc:6.2.0:8.5.0:9.10.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2932	20081260_f1_1	5886	19989	714	238	YOR089C	723	1.3(10)-71	Saccharomyces cerevisiae	[ui:yor089c] [pn:gtp-binding protein:gtp-binding protein:ypt51/vps21] [gn:ypt51:vps21:yor3154c] [gtcfc:10.7:11.1:12.10:12.13:12.16:12.6] [keggfc:14.2] [sgdfc:6.2.0:8.5.0:8.7.0.9.9.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2891	22460877_c3_4	5887	19990	492	164	YOR132W	205	9.1(10)-16	Saccharomyces cerevisiae	[ui:yor132w] [pn:vacuolar protein sorting-associated protein:vacuolar protein sorting-associated protein vps17] [gn:vps17] [sgdfc:6.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG707	25673905_f3_2	5888	19991	957	319	YOR132W	380	3.6(10)-39	Saccharomyces cerevisiae	[ui:yor132w] [pn:vacuolar protein sorting-associated protein:vacuolar protein sorting-associated protein vps17] [gn:vps17:pep21:o3314:yor3314w] [gtcfc:10.7:11.1] [keggfc:14.2] [sgdfc:6.2.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5413	4725328_c1_15	5889	19992	2031	677	YOR254C	1021	3.7(10)-103	Saccharomyces cerevisiae	[ui:yor254c] [pn:er protein-translocation complex subunit:npl1 protein:sec63 protein] [gn:npl1:sec63 protein] [gtcfc:10.7:11.1:12.16:12.6] [keggfc:14.2] [sgdfc:6.2.0:7.11.0:8.8.0:9.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4807	33260968_f2_5	5890	19993	285	95	YOR286W	221	2.2(10)-18	Saccharomyces cerevisiae	[ui:yor286w] [pn:similarity to d.melanogaster heat shock protein 67b2] [gtcfc:12.7:11.1] [keggfc:14.2] [sgdfc:6.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1534	25597186_c2_4	5891	19994	228	76	YOR327C	288	1.8(10)-25	Saccharomyces cerevisiae	[ui:yor327c] [pn:strong similarity to synaptobrevin:synaptobrevin homolog 2] [gn:snc2] [gtcfc:10.7:11.1:12.10:12.16] [keggfc:14.2] [sgdfc:6.2.0:8.3.0:9.9.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3832	19540675_f2_3	5892	19995	1422	474	YOR329C	203	3.7(10)-18	Saccharomyces cerevisiae	[ui:yor329c] [pn:suppressor of clathrin deficiency:scd5 protein:ffb1 protein] [gn:scd5:ffb1] [gtcfc:10.7:11.1:12.6] [keggfc:14.2] [sgdfc:6.2.0:8.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5798	23875200_f1_9	5893	19996	627	209	YPL259C	588	2.8(10)-57	Saccharomyces cerevisiae	[ui:ypl259c] [pn:clathrin-associated protein:clathrin coat assembly protein ap54:clathrin coat associated protein ap54:golgi adaptor ap-1 54 kd protein:hal 54 kd subunit:clathrin assembly protein complex 1 medium chain] [gn:apm1:yap54:

CONTIG									
CONTIG4518	22344008_f2_2	5894	19997	1131	YPL243W	134	7.2(10)-6	Saccharomyces cerevisiae	[ui:ypl243w] [pn:signal recognition particle protein:signal recognition particle 68 kd protein homolog] [gn:srp68] [gtcfc:12.13:11.3] [keggfc:14.2] [sgdfc:6.2.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3924	11805416_f1_1	5895	19998	1353	YPL210C	114	1.3(10)-7	Saccharomyces cerevisiae	[ui:ypl210c] [pn:signal recognition particle protein:signal recognition particle 72 kd protein homolog] [gn:srp72] [gtcfc:12.13:11.3] [keggfc:14.2] [sgdfc:6.2.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4942	22850187_c2_20	5896	19999	960	YPL094C	383	1.5(10)-35	Saccharomyces cerevisiae	[ui:ypl094c] [pn:er protein-translocation complex subunit:translocation protein sec62] [gn:sec62:lpg14c] [gtcfc:10.7:11.1:12.16:12.6] [keggfc:14.2] [sgdfc:6.2.0:7.11.0:8.8.0:9.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3632	16882330_c3_9	5897	20000	975	YPL045W	201	2.3(10)-13	Saccharomyces cerevisiae	[ui:ypl045w] [pn:vacuolar sorting protein:vacuolar protein sorting-associated protein vps16] [gn:vps16:vam9] [gtcfc:10.7:11.1:12.13:12.16] [keggfc:14.2] [sgdfc:6.2.0:8.5.0:9.3.0:9.10.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3717	820337_c3_9	5898	20001	837	279	YPL045W	256	7.4(10)-28	Saccharomyces cerevisiae	[ui:ypl045w] [pn:vacuolar sorting protein:vacuolar protein sorting-associated protein vps16] [gn:vps16:vam9] [gtfc:10.7:11.1:12.13:12.16] [keggfc:14.2] [sgdfc:6.2.0:8.5.0:9.3.0:9.10.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3717	10650305_c1_6	5899	20002	543	181	YPL045W	113	0.00033	Saccharomyces cerevisiae	[ui:ypl045w] [pn:vacuolar sorting protein:vacuolar protein sorting-associated protein vps16] [gn:vps16:vam9] [gtfc:10.7:11.1:12.13:12.16] [keggfc:14.2] [sgdfc:6.2.0:8.5.0:9.3.0:9.10.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2805	9860458_f3_4	5900	20003	759	253	YPR088C	372	2.3(10)-34	Saccharomyces cerevisiae	[ui:ypr088c] [pn:signal recognition particle subunit:signal recognition particle 54 kd protein homolog:srp54] [gn:srp54:srh1:p9513] [gtfc:12.13:11.3] [keggfc:14.2] [sgdfc:6.2.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1222	4954650_c1_4	5901	20004	888	296	YCR077C	98	0.019	Saccharomyces cerevisiae	[ui:ycr077c] [pn:topoisomerase ii-associated protein:88.5 kd protein in ers1-srb8 intergenic region] [gtfc:10.8] [keggfc:14.2] [sgdfc:3.6.0:3.7.0:9.2.0] [db:gtc-saccharomyces cerevisiae]

CONTIG1542	787811_c3_7	5902	20005	762	254	YCR077C	415	4.4(10)-38	Saccharomyces cerevisiae	[ui:ycr077c] [pn:topoisomerase ii-associated protein:88.5 kd protein in ers1-srb8 intergenic region] [gtcfc:10.8] [keggfc:14.2] [sgdfc:3.6.0:3.7.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5531	417969l_c2_33	5903	20006	1692	564	YDR206W	134	9.8(10)-10	Saccharomyces cerevisiae	[ui:ydr206w] [pn:similarity to est1 protein] [gtcfc:10.8] [keggfc:14.2] [sgdfc:3.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4719	36210197_c2_4	5904	20007	1488	496	YGL201C	1446	2.2(10)-174	Saccharomyces cerevisiae	[ui:ygl201c] [pn:similarity with rat intestinal dna replication protein:hypothetical 113.0 kd protein in kex1-emp24 intergenic region] [gtcfc:10.8] [keggfc:14.2] [sgdfc:3.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5624	10975253_c3_19	5905	20008	1059	353	YGL201C	662	1.8(10)-94	Saccharomyces cerevisiae	[ui:ygl201c] [pn:similarity with rat intestinal dna replication protein:hypothetical 113.0 kd protein in kex1-emp24 intergenic region] [gtcfc:10.8] [keggfc:14.2] [sgdfc:3.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5612	10973406_f3_7	5906	20009	858	286	YGR132C	979	1.1(10)-98	Saccharomyces cerevisiae	[ui:ygr132c] [pn:prohibitin, antiproliferative protein:prohibitin] [gn:phb1:phb] [gtcfc:10.8:12.8] [keggfc:14.2] [sgdfc:3.6.0:3.8.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4491	20601678_c2_5	5907	20010	975	325	YGR231C	1010	5.5(10)-102	Saccharomyces cerevisiae	[ui:ygr231c] [pn:strong similarity to prohibitins:hypothetical 34.9 kd protein in smi1-pho81 intergenic region] [gn:g8561] [gtcfc:10.8:12.8] [keggfc:14.2] [sgdfc:3.6.0:3.8.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2191	24336567_c3_5	5908	20011	1299	433	YIL150C	290	1.2(10)-23	Saccharomyces cerevisiae	[ui:yil150c] [pn:required for s-phase initiation or completion:protein] [gn:dna43] [gtcfc:10.8:12.8] [keggfc:14.2] [sgdfc:3.6.0:3.8.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4281	36597763_f3_2	5909	20012	258	86	YKL113C	128	1.0(10)-7	Saccharomyces cerevisiae	[ui:ykl113c] [pn:ssdna endonuclease and 5"-3"exonuclease:structure specific endonuclease ykl113c/] [gn:rad27:ykl510] [gtcfc:10.8] [keggfc:14.2] [sgdfc:3.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4404	14477175_c1_7	5910	20013	675	225	YKL113C	671	4.7(10)-66	Saccharomyces cerevisiae	[ui:ykl113c] [pn:ssdna endonuclease and 5"-3"exonuclease:structure specific endonuclease ykl113c/] [gn:rad27:ykl510] [gtcfc:10.8] [keggfc:14.2] [sgdfc:3.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5535	39125_f2_5	5911	20014	1803	601	YLR103C	310	6.2(10)-67	Saccharomyces cerevisiae	[ui:ylr103c] [pn:required for minichromosome maintenance and initiation of chromosomal dna replication] [gn:cdc45] [gtcfc:10.8:12.8] [keggfc:13.2] [sgdfc:3.6.0:3.8.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5343	6251_f2_4	5912	20015	1962	654	YOL095C	278	5.2(10)-32	Saccharomyces cerevisiae	[ui:yol095c] [pn:similarity to s.aureus dna helicase pcra] [gtcfc:10.8] [keggfc:14.2] [sgdfc:3.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2784	11751500_f3_3	5913	20016	1536	512	YPL256C	336	3.8(10)-30	Saccharomyces cerevisiae	[ui:ypl256c] [pn:cyclin, g1/s-specific cyclin] [gn:cln2] [gtcfc:10.8:12.8:12.9] [keggfc:13.1] [sgdfc:3.2.0:3.3.0:3.6.0:3.8.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1980	4413900_f3_3	5914	20017	684	228	YPR019W	271	1.8(10)-22	Saccharomyces cerevisiae	[ui:ypr019w] [pn:member of the cdc46p/mcm2p/mcm3p family:cell division control protein 54] [gn:cdc54:hcd21:yp9531] [gtcfc:10.8:12.8] [sgdfc:3.6.0:3.8.0] [db:gtc-saccharomyces cerevisiae]
CONTIG474	7159683_c3_3	5915	20018	492	164	YPR019W	359	7.2(10)-32	Saccharomyces cerevisiae	[ui:ypr019w] [pn:member of the cdc46p/mcm2p/mcm3p family:cell division control protein 54] [gn:cdc54:hcd21:yp9531] [gtcfc:10.8:12.8] [sgdfc:3.6.0:3.8.0] [keggfc:14.2] [db:gtc-saccharomyces cerevisiae]
b9x12m21.y	236094_c1_1	5916	20019	519	173	YPR019W	593	3.2(10)-57	Saccharomyces cerevisiae	[ui:ypr019w] [pn:member of the cdc46p/mcm2p/mcm3p family:cell division control protein 54] [gn:cdc54:hcd21:yp9531] [gtcfc:10.8:12.8] [sgdfc:3.6.0:3.8.0] [keggfc:14.2] [db:gtc-saccharomyces cerevisiae]

CONTIG4270	10413432_c2_5	5917	20020	1497	499	YPR120C	507	1.1(10)-48	Saccharomyces cerevisiae	[ui:ypr120c] [pn:cyclin, b-type:s-phase entry cyclin 5] [gn:clb5:p9642] [gtcfc:10.8:12.8] [keggfc:13.3] [sgdfc:3.6.0:3.8.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2912	36224063_f2_2	5918	20021	1308	436	YBR136W	780	5.2(10)-76	Saccharomyces cerevisiae	[ui:ybr136w] [pn:cell cycle checkpoint protein:esr1 protein] [gn:esr1:mec1:sad3:ybr1012] [gtcfc:10.8:12.8] [keggfc:14.2] [sgdfc:3.5.0:3.7.0:3.8.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3833	1986000_c2_11	5919	20022	345	115	YBR136W	154	1.8(10)-9	Saccharomyces cerevisiae	[ui:ybr136w] [pn:cell cycle checkpoint protein:esr1 protein] [gn:esr1:mec1:sad3:ybr1012] [gtcfc:10.8:12.8] [keggfc:14.2] [sgdfc:3.5.0:3.7.0:3.8.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3833	35212787_c2_10	5920	20023	1440	480	YBR136W	526	5.4(10)-49	Saccharomyces cerevisiae	[ui:ybr136w] [pn:cell cycle checkpoint protein:esr1 protein] [gn:esr1:mec1:sad3:ybr1012] [gtcfc:10.8:12.8] [keggfc:14.2] [sgdfc:3.5.0:3.7.0:3.8.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3833	14195175_c3_12	5921	20024	966	322	YBR136W	302	3.5(10)-25	Saccharomyces cerevisiae	[ui:ybr136w] [pn:cell cycle checkpoint protein:esr1 protein] [gn:esr1:mec1:sad3:ybr1012] [gtcfc:10.8:12.8] [keggfc:14.2] [sgdfc:3.5.0:3.7.0:3.8.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4697	30515925_f2_1	5922	20025	2334	778	YBR136W	122	0.0027	Saccharomyces cerevisiae	[ui:ybr136w] [pn:cell cycle checkpoint protein:esr1 protein] [gn:esr1:mec1:sad3:ybr1012] [gtcfc:10.8:12.8] [keggfc:14.2] [sgdfc:3.5.0:3.7.0:3.8.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4748	10647936_c3_12	5923	20026	690	230	YDL059C	184	1.8(10)-14	Saccharomyces cerevisiae	[ui:ydl059c] [pn:recombination and dna repair protein] [gn:rad59] [gtcfc:10.8] [keggfc:14.2] [sgdfc:3.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5676	1178882_c2_22	5924	20027	1284	428	YDR182W	872	2.3(10)-87	Saccharomyces cerevisiae	[ui:ydr182w] [pn:cell division control protein:cell division control protein 1] [gn:cdc1:dsr1:esp2:yd9395] [gtcfc:10.8:12:15:12.8] [keggfc:14.2] [sgdfc:3.2.0:3.4.0:3.7.0:3.8.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5727	4079660_f1_3	5925	20028	1467	489	YDR182W	552	1.8(10)-53	Saccharomyces cerevisiae	[ui:ydr182w] [pn:cell division control protein:cell division control protein 1] [gn:cdc1:dsr1:esp2:yd9395] [gtcfc:10.8:12:15:12.8] [keggfc:14.2] [sgdfc:3.2.0:3.4.0:3.7.0:3.8.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5715	6910183_f1_1	5926	20029	660	220	YER173W	244	2.6(10)-25	Saccharomyces cerevisiae	[ui:yer173w] [pn:cell cycle checkpoint protein:checkpoint protein rad24] [gn:rad24:sygp-orf60] [gtcfc:10.8:12.8] [keggfc:14.2] [sgdfc:3.7.0:3.8.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5715	5312513_f2_4	5927	20030	978	326	YER173W	119	3.6(10)-7	Saccharomyces cerevisiae	[ui:yer173w] [pn:cell cycle checkpoint protein:checkpoint protein rad24] [gn:rad24:sygp-orf60] [gtcfc:10.8:12.8] [keggfc:14.2] [sgdfc:3.7.0:3.8.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5553	976556_c2_22	5928	20031	1530	510	YHR031C	711	2.7(10)-70	Saccharomyces cerevisiae	[ui:yhr031c] [pn:similarity to pif1p:hypothetical helicase in slt2-put2 intergenic region] [gtcfc:10.8] [keggfc:14.2] [sgdfc:3.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5801	21657817_f2_9	5929	20032	2739	913	YHR031C	743	9.0(10)-96	Saccharomyces cerevisiae	[ui:yhr031c] [pn:similarity to pif1p:hypothetical helicase in slt2-put2 intergenic region] [gtcfc:10.8] [keggfc:14.2] [sgdfc:3.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5553	23829836_c1_18	5930	20033	303	101	YHR031C	221	2.8(10)-17	Saccharomyces cerevisiae	[ui:yhr031c] [pn:similarity to pif1p:hypothetical helicase in slt2-put2 intergenic region] [gtcfc:10.8] [keggfc:14.2] [sgdfc:3.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4667	23611251_c3_11	5931	20034	342	114	YHR154W	154	7.4(10)-10	Saccharomyces cerevisiae	[ui:yhr154w] [pn:putative dna damage responsive cell cycle checkpoint protein:hypothetical 123.0 kd protein in spo16-rec104 intergenic region] [gtcfc:10.8:12.8] [keggfc:14.2] [sgdfc:3.7.0:3.8.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4709	14729561_c1_13	5932	20035	807	269	YHR154W	97	0.11	Saccharomyces cerevisiae	[ui:yhr154w] [pn:putative dna damage responsive cell cycle checkpoint protein:hypothetical 123.0 kd protein in spo16-rec104 intergenic region] [keggfc:14.2] [sgdfc:3.7.0:3.8.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5190	14554813_f3_5	5933	20036	1629	543	YHR154W	350	5.0(10)-29	Saccharomyces cerevisiae	[ui:yhr154w] [pn:putative dna damage responsive cell cycle checkpoint protein:hypothetical 123.0 kd protein in spo16-rec104 intergenic region] [gtcfc:10.8:12.8] [keggfc:14.2] [sgdfc:3.7.0:3.8.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1194	15818812_f3_1	5934	20037	471	157	YLR383W	306	4.7(10)-26	Saccharomyces cerevisiae	[ui:ylr383w] [pn:recombination repair protein] [gn:rhc18] [gtcfc:10.8] [keggfc:14.2] [sgdfc:3.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2232	16462551_c1_2	5935	20038	1227	409	YLR383W	218	8.5(10)-15	Saccharomyces cerevisiae	[ui:ylr383w] [pn:recombination repair protein] [gn:rhc18] [gtcfc:10.8] [keggfc:14.2] [sgdfc:3.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG865	35370305_c2_6	5936	20039	921	307	YLR383W	328	2.1(10)-28	Saccharomyces cerevisiae	[ui:ylr383w] [pn:recombination repair protein] [gn:rhc18] [gtcfc:10.8] [keggfc:14.2] [sgdfc:3.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5815	26354683_f2_12	5937	20040	2640	880	YMR190C	1739	3.0(10)-183	Saccharomyces cerevisiae	[ui:ymr190c] [pn:dna helicase:helicase sgs1:helicase tps1] [gn:sgs1:tps1:ym9646] [gtcfc:10.8] [keggfc:14.2] [sgdfc:3.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5430	20426588_f3_8	5938	20041	825	275	YOR077W	347	1.0(10)-31	Saccharomyces cerevisiae	[ui:yor077w] [pn:similarity to mouse kin17 protein:protein] [gn:rts2] [gtcfc:10.8] [keggfc:14.2] [sgdfc:3.7.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5699	24275806_c1_21	5939	20042	993	331	YPL164C	291	8.3(10)-25	Saccharomyces cerevisiae	[ui:ypl164c] [pn:similarity to mismatch repair protein mlh1p] [gtcfc:10.8] [keggfc:14.2] [sgdfc:3.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1704	12694430_f2_2	5940	20043	606	202	YPL164C	197	1.1(10)-14	Saccharomyces cerevisiae	[ui:ypl164c] [pn:similarity to mismatch repair protein mlh1p] [gtcfc:10.8] [keggfc:14.2] [sgdfc:3.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5807	9972786_f3_5	5941	20044	528	176	YPL121C	151	5.9(10)-11	Saccharomyces cerevisiae	[ui:ypl121c] [pn:meiotic protein:meiosis protein 5] [gn:mei5] [gtcfc:10.8:12.8] [keggfc:14.2] [sgdfc:3.5.0:3.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5650	265902_c3_23	5942	20045	1449	483	YBR236C	612	8.4(10)-60	Saccharomyces cerevisiae	[ui:ybr236c] [pn:methyltransferase:abd1 protein] [gn:abd1:ybr1602] [gtcfc:10.9] [keggfc:14.2] [sgdfc:4.10.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4457	4331510_c2_9	5943	20046	543	181	YJR017C	355	1.3(10)-32	Saccharomyces cerevisiae	[ui:yjr017c] [pn:ess1 protein:processing/termination factor 1] [gn:ess1:ptf1:j1452] [gtcfc:10.9] [keggfc:14.2] [sgdfc:4.10.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2527	11179687_c1_6	5944	20047	1617	539	YKL025C	404	9.4(10)-47	Saccharomyces cerevisiae	[ui:ykl025c] [pn:component of the pab1p-dependent poly-a ribonuclease:hypothetical 76.5 kd protein in tfa1-ura6 intergenic region] [gn:pan3] [gtcfc:10.9] [keggfc:14.2] [sgdfc:4.10.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3251	21682687_c2_5	5945	20048	414	138	YLR115W	143	8.3(10)-9	Saccharomyces cerevisiae	[ui:lr115w] [pn:similarity to cattle cleavage and polyadenylation specificity factor] [gtcfc:10.9] [keggfc:14.2] [sgdfc:4.10.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4585	14648437_c3_12	5946	20049	1038	346	YLR115W	495	1.2(10)-46	Saccharomyces cerevisiae	[ui:lr115w] [pn:similarity to cattle cleavage and polyadenylation specificity factor] [gtcfc:10.9] [keggfc:14.2] [sgdfc:4.10.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3608	14640686_f2_3	5947	20050	579	193	YOL149W	168	6.5(10)-26	Saccharomyces cerevisiae	[ui:yol149w] [pn:component of the yeast decapping enzyme] [gn:dcp1] [gtcfc:10.9] [keggfc:14.2] [sgdfc:4.10.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5771	24414192_f3_18	5948	20051	426	142	YPL178W	355	1.3(10)-32	Saccharomyces cerevisiae	[ui:ypl178w] [pn:cell cycle block in meiotic prophase] [gn:sae1] [gtcfc:10.9:12.8] [keggfc:14.2] [sgdfc:3.8.0:4.10.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5785	14511013_c3_35	5949	20052	696	232	YAL059W	109	2.8(10)-5	Saccharomyces cerevisiae	[ui:yal059w] [pn:involved in cell wall biosynthesis:protein] [gn:sim1] [gtcfc:11.1] [keggfc:14.2] [sgdfc:9.1.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2940	21600465_f2_4	5950	20053	306	102	YBR068C	143	5.2(10)-9	Saccharomyces cerevisiae	[ui:ybr068c] [pn:amino acid permease:leu/val/ile amino-acid permease bap2] [gn:bap2:ybr0629] [gtcfc:11.1:12.1:12.6] [keggfc:14.2] [sgdfc:1.1.3:7.4.0:8.7.0:9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4339	20593915_f1_1	5951	20054	1020	340	YBR298C	681	4.0(10)-67	Saccharomyces cerevisiae	[ui:ybr298c] [pn:maltose permease] [gn:mal31:mal31:mal61:mal6t:ybr21 6] [gtcfc:11.1:12.2:12.6] [keggfc:14.2] [sgdfc:1.5.3:7.3.0:8.7.0:9.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2329	448958_f2_1	5952	20055	606	202	YCL027W	122	2.0(10)-5	Saccharomyces cerevisiae	[ui:ycl027w] [pn:cell fusion protein:nuclear fusion protein fus1] [gn:fus1:ycl27w] [gtcfc:11.1:12.8:12.9] [keggfc:14.2] [sgdfc:3.3.0:9.1.0:10.1.6] [db:gtc-saccharomyces cerevisiae]
CONTIG1755	34117012_c3_5	5953	20056	393	131	YCR011C	292	1.3(10)-24	Saccharomyces cerevisiae	[ui:ycr011c] [pn:atp-dependent permease:probable atp-dependent permease precursor] [gn:adp1:yer11c:ycr105] [gtcfc:11.1:12.6] [keggfc:14.2] [sgdfc:7.9.0.9.1.0] [db:gtc-saccharomyces cerevisiae]

CONTIG1755	21687875_c1_3	5954	20057	861	287	YCR011C	676	5.5(10)-66	Saccharomyces cerevisiae	[ui:ycr011c] [pn:atp-dependent permease;probable atp-dependent permease precursor] [gn:adp1:yer11c:ycr105] [gtcfc:11.1:12.6] [keggfc:14.2] [sgdfc:7.9.0:9.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2857	4394530_c3_5	5955	20058	1008	336	YCR011C	957	2.2(10)-96	Saccharomyces cerevisiae	[ui:ycr011c] [pn:atp-dependent permease;probable atp-dependent permease precursor] [gn:adp1:yer11c:ycr105] [gtcfc:11.1:12.6] [keggfc:14.2] [sgdfc:7.9.0:9.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3284	1408501_f3_2	5956	20059	465	155	YCR011C	238	7.7(10)-19	Saccharomyces cerevisiae	[ui:ycr011c] [pn:atp-dependent permease;probable atp-dependent permease precursor] [gn:adp1:yer11c:ycr105] [gtcfc:11.1:12.6] [keggfc:14.2] [sgdfc:7.9.0:9.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5055	32305143_c2_11	5957	20060	4089	1363	YCR038C	305	2.7(10)-31	Saccharomyces cerevisiae	[ui:ycr038c] [pn:gdp/gtp exchange factor for rsr1p/bud1 p:bud site selection protein bud5] [gn:bud5:ycr38c:ycr526] [gtcfc:11.1:12.8] [keggfc:13.3] [sgdfc:3.2.0:9.1.0] [db:gtc-saccharomyces cerevisiae]

CONTIG1269	14472817_f1_1	5958	20061	984	328	YCR098C	385	9.5(10)-36	Saccharomyces cerevisiae	[ui:ycr098c] [pn:similarity to phosphate transporter proteins:probable metabolite transport protein ycr98c] [gn:git1:ycr98c:ycr137] [gtcfc:12.4:11.1:13.10] [keggfc:14.2] [sgdfc:1.4.3:7.2.3:7.3.0:9.1.0:17.0.0] [db:gtc-saccharomyces cer
CONTIG4599	484681_c3_9	5959	20062	999	333	YCR098C	297	6.9(10)-26	Saccharomyces cerevisiae	[ui:ycr098c] [pn:similarity to phosphate transporter proteins:probable metabolite transport protein ycr98c] [gn:git1:ycr98c:ycr137] [gtcfc:12.4:11.1:13.10] [keggfc:14.2] [sgdfc:1.4.3:7.2.3:7.3.0:9.1.0:17.0.0] [db:gtc-saccharomyces cer
CONTIG4599	5913317_c3_8	5960	20063	468	156	YCR098C	174	1.8(10)-12	Saccharomyces cerevisiae	[ui:ycr098c] [pn:similarity to phosphate transporter proteins:probable metabolite transport protein ycr98c] [gn:git1:ycr98c:ycr137] [gtcfc:12.4:11.1:13.10] [keggfc:14.2] [sgdfc:1.4.3:7.2.3:7.3.0:9.1.0:17.0.0] [db:gtc-saccharomyces cer

CONTIG4947	4334552_f1_1	5961	20064	930		YCR098C	921	1.5(10)-92	Saccharomyces cerevisiae	[ui:ycr098c] [pn:similarity to phosphate transporter proteins:probable metabolite transport protein ycr98c] [gn:git1:ycr98c:ycr137] [gtcfc:12.4:11.1:13.10] [keggfc:14.2] [sgdfc:1.4.3:7.2:3:7.3.0:9.1.0:17.0.0] [db:gtc-saccharomyces cer
CONTIG98	20959800_c1_1	5962	20065	594	198	YCR098C	224	7.0(10)-18	Saccharomyces cerevisiae	[ui:ycr098c] [pn:similarity to phosphate transporter proteins:probable metabolite transport protein ycr98c] [gn:git1:ycr98c:ycr137] [gtcfc:12.4:11.1:13.10] [keggfc:14.2] [sgdfc:1.4.3:7.2:3:7.3.0:9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3589	14235307_f2_1	5963	20066	1599	533	YDL210W	1196	1.1(10)-121	Saccharomyces cerevisiae	[ui:ydl210w] [pn:gaba-specific high-affinity permease:gaba-specific permease:gaba-specific transport protein] [gn:uga4:dl037] [gtcfc:11.1:12.1] [keggfc:14.2] [sgdfc:7.4.0:8.7.0:9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5100	11844785_f3_1	5964	20067	1428	476	YDL210W	1063	1.3(10)-107	Saccharomyces cerevisiae	[ui:ydl210w] [pn:gaba-specific high-affinity permease:gaba-specific permease:gaba-specific transport protein] [gn:uga4:dl037] [gtcfc:11.1:12.1] [keggfc:14.2] [sgdfc:7.4.0:8.7.0:9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5563	20969078_f2_6	5965	20068	2298	766	YDL194W	1369	5.0(10)-140	Saccharomyces cerevisiae	[ui:ydl194w] [pn:high-affinity glucose transporter/regulatory protein:high-affinity glucose transporter snf3] [gn:snf3:d1234] [keggfc:14.2] [sgdfc:1.5.2:1.5.3:7.3.0:8.7.0:9.1.0:1 7.0.0] [db:gtc-saccharomyces cer
b4x10274.y	9860017_f1_1	5966	20069	405	135	YDL194W	135	6.2(10)-8	Saccharomyces cerevisiae	[ui:ydl194w] [pn:high-affinity glucose transporter/regulatory protein:high-affinity glucose transporter snf3] [gn:snf3:d1234] [keggfc:14.2] [sgdfc:1.5.2:1.5.3:7.3.0:8.7.0:9.1.0:1 7.0.0] [db:gtc-saccharomyces cer
CONTIG1940	26172692_c1_2	5967	20070	1077	359	YDR011W	1022	1.0(10)-102	Saccharomyces cerevisiae	[ui:ydr011w] [pn:multidrug resistance protein:snq2 protein] [gn:snq2:yd8119] [gtcfc:11.1:12.12.6] [keggfc:14.2] [sgdfc:7.9.0:9.1.0:11.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG665	23838938_c3_4	5968	20071	915	305	YDR011W	535	2.7(10)-50	Saccharomyces cerevisiae	[ui:ydr011w] [pn:multidrug resistance protein:snq2 protein] [gn:snq2:yd8119] [gtcfc:11.1:12.12.6] [keggfc:14.2] [sgdfc:7.9.0:9.1.0:11.3.0] [db:gtc-saccharomyces cerevisiae]

CONTIG900	5269432_f3_1	5969	20072	801	267	YDR011W	244	2.8(10)-19	Saccharomyces cerevisiae	[ui:ydr011w] [pn:multidrug resistance protein:snq2 protein] [gn:snq2:yd8119] [gtcfc:11.1:12.12-12.6] [keggfc:14.2] [sgdfc:7.9.0:9.1.0:11.3.0] [db:gtc-saccharomyces cerevisiae]
b1x17948.x	21611632_c1_1	5970	20073	831	277	YDR011W	618	3.8(10)-59	Saccharomyces cerevisiae	[ui:ydr011w] [pn:multidrug resistance protein:snq2 protein] [gn:snq2:yd8119] [gtcfc:11.1:12.12-12.6] [keggfc:14.2] [sgdfc:7.9.0:9.1.0:11.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4946	26354552_c2_7	5971	20074	339	113	YDR342C	108	2.7(10)-5	Saccharomyces cerevisiae	[ui:ydr342c] [pn:high-affinity hexose transporter:high affinity hexose transporter hxt6] [gn:hxt7:d9651] [gtcfc:12.2:11.1] [keggfc:14.2] [sgdfc:1.5.3:7.3.0:8.7.0:9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5043	814092_c2_10	5972	20075	1521	507	YDR342C	1320	7.9(10)-135	Saccharomyces cerevisiae	[ui:ydr342c] [pn:high-affinity hexose transporter:high affinity hexose transporter hxt6] [gn:hxt7:d9651] [keggfc:14.2] [sgdfc:1.5.3:7.3.0:8.7.0:9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5004	5866544_c1_2	5973	20076	1257	419	YDR342C	1100	1.6(10)-111	Saccharomyces cerevisiae	[ui:ydr342c] [pn:high-affinity hexose transporter:high affinity hexose transporter hxt6] [gn:hxt7:d9651] [gtcfc:12.2:11.1] [keggfc:14.2] [sgdfc:1.5.3:7.3.0:8.7.0:9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG473	25423837_f1_1	5974	20077	648	216	YDR497C	256	3.1(10)-21	Saccharomyces cerevisiae	[ui:ydr497c] [pn:myo-inositol permease, major myo-inositol transporter 1] [gn:itr1:d9719] [gtcfc:12.2:11.1:8.2] [keggfc:14.2] [sgdfc:1.5.3:7.3.0:8.7.0:9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5237	4069677_f1_2	5975	20078	1662	554	YDR536W	1639	1.2(10)-168	Saccharomyces cerevisiae	[ui:ydr536w] [pn:strong similarity to members of the sugar permease family:sugar transporter stl1] [gn:stl1:d9719] [gtcfc:12.2:11.1] [keggfc:14.2] [sgdfc:1.5.3:7.3.0:9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5348	26360285_f1_3	5976	20079	1503	501	YDR536W	549	4.0(10)-53	Saccharomyces cerevisiae	[ui:ydr536w] [pn:strong similarity to members of the sugar permease family:sugar transporter stl1] [gn:stl1:d9719] [gtcfc:12.2:11.1] [keggfc:14.2] [sgdfc:1.5.3:7.3.0:9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5348	13712753_f3_10	5977	20080	273	91	YDR536W	150	8.3(10)-10	Saccharomyces cerevisiae	[ui:ydr536w] [pn:strong similarity to members of the sugar permease family:sugar transporter stl1] [gn:stl1:d97191] [gtcfc:12.2:11.1] [keggfc:14.2] [sgdfc:1.5:3:7.3.0:9.1.0.17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5655	32455327_c3_22	5978	20081	978	326	YEL069C	289	7.2(10)-25	Saccharomyces cerevisiae	[ui:yel069c] [pn:high-affinity hexose transporter:hexose transporter hxt13] [gn:hxt13:hxt8] [gtcfc:12.2:11.1] [keggfc:14.2] [sgdfc:1.5:3:7.3.0:8.7.0:9.1.0.17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2731	19532625_c1_3	5979	20082	1317	439	YEL063C	1315	2.7(10)-134	Saccharomyces cerevisiae	[ui:yel063c] [pn:amino acid permease:arginine permease] [gn:can1] [gtcfc:11.1:12.1:12.6] [keggfc:14.2] [sgdfc:1.1.3:7.4.0:8.7.0:9.1.0.17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3177	2914055_c2_3	5980	20083	432	144	YEL063C	232	1.3(10)-18	Saccharomyces cerevisiae	[ui:yel063c] [pn:amino acid permease:arginine permease] [gn:can1] [gtcfc:11.1:12.1:12.6] [keggfc:14.2] [sgdfc:1.1.3:7.4.0:8.7.0:9.1.0.17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3579	10033577_c2_6	5981	20084	798	266	YEL063C	709	4.4(10)-70	Saccharomyces cerevisiae	[ui:yel063c] [pn:amino acid permease:arginine permease] [gn:can1] [gtcfc:11.1:12.1:12.6] [keggfc:14.2] [sgdfc:1.1.3:7.4.0:8.7.0:9.1.0.17.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4383	2397692_f1_1	5982	20085	594	198	YEL063C	540	3.6(10)-52	Saccharomyces cerevisiae	[ui:yel063c] [pn:amino acid permease:arginine permease] [gn:can1] [gtcfc:11.1:12.1:12.6] [sgdfc:1.1.3:7.4.0:8.7.0:9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4559	36564036_f2_1	5983	20086	1215	405	YEL063C	1160	7.0(10)-118	Saccharomyces cerevisiae	[ui:yel063c] [pn:amino acid permease:arginine permease] [gn:can1] [gtcfc:11.1:12.1:12.6] [sgdfc:1.1.3:7.4.0:8.7.0:9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG96	13719753_c2_1	5984	20087	618	206	YEL063C	575	7.0(10)-56	Saccharomyces cerevisiae	[ui:yel063c] [pn:amino acid permease:arginine permease] [gn:can1] [gtcfc:11.1:12.1:12.6] [sgdfc:1.1.3:7.4.0:8.7.0:9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2651	15126675_c1_6	5985	20088	1221	407	YER056C	1172	3.7(10)-119	Saccharomyces cerevisiae	[ui:yer056c] [pn:purine-cytosine permease:pcp:cytosine/purine transport protein] [gn:fcy2] [gtcfc:12.3:11.1:4.1:4.2] [sgdfc:1.3.7:7.6.0:8.7.0:9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG105	35267137_c2_2	5986	20089	444	148	YER118C	199	1.3(10)-15	Saccharomyces cerevisiae	[ui:yer118c] [pn:involved in the hog1 high-osmolarity signal transduction pathway:ssu81 protein:sho1 osmosensor] [gn:ssu81:sho1] [gtcfc:12.13:11.3] [keggfc:14.2] [sgdfc:9.1.0:10.3.3:11.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4313	160902_f1_3	5987	20090	1155	385	YER118C	270	1.3(10)-27	Saccharomyces cerevisiae	[ui:yer118c] [pn:involved in the hog1 high-osmolarity signal transduction pathway:ssu81 protein:sho1 osmosensor] [gn:ssu81:sho1] [gtcfc:12.13:11.3] [keggfc:14.2] [sgdfc:9.1.0:10.3.3:11.1.0] [db:gtc-saccharomyces cerevisiae]
b9x10g01.y	1032761_c1_2	5988	20091	573	191	YFL026W	201	1.3(10)-15	Saccharomyces cerevisiae	[ui:yfl026w] [pn:pheromone alpha-factor receptor:pheromone alpha-factor receptor] [gn:ste2] [gtcfc:11.1:11.3:12.8:12.9] [keggfc:13.1] [sgdfc:3.3.0:9.1.0:10.1.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5813	35189635_c2_52	5989	20092	1224	408	YFL011W	331	1.5(10)-29	Saccharomyces cerevisiae	[ui:yfl011w] [pn:hexose transporter] [gn:hxt10] [gtcfc:12.2:11.1] [keggfc:14.2] [sgdfc:1.5.3:7.3.0:8.7.0:9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4079	23939651_c1_4	5990	20093	1872	624	YGL233W	282	2.6(10)-21	Saccharomyces cerevisiae	[ui:ygl233w] [pn:vesicular traffic control protein] [gn:sec15] [gtcfc:11.1:12.10] [keggfc:14.2] [sgdfc:8.3.0:8.6.0:9.1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4714	12897316_f2_1	5991	20094	678	226	YGL233W	113	2.7(10)-10	Saccharomyces cerevisiae	[ui:ygl233w] [pn:vesicular traffic control protein] [gn:sec15] [gtcfc:11.1:12.10] [keggfc:14.2] [sgdfc:8.3.0:8.6.0:9.1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3746	12188155_f2_2	5992	20095	1353	451	YGL077C	1117	2.6(10)-113	Saccharomyces cerevisiae	[ui:ygl077c] [pn:choline permease:choline transport protein] [gn:hnm1:ctr1:ctr] [gtcfc:12.2:11.1] [keggfc:14.2] [sgdfc:7.4.0:8.7.0:9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5418	26189005_c1_10	5993	20096	1758	586	YGL077C	1185	1.6(10)-120	Saccharomyces cerevisiae	[ui:ygl077c] [pn:choline permease:choline transport protein] [gn:hnm1:ctr1:ctr] [gtcfc:12.2:11.1] [keggfc:14.2] [sgdfc:7.4.0:8.7.0:9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG848	24882176_c2_6	5994	20097	1143	381	YGL008C	412	1.3(10)-38	Saccharomyces cerevisiae	[ui:ygl077c] [pn:choline permease:choline transport protein] [gn:hnm1:ctr1:ctr] [gtcfc:12.2:11.1] [sgdfc:7.4.0:8.7.0:9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3434	10725014_c1_7	5995	20098	1695	565	YGL008C	2253	1.1(10)-233	Saccharomyces cerevisiae	[ui:ygl008c] [pn:h+-transporting p-type atpase:plasma membrane atpase 1:proton pump] [gn:pma1] [gtcfc:12.5:11.1] [ec:3.6.1.35] [keggfc:14.1] [sgdfc:1.8.2:7.2.2:7.8.0:9.1.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4102	24397650_c2_3	5996	20009	1083	361	YGR009C	260	1.5(10)-21	Saccharomyces cerevisiae	[ui:ygr009c] [pn:protein transport protein sec9] [gn:sec9:hss7] [gtcfc:12.6:11.1:12.10] [keggfc:14.2] [sgdfc:8.3.0:8.6.0:9.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG764	24509563_c2_1	5997	20100	192	64	YGR009C	147	2.1(10)-9	Saccharomyces cerevisiae	[ui:ygr009c] [pn:protein transport protein sec9] [gn:sec9:hss7] [gtcfc:12.6:11.1:12.10] [keggfc:14.2] [sgdfc:8.3.0:8.6.0:9.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5663	4195250_c2_16	5998	20101	2403	801	YGR014W	94	0.76	Saccharomyces cerevisiae	[ui:ygr014w] [pn:multicopy suppressor of a cdc24 bud emergence defect:protein:multicopy suppression of a budding defect 2] [gn:msb2] [gtcfc:11.1:12.8] [keggfc:14.2] [sgdfc:3.2.0:9.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3541	553336_c3_3	5999	20102	666	222	YGR055W	340	1.8(10)-30	Saccharomyces cerevisiae	[ui:ygr055w] [pn:high affinity methionine permease] [gn:mup1] [gtcfc:11.1:12.1:12.6] [keggfc:14.2] [sgdfc:1.1.3:7.4.0:8.7.0:9.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2940	813803_f1_1	6000	20103	852	284	YGR191W	451	9.5(10)-43	Saccharomyces cerevisiae	[ui:ygr191w] [pn:histidine permease] [gn:hip1:g7572] [gtcfc:11.1:12.1:12.6] [keggfc:14.2] [sgdfc:1.1.3:7.4.0:8.7.0:9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG57	31533281_f3_2	6001	20104	630	210	YGR191W	497	1.3(10)-47	Saccharomyces cerevisiae	[ui:ygr191w] [pn:histidine permease] [gn:hip1:g7572] [gtcfc:11.1:12.1:12.6] [sgdfc:1.1.3:7.4.0:8.7.0:9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1342	3172050_c2_2	6002	20105	1086	362	YGR281W	464	5.5(10)-48	Saccharomyces cerevisiae	[ui:ygr281w] [pn:atp-binding cassette transporter protein:oligomycin resistance atp-dependent permease] [gn:yor1] [gtcfc:11.1:12.6:13.3] [sgdfc:7.9.0:7.10.0:9.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1526	4469127_f2_2	6003	20106	462	154	YGR281W	234	3.2(10)-18	Saccharomyces cerevisiae	[ui:ygr281w] [pn:atp-binding cassette transporter protein:oligomycin resistance atp-dependent permease] [gn:yor1] [gtcfc:11.1:12.6:13.3] [keggfc:14.2] [sgdfc:7.9.0:7.10.0:9.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1500	24901912_f1_1	6004	20107	723	241	YGR281W	512	9.6(10)-72	Saccharomyces cerevisiae	[ui:ygr281w] [pn:atp-binding cassette transporter protein:oligomycin resistance atp-dependent permease] [gn:yor1] [gtcfc:11.1:12.6:13.3] [sgdfc:7.9.0:7.10.0:9.1.0] [db:gtc-saccharomyces cerevisiae]

b2x10882.x	24891016_c3_2	6005	20108		165	YGR281W	182	1.1(10)-12	Saccharomyces cerevisiae	[ui:ygr281w] [pn:atp-binding cassette transporter protein:oligomycin resistance atp-dependent permease] [gn:yor1] [gtcfc:11.1:12.6:13.3] [keggfc:14.2] [sgdfc:7.9.0:7.10.0:9.1.0] [db:gtc-saccharomyces cerevisiae]
b3x10485.y	4004139_c1_1	6006	20109		171	YGR281W	499	1.8(10)-46	Saccharomyces cerevisiae	[ui:ygr281w] [pn:atp-binding cassette transporter protein:oligomycin resistance atp-dependent permease] [gn:yor1] [gtcfc:11.1:12.6:13.3] [keggfc:14.2] [sgdfc:7.9.0:7.10.0:9.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3184	4884677_c3_9	6007	20110	384	128	YHL028W	95	0.00072	Saccharomyces cerevisiae	[ui:yhl028w] [pn:similarity to mucin and other ser-thr rich proteins:hypothetical 63.8 kd protein in gut1-rim1 intergenic region precursor] [gtcfc:11.1:5.3] [keggfc:14.2] [sgdfc:9.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4476	25397177_c2_10	6008	20111		581	YHL028W	109	0.0077	Saccharomyces cerevisiae	[ui:yhl028w] [pn:similarity to mucin and other ser-thr rich proteins:hypothetical 63.8 kd protein in gut1-rim1 intergenic region precursor] [gtcfc:11.1:5.3] [keggfc:14.2] [sgdfc:9.1.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5699	14629382_c1_25	6009	20112	1473	491	YHL028W	153	4.5(10)-8	Saccharomyces cerevisiae	[ui:yhl028w] [pn:similarity to mucin and other ser-thr rich proteins:hypothetical 63.8 kd protein in gut1-rim1 intergenic region precursor] [gtcfc:11.1:5.3] [keggfc:14.2] [sgdfc:9.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1827	35797776_f1_1	6010	20113	342	114	YHL019C	152	5.5(10)-10	Saccharomyces cerevisiae	[ui:yhl019c] [pn:involved in clathrin-dependent transport processes:adaptin medium chain homolog] [gn:apm2] [gtcfc:11.1:12.16] [keggfc:14.2] [sgdfc:8.8.0:9.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1827	23948587_f1_2	6011	20114	714	238	YHL019C	141	8.4(10)-9	Saccharomyces cerevisiae	[ui:yhl019c] [pn:involved in clathrin-dependent transport processes:adaptin medium chain homolog] [gn:apm2] [gtcfc:11.1:12.16] [keggfc:14.2] [sgdfc:8.8.0:9.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1827	9805182_f2_3	6012	20115	660	220	YHL019C	130	5.5(10)-6	Saccharomyces cerevisiae	[ui:yhl019c] [pn:involved in clathrin-dependent transport processes:adaptin medium chain homolog] [gn:apm2] [gtcfc:11.1:12.16] [keggfc:14.2] [sgdfc:8.8.0:9.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1042	23863842_f1_1	6013	20116	825	275	YHL016C	269	4.0(10)-30	Saccharomyces cerevisiae	[ui:yhl016c] [pn:urea active transporter] [gn:dur3] [gtcfc:12.4:5.16:11.1] [keggfc:14.2] [sgdfc:1.2.3:1.8.2:7.2.2:9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3399	2913577_c1_5	6014	20117	819	273	YHL016C	124	.	7.0(10)-5	Saccharomyces cerevisiae	[ui:yhl016c] [pn:urea transport protein:urea active transporter] [gn:dur3] [gtcfc:12.4:5.16:11.1] [sgdfc:1.2.3:1.8.2:7.2.2:9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG371	6843750_c3_4	6015	20118	1038	346	YHL016C	432		4.4(10)-40	Saccharomyces cerevisiae	[ui:yhl016c] [pn:urea transport protein:urea active transporter] [gn:dur3] [gtcfc:12.4:5.16:11.1] [sgdfc:1.2.3:1.8.2:7.2.2:9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5303	21492838_c2_15	6016	20119	1152	384	YHL016C	527		8.5(10)-51	Saccharomyces cerevisiae	[ui:yhl016c] [pn:urea transport protein:urea active transporter] [gn:dur3] [gtcfc:12.4:5.16:11.1] [sgdfc:1.2.3:1.8.2:7.2.2:9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5355	29344811_f2_1	6017	20120	1512	504	YHL016C	715		1.3(10)-107	Saccharomyces cerevisiae	[ui:yhl016c] [pn:urea transport protein:urea active transporter] [gn:dur3] [gtcfc:12.4:5.16:11.1] [sgdfc:1.2.3:1.8.2:7.2.2:9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5379	10975902_c2_18	6018	20121	2043	681	YHL016C	921		5.9(10)-105	Saccharomyces cerevisiae	[ui:yhl016c] [pn:urea transport protein:urea active transporter] [gn:dur3] [gtcfc:12.4:5.16:11.1] [sgdfc:1.2.3:1.8.2:7.2.2:9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5611	7070305_f1_3	6019	20122	609	203	YHL016C	484	7.2(10)-46	Saccharomyces cerevisiae	[ui:yhl016c] [pn:urea transport protein:urea active transporter] [gn:dur3] [gtcfc:12.4:5.16:11.1] [keggfc:14.2] [sgdfc:1.2.3:1.8.2:7.2:2.9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG747	24297337_c3_9	6020	20123	1203	401	YHL016C	507	1.6(10)-48	Saccharomyces cerevisiae	[ui:yhl016c] [pn:urea transport protein:urea active transporter] [gn:dur3] [gtcfc:12.4:5.16:11.1] [keggfc:14.2] [sgdfc:1.2.3:1.8.2:7.2:2.9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
b9x11469.x	9855416_f3_1	6021	20124	540	180	YHL016C	109	3.0(10)-5	Saccharomyces cerevisiae	[ui:yhl016c] [pn:urea transport protein:urea active transporter] [gn:dur3] [gtcfc:12.4:5.16:11.1] [keggfc:14.2] [sgdfc:1.2.3:1.8.2:7.2:2.9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4312	21673261_f1_1	6022	20125	429	143	YHR096C	183	2.5(10)-13	Saccharomyces cerevisiae	[ui:yhr096c] [pn:strong similarity to hexose transporters:probable glucose transporter] [gn:hxt5] [gtcfc:12.2:11.1] [keggfc:14.2] [sgdfc:1.5.3:7.3.0:8.7.0:9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4946	2157665_c1_4	6023	20126	417	139	YHR096C	286	1.8(10)-24	Saccharomyces cerevisiae	[ui:yhr096c] [pn:strong similarity to hexose transporters:probable glucose transporter] [gn:hxt5] [gtcfc:12.2:11.1] [keggfc:14.2] [sgdfc:1.5.3:7.3.0:8.7.0:9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5319	24303912_c1_6	6024	20127	1125	375	YHR096C	334	1.0(10)-29	Saccharomyces cerevisiae	[ui:yhr096c] [pn:strong similarity to hexose transporters;probable glucose transporter] [gn:hxt5] [gtcfc:12.2:11.1] [keggfc:14.2] [sgdfc:1.5.3:7.3.0:8.7.0:9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
b3x16095.y	33460818_c2_6	6025	20128	228	76	YIL147C	96	0.00129	Saccharomyces cerevisiae	[ui:yil147c] [pn:two-component signal transducer:osomolarity two-component system protein sln1] [gn:sln1:ypd2] [gtcfc:12.11:11.3:12.13] [ec:2.7.3.-] [sgdfc:1.5.2:9.1.0:10.3.2:11.1.0] [keggfc:14.1] [db:gtc-saccharomyces cerevisiae]
CONTIG2824	23604063_c2_1	6026	20129	1047	349	YIL140W	635	3.1(10)-62	Saccharomyces cerevisiae	[ui:yil140w] [pn:required for axial pattern of budding:axl2 protein precursor:sro4 protein] [gn:axl2:sro4] [gtcfc:11.1:12.8] [keggfc:14.2] [sgdfc:3.2.0:9.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2142	16187630_f2_3	6027	20130	228	76	YIL047C	96	0.00093	Saccharomyces cerevisiae	[ui:yil047c] [pn:member of the major facilitator superfamily:protein] [gn:syg1] [gtcfc:11.1:12.6:12.8:12.9] [keggfc:14.2] [sgdfc:3.3.0:9.1.0:10.1.6:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3415	19609375_f3_3	6028	20131	1059	353	YIL047C	640	9.1(10)-63	Saccharomyces cerevisiae	[ui:yil047c] [pn:member of the major facilitator superfamily:protein] [gn:syg1] [gtcfc:11.1:12.6:12.8:12.9] [keggfc:14.2] [sgdfc:3.3.0:9.1.0:10.1.6:17.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5360	24083326_f3_5	6029	20132	1725	575		3.2(10)-147	Saccharomyces cerevisiae	[ui:yir028w] [pn:allantoin permease:allantoin transport protein] [gn:dal4] [gtcfc:12.6:11.1] [keggfc:14.2] [sgdfc:7.7.0:8.7.0.9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3735	13759450_f2_4	6030	20133	633	211	YJL219W	238	2.6(10)-19	Saccharomyces cerevisiae	[ui:yjl219w] [pn:hexose transport protein:hexose transporter hxt9] [gn:hxt9:j0222:hrc567] [gtcfc:12.2:11.1] [keggfc:14.2] [sgdfc:1.5.3:7.3.0:8.7.0.9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5448	21489688_c1_13	6031	20134	927	309	YJL093C	366	5.7(10)-33	Saccharomyces cerevisiae	[ui:yjl093c] [pn:outward-rectifier potassium channel:outward-rectifier potassium channel tok1:two-domain outward rectifier k+ channel york] [gn:tok1:duk1:j0911] [gtcfc:11.1:11.3:12.10:12.6] [keggfc:14.2] [sgdfc:1.8.2:7.1.0:8.6.0:9.1.
CONTIG5448	25813802_c1_12	6032	20135	1287	429	YJL093C	590	1.8(10)-57	Saccharomyces cerevisiae	[ui:yjl093c] [pn:outward-rectifier potassium channel:outward-rectifier potassium channel tok1:two-domain outward rectifier k+ channel york] [gn:tok1:duk1:j0911] [gtcfc:11.1:11.3:12.10:12.6] [keggfc:14.2] [sgdfc:1.8.2:7.1.0:8.6.0:9.1.

CONTIG2735	15705057_f2_1	6033	20136	1440	480	YJR040W	320	7.5(10)-28	Saccharomyces cerevisiae	[ui:yjr040w] [pn:voltage-gated chloride channel protein:gef1 protein:voltage-gated chloride channel:clc-y1:clc-a] [gn:gef1:clcy1:j1616] [gtcfc:11.1:11.3:12.6] [sgdfc:1.8.2:7.1.0:8.7.0:9.1.0] [db:gtc-saccharomyces cerevis
CONTIG3806	972933_f2_3	6034	20137	465	155	YJR040W	376	6.9(10)-34	Saccharomyces cerevisiae	[ui:yjr040w] [pn:voltage-gated chloride channel protein:gef1 protein:voltage-gated chloride channel:clc-y1:clc-a] [gn:gef1:clcy1:j1616] [gtcfc:11.1:11.3:12.6] [sgdfc:1.8.2:7.1.0:8.7.0:9.1.0] [db:gtc-saccharomyces cerevis
CONTIG3806	13850627_f1_2	6035	20138	1248	416	YJR040W	556	7.2(10)-54	Saccharomyces cerevisiae	[ui:yjr040w] [pn:voltage-gated chloride channel protein:gef1 protein:voltage-gated chloride channel:clc-y1:clc-a] [gn:gef1:clcy1:j1616] [gtcfc:11.1:11.3:12.6] [sgdfc:1.8.2:7.1.0:8.7.0:9.1.0] [db:gtc-saccharomyces cerevis
							.	.		

CONTIG4484	9781912_c3_7	6036	20139	2466	822	YJR040W	384	2.7(10)-41	Saccharomyces cerevisiae	[ui:yjr040w] [pn:voltage-gated chloride channel protein:gef1 protein:voltage-gated chloride channel:clc-y1:clc-a] [gn:gef1:clcy1:j1616] [gtcfc:11.1:11.3:12.6] [sgdfc:1.8.2:7.1.0:8.7.0:9.1.0] [db:gtc-saccharomyces cerevis
CONTIG5246	9777082_f3_6	6037	20140	759	253	YJR040W	116	0.00038	Saccharomyces cerevisiae	[ui:yjr040w] [pn:voltage-gated chloride channel protein:gef1 protein:voltage-gated chloride channel:clc-y1:clc-a] [gn:gef1:clcy1:j1616] [gtcfc:11.1:11.3:12.6] [sgdfc:1.8.2:7.1.0:8.7.0:9.1.0] [db:gtc-saccharomyces cerevis
CONTIG5649	2151425_c1_15	6038	20141	534	178	YJR040W	135	5.2(10)-8	Saccharomyces cerevisiae	[ui:yjr040w] [pn:voltage-gated chloride channel protein:gef1 protein:voltage-gated chloride channel:clc-y1:clc-a] [gn:gef1:clcy1:j1616] [gtcfc:11.1:11.3:12.6] [sgdfc:1.8.2:7.1.0:8.7.0:9.1.0] [db:gtc-saccharomyces cerevis
CONTIG1183	4871053_f3_1	6039	20142	990	330	YJR151C	148	1.5(10)-7	Saccharomyces cerevisiae	[ui:yjr151c] [pn:similarity to mucin proteins, ykl224c, sta1p:hypothetical 118.4 kd protein in rps7b-dal5 intergenic region precursor] [gn:j2223] [gtcfc:11.1] [keggfc:14.2] [sgdfc:9.1.0] [db:gtc-saccharomyces cerevisiae]

CONTIG1562	23641263_c2_4	6040	20143	939	313	YJR151C	92	0.22	Saccharomyces cerevisiae	[ui:yjr151c] [pn:similarity to mucin proteins, sta1p:hypothetical 118.4 kd protein in rps7b-dal5 intergenic region precursor] [gn:j2223] [sgdfc:9.1.0] [gtcfc:11.1] [db:gtc-saccharomyces cerevisiae]
CONTIG2128	14568812_f2_1	6041	20144	402	134	YJR151C	91	0.03699	Saccharomyces cerevisiae	[ui:yjr151c] [pn:similarity to mucin proteins, ykl224c, sta1p:hypothetical 118.4 kd protein in rps7b-dal5 intergenic region precursor] [gn:j2223] [sgdfc:9.1.0] [gtcfc:11.1] [db:gtc-saccharomyces cerevisiae]
CONTIG2535	14884637_f3_3	6042	20145	2490	830	YJR151C	94	0.71999	Saccharomyces cerevisiae	[ui:yjr151c] [pn:similarity to mucin proteins, ykl224c, sta1p:hypothetical 118.4 kd protein in rps7b-dal5 intergenic region precursor] [gn:j2223] [keggfc:14.2] [sgdfc:9.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5387	22667311_f3_11	6043	20146	966	322	YJR151C	106	0.01499	Saccharomyces cerevisiae	[ui:yjr151c] [pn:similarity to mucin proteins, ykl224c, sta1p:hypothetical 118.4 kd protein in rps7b-dal5 intergenic region precursor] [gn:j2223] [sgdfc:9.1.0] [gtcfc:11.1] [db:gtc-saccharomyces cerevisiae]

CONTIG1416	13704127_c2_5	6044	20147	1374	458	YJR152W	1149	1.0(10)-116	Saccharomyces cerevisiae	[ui:yjr152w] [pn:allantoate permease] [gn:dal5:urep1:j2230] [gtcfc:11.1:12.6] [sgdfc:7.7.0:8.7.0:9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1150	26445192_c3_1	6045	20148	774	258	YJR152W	560	2.7(10)-54	Saccharomyces cerevisiae	[ui:yjr152w] [pn:allantoate permease] [gn:dal5:urep1:j2230] [gtcfc:11.1:12.6] [sgdfc:7.7.0:8.7.0:9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1605	32078317_f3_1	6046	20149	705	235	YJR152W	562	1.7(10)-54	Saccharomyces cerevisiae	[ui:yjr152w] [pn:allantoate permease] [gn:dal5:urep1:j2230] [gtcfc:11.1:12.6] [sgdfc:7.7.0:8.7.0:9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3088	24651561_c1_3	6047	20150	660	220	YJR152W	325	6.5(10)-29	Saccharomyces cerevisiae	[ui:yjr152w] [pn:allantoate permease] [gn:dal5:urep1:j2230] [gtcfc:11.1:12.6] [sgdfc:7.7.0:8.7.0:9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5778	24250927_c1_23	6048	20151	1659	553	YJR152W	1205	1.2(10)-122	Saccharomyces cerevisiae	[ui:yjr152w] [pn:allantoate permease] [gn:dal5:urep1:j2230] [gtcfc:11.1:12.6] [sgdfc:7.7.0:8.7.0:9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
b1x18608.x	6055325_f3_1	6049	20152	189	63	YJR152W	95	0.00063	Saccharomyces cerevisiae	[ui:yjr152w] [pn:allantoate permease] [gn:dal5:urep1:j2230] [gtcfc:11.1:12.6] [sgdfc:7.7.0:8.7.0:9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG171	31267580_f2_1	6050	20153	756	252	YKL220C	289	1.3(10)-24	Saccharomyces cerevisiae	[ui:ykl220c] [pn:ferric and cupric reductase:ferric reductase transmembrane component 2 precursor] [gn:fre2] [gtcfc:11.1:12.6] [keggfc:14.2] [sgdfc:1.8.1:9.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4756	7040907_c1_12	6051	20154	1722	574	YKL220C	494	3.2(10)-47	Saccharomyces cerevisiae	[ui:kl220c] [pn:ferric and cupric reductase:ferric reductase transmembrane component 2 precursor] [gn:fre2] [gtcfc:11.1:12.6] [keggfc:14.2] [sgdfc:1.8.1:9.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1914	20742167_c1_8	6052	20155	549	183	YKL178C	338	9.0(10)-31	Saccharomyces cerevisiae	[ui:ykl178c] [pn:pheromone a-factor receptor:pheromone a factor receptor] [gn:ste3] [gtcfc:11.1:11.3:12.8:12.9] [keggfc:13.1] [sgdfc:3.3.0:9.1.0:10.1.1] [db:gtc-saccharomyces cerevisiae]
CONTIG1879	1067693_f1_1	6053	20156	633	211	YKR039W	559	3.5(10)-54	Saccharomyces cerevisiae	[ui:ykr039w] [pn:general amino acid permease:general amino-acid permease] [gn:gap1] [gtcfc:11.1:12.1:12.6] [keggfc:14.2] [sgdfc:1.1.3:7.4.0:8.7.0:9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2695	2386458_f2_1	6054	20157	771	257	YKR039W	625	3.5(10)-61	Saccharomyces cerevisiae	[ui:ykr039w] [pn:general amino acid permease:general amino-acid permease] [gn:gap1] [gtcfc:11.1:12.1:12.6] [keggfc:14.2] [sgdfc:1.1.3:7.4.0:8.7.0:9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2933	3908427_f3_1	6055	20158	1038	346	YKR039W	581	1.6(10)-56	Saccharomyces cerevisiae	[ui:ykr039w] [pn:general amino acid permease:general amino-acid permease] [gn:gap1] [gtcfc:11.1:12.1:12.6] [keggfc:14.2] [sgdfc:1.1.3:7.4.0:8.7.0:9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4473	289027_c3_7	6056	20159	702	234	YKR039W	700	4.0(10)-69	Saccharomyces cerevisiae	[ui:ykr039w] [pn:general amino acid permease:general amino-acid permease] [gn:gap1] [gtcfc:11.1:12.1:12.6] [keggfc:14.2] [sgdfc:1.1.3:7.4.0:8.7.0:9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG458	13062660_f1_1	6057	20160	915	305	YKR039W	783	6.2(10)-78	Saccharomyces cerevisiae	[ui:ykr039w] [pn:general amino acid permease:general amino-acid permease] [gn:gap1] [gtcfc:11.1:12.1:12.6] [keggfc:14.2] [sgdfc:1.1.3:7.4.0:8.7.0:9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4723	4879405_fl_1	6058	20161	1527	509	YKR039W	1023	2.2(10)-103	Saccharomyces cerevisiae	[ui:ykr039w] [pn:general amino acid permease:general amino-acid permease] [gn:gap1] [gtcfc:11.1:12.1:12.6] [keggfc:14.2] [sgdfc:1.1.3:7.4.0:8.7.0:9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4899	6147812_c2_9	6059	20162	345	115	YKR039W	108	2.8(10)-5	Saccharomyces cerevisiae	[ui:ykr039w] [pn:general amino acid permease:general amino-acid permease] [gn:gap1] [gtcfc:11.1:12.1:12.6] [keggfc:14.2] [sgdfc:1.1.3:7.4.0:8.7.0:9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
b1x18591.y	391899_c1_1	6060	20163	528	176	YKR039W	462	6.5(10)-44	Saccharomyces cerevisiae	[ui:ykr039w] [pn:general amino acid permease:general amino-acid permease] [gn:gap1] [gtcfc:11.1:12.1:12.6] [keggfc:14.2] [sgdfc:1.1.3:7.4.0:8.7.0:9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4208	25986017_fl_1	6061	20164	1734	578	YKR050W	871	3.1(10)-129	Saccharomyces cerevisiae	[ui:ykr050w] [pn:moderate-affinity potassium transport protein:potassium transport protein, low-affinity] [gn:trk2:rpd2] [gtcfc:12.5:11.1] [keggfc:14.2] [sgdfc:7.2.2:8.7.0:9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5487	16526511_f2_6	6062	20165	1341	447	YKR050W	391	1.1(10)-39	Saccharomyces cerevisiae	[ui:ykr050w] [pn:moderate-affinity potassium transport protein:potassium transport protein, low-affinity] [gn:trk2:rpd2] [gtcfc:12.5:11.1] [keggfc:14.2] [sgdfc:7.2.2:8.7.0:9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4679	25975752_f1_1	6063	20166	624	208	YKR093W	651	6.2(10)-64	Saccharomyces cerevisiae	[ui:ykr093w] [pn:peptide transporter:peptide transporter ptr2:peptide permease ptr2] [gn:ptr2:ykr413] [gtcfc:12.1:11.1] [keggfc:14.2] [sgdfc:7.11.0:8.8.0:9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4793	10976000_c2_11	6064	20167	963	321	YKR093W	780	1.3(10)-77	Saccharomyces cerevisiae	[ui:ykr093w] [pn:peptide transporter:peptide transporter ptr2:peptide permease ptr2] [gn:ptr2:ykr413] [gtcfc:12.1:11.1] [keggfc:14.2] [sgdfc:7.11.0:8.8.0:9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4946	15517080_c2_5	6065	20168	816	272	YLR081W	692	2.7(10)-68	Saccharomyces cerevisiae	[ui:ylr081w] [pn:galactose and glucose permease:galactose transporter:galactose permease] [gn:gal2:imp1] [gtcfc:12.2:11.1.1.6] [keggfc:14.2] [sgdfc:1.5.3.7.3.0:8.7.0:9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG1005	9886332_f1_1	6066	20169	372	124	YLR081W	157	1.5(10)-10	Saccharomyces cerevisiae	[ui:ylr081w] [pn:galactose and glucose permease:galactose transporter:galactose permease] [gn:gal2:imp1] [gtcfc:12.2:11.1:1.6] [keggfc:14.2] [sgdfc:1.5:3:7.3.0:8.7.0:9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2624	24225907_f2_2	6067	20170	534	178	YLR110C	138	1.3(10)-9	Saccharomyces cerevisiae	[ui:ylr110c] [pn:putative pseudogene] [gtcfc:11.1] [keggfc:14.2] [sgdfc:9.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2890	1291390_c1_3	6068	20171	1323	441	YLR110C	108	9.3(10)-6	Saccharomyces cerevisiae	[ui:ylr110c] [pn:putative pseudogene] [gtcfc:11.1] [keggfc:14.2] [sgdfc:9.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4658	6503752_f3_3	6069	20172	492	164	YLR229C	645	2.7(10)-63	Saccharomyces cerevisiae	[ui:ylr229c] [pn:gtp-binding protein of ras superfamily:cell division control protein 42] [gn:cdc42:sro2:l8083] [gtcfc:11.1:11.3:12.13:12.8:12.9] [keggfc:13.1:13.3] [sgdfc:3.2.0:3.3.0:3.8.0.9.1.0:10.1.2:10.2.3] [db:gtc-saccharomyces c
CONTIG4763	11881550_f3_5	6070	20173	198	66	YLR229C	247	4.0(10)-21	Saccharomyces cerevisiae	[ui:ylr229c] [pn:gtp-binding protein of ras superfamily:cell division control protein 42] [gn:cdc42:sro2:l8083] [gtcfc:11.1:11.3:12.13:12.8:12.9] [keggfc:13.1:13.3] [sgdfc:3.2.0:3.3.0:3.8.0.9.1.0:10.1.2: 10.2.3] [db:gtc-saccharomyces c

CONTIG1985	14878405_f2_2	6071	20174	762	254	YLR343W	627	2.2(10)-61	Saccharomyces cerevisiae	[ui:ylr343w] [pn:strong similarity to gas1p and c.albicans ph responsive protein] [gtcfc:11.1] [keggfc:14.2] [sgdfc:9.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3168	20600817_f1_1	6072	20175	1074	358	YLR343W	415	6.2(10)-39	Saccharomyces cerevisiae	[ui:ylr343w] [pn:strong similarity to gas1p and c.albicans ph responsive protein] [gtcfc:11.1] [keggfc:14.2] [sgdfc:9.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2344	12129432_c1_4	6073	20176	1755	585	YML123C	1014	1.5(10)-194	Saccharomyces cerevisiae	[ui:yml123c] [pn:high-affinity inorganic phosphate/h+ symporter:inorganic phosphate transporter pho84] [gn:pho84:ym7o56] [gtcfc:12.4.11.1:13.10] [keggfc:14.2] [sgdfc:1.4.3:1.8.2:7.2.3:7.3.0:8.7.0:9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG276	14886718_f3_1	6074	20177	573	191	YMR058W	577	4.2(10)-56	Saccharomyces cerevisiae	[ui:ymr058w] [pn:cell surface ferroxidase:iron transport multicopper oxidase] [gn:fet3:ym9796] [gtcfc:12.6:11.3] [keggfc:14.2] [sgdfc:1.8.1:8.7.0:9.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4427	4688293_c2_2	6075	20178	1827	609	YMR058W	1480	8.8(10)-152	Saccharomyces cerevisiae	[ui:ymr058w] [pn:cell surface ferroxidase:iron transport multicopper oxidase] [gn:fet3:ym9796] [gtcfc:12.6:11.3] [keggfc:14.2] [sgdfc:1.8.1:8.7.0:9.1.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4629	5351452_c3_9	6076	20179	963	321	YMR058W	910	2.2(10)-91	Saccharomyces cerevisiae	[ui:ymr058w] [pn:cell surface ferroxidase:iron transport multicopper oxidase] [gn:fet3:ym9796] [gtcfc:12.6:11.3] [keggfc:14.2] [sgdfc:1.8.1:8.7.0:9.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5726	25672061_c2_27	6077	20180	1728	576	YMR058W	1658	1.2(10)-170	Saccharomyces cerevisiae	[ui:ymr058w] [pn:cell surface ferroxidase:iron transport multicopper oxidase] [gn:fet3:ym9796] [gtcfc:12.6:11.3] [keggfc:14.2] [sgdfc:1.8.1:8.7.0:9.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG806	15041078_f1_1	6078	20181	1179	393	YMR058W	1093	9.0(10)-111	Saccharomyces cerevisiae	[ui:ymr058w] [pn:cell surface ferroxidase:iron transport multicopper oxidase] [gn:fet3:ym9796] [gtcfc:12.6:11.3] [keggfc:14.2] [sgdfc:1.8.1:8.7.0:9.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4895	14570426_f2_2	6079	20182	561	187	YMR183C	331	5.0(10)-30	Saccharomyces cerevisiae	[ui:ymr183c] [pn:involved in vesicle transport from golgi to plasma membrane:sso2 protein] [gn:sso2:ym8010] [gtcfc:12.6:11.1:12.10:12.16] [keggfc:14.2] [sgdfc:8.3.0:9.1.0] [db:gtc-saccharomyces cerevisiae]

CONTIG1375	206887_c1_3	6080	20183	750	250	YMR243C	494	2.7(10)-47	Saccharomyces cerevisiae	[ui:ymr243c] [pn:zinc- and cadmium resistance protein:zinc/cadmium resistance protein] [gn:zrc1:ym9408] [gtcfc:11.1:12.12:12.6] [keggfc:14.2] [sgdfc:1.8.1:7.2.1:8.7.0:9.1.0:11.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5794	24610312_f3_15	6081	20184	771	257	YMR243C	173	2.0(10)-21	Saccharomyces cerevisiae	[ui:ymr243c] [pn:zinc- and cadmium resistance protein:zinc/cadmium resistance protein] [gn:zrc1:ym9408] [gtcfc:11.1:12.12:12.6] [keggfc:14.2] [sgdfc:1.8.1:7.2.1:8.7.0:9.1.0:11.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2873	7291678_c1_6	6082	20185	735	245	YMR307W	776	3.5(10)-77	Saccharomyces cerevisiae	[ui:ymr307w] [pn:glycophospholipid-anchored surface glycoprotein:glycolipid anchored surface protein precursor:glycoprotein gp115] [gn:gas1:ggp1:ym9952] [gtcfc:11.1] [keggfc:14.2] [sgdfc:9.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2446	29320327_c3_9	6083	20186	1590	530	YMR317W	133	2.8(10)-5	Saccharomyces cerevisiae	[ui:ymr317w] [pn:similarity to mucins, glucan 1,4-alpha-glucosidase and exo-alpha-sialidase:hypothetical 113.1 kd protein in pre5-fet4 intergenic region] [gn:ymr316w:ym9924] [gtcfc:11.1] [keggfc:14.2] [sgdfc:9.1.0] [db:gtc-saccharomy

CONTIG3169	10547807_c3_2	6084	20187	1065	355	YMR317W	120	0.00036	Saccharomyces cerevisiae	[ui:ymr317w] [pn:similarity to mucins, glucan 1,4-alpha-glucosidase and exo-alpha-sialidase:hypothetical 113.1 kd protein in pre5-fet4 intergenic region] [gn:ymr316w:ym9924] [gtcfc:11.1] [sgdfc:9.1.0] [db:gtc-saccharomy
CONTIG2446	9821013_f3_4	6085	20188	597	199	YMR317W	104	0.00979	Saccharomyces cerevisiae	[ui:ymr317w] [pn:similarity to mucins, glucan 1,4-alpha-glucosidase and exo-alpha-sialidase:hypothetical 113.1 kd protein in pre5-fet4 intergenic region] [gn:ymr316w:ym9924] [gtcfc:11.1] [sgdfc:9.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4341	131306_f3_3	6086	20189	999	333	YNL291C	374	1.7(10)-34	Saccharomyces cerevisiae	[ui:ynl291c] [pn:involved in ca2+ influx during mating:mid1 protein] [gn:mid1:n0530] [gtcfc:11.1:12.9] [keggfc:14.2] [sgdfc:3.3.0:9.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4341	22318952_f1_1	6087	20190	738	246	YNL291C	448	2.0(10)-42	Saccharomyces cerevisiae	[ui:ynl291c] [pn:involved in ca2+ influx during mating:mid1 protein] [gn:mid1:n0530] [gtcfc:11.1:12.9] [keggfc:14.2] [sgdfc:3.3.0:9.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4258	35422500_c2_4	6088	20191	702	234	YNL268W	203	1.8(10)-15	Saccharomyces cerevisiae	[ui:ynl268w] [pn:lysine-specific high-affinity permease:lysine-specific permease] [gn:lyp1:n0790] [gtcfc:1.1.12.1:12.6] [keggfc:14.2] [sgdfc:1.1.3:7.4.0:8.7.0.9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG										
CONTIG5516	9787553_c3_17	6089	20192	432	144	YNL268W	150	9.3(10)-10	Saccharomyces cerevisiae	[ui:ynl268w] [pn:lysine-specific high-affinity permease:lysine-specific permease] [gn:lyp1:n0790] [gtcfc:11.1:12.1:12.6] [sgdfc:1.1.3:7.4.0:8.7.0:9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4856	35425753_c2_11	6090	20193	723	241	YNL142W	555	9.1(10)-54	Saccharomyces cerevisiae	[ui:ynl142w] [pn:high affinity low capacity ammonia permease:ammonium transporter mep2] [gn:mep2:n1207:n1820] [sgdfc:1.2.3:7.2.2:8.7.0:9.1.0:17.0.0] [gtcfc:12.5:11.1] [keggfc:14.2] [db:gtc-saccharomyces cerevisiae]
CONTIG3294	23885417_f3_1	6091	20194	231	77	YNL142W	123	5.5(10)-7	Saccharomyces cerevisiae	[ui:ynl142w] [pn:high affinity low capacity ammonia permease:ammonium transporter mep2] [gn:mep2:n1207:n1820] [gtcfc:12.5:11.1] [sgdfc:1.2.3:7.2.2:8.7.0:9.1.0:17.0.0] [keggfc:14.2] [db:gtc-saccharomyces cerevisiae]
CONTIG5673	23944050_f3_22	6092	20195	387	129	YNL142W	297	5.7(10)-26	Saccharomyces cerevisiae	[ui:ynl142w] [pn:high affinity low capacity ammonia permease:ammonium transporter mep2] [gn:mep2:n1207:n1820] [gtcfc:12.5:11.1] [keggfc:14.2] [sgdfc:1.2.3:7.2.2:8.7.0:9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2519	972775_c2_3	6093	20196	492	164	YNR044W	92	0.0019	Saccharomyces cerevisiae	[ui:ynr044w] [pn:a-agglutinin anchor subunit:a-agglutinin attachment subunit precursor] [gn:agai:n3431] [gtcfc:11.1:12.9] [keggfc:14.2] [sgdfc:3.3.0:9.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3537	7119442_f2_1	6094	20197	2055	685	YNR044W	177	4.2(10)-10	Saccharomyces cerevisiae	[ui:ynr044w] [pn:a-agglutinin anchor subunit:a-agglutinin attachment subunit precursor] [gn:agai:n3431] [gtcfc:11.1:12.9] [keggfc:14.2] [sgdfc:3.3.0:9.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3914	16438431_f2_1	6095	20198	666	222	YNR044W	93	0.11	Saccharomyces cerevisiae	[ui:ynr044w] [pn:a-agglutinin anchor subunit:a-agglutinin attachment subunit precursor] [gn:agai:n3431] [gtcfc:11.1:12.9] [keggfc:14.2] [sgdfc:3.3.0:9.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4784	19707027_f2_5	6096	20199	1305	435	YNR044W	104	0.02199	Saccharomyces cerevisiae	[ui:ynr044w] [pn:a-agglutinin anchor subunit:a-agglutinin attachment subunit precursor] [gn:agai:n3431] [gtcfc:11.1:12.9] [keggfc:14.2] [sgdfc:3.3.0:9.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4984	979811_c2_10	6097	20200	666	222	YNR044W	98	0.033	Saccharomyces cerevisiae	[ui:ynr044w] [pn:a-agglutinin anchor subunit:a-agglutinin attachment subunit precursor] [gn:agai:n3431] [gtcfc:11.1:12.9] [keggfc:14.2] [sgdfc:3.3.0:9.1.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5771	7223407_f2_14	6098	20201	2118	706	YNR044W	122	0.00054	Saccharomyces cerevisiae	[ui:ynr044w] [pn:a-agglutinin anchor subunit:a-agglutinin attachment subunit precursor] [gn:agal:n343l] [gtcfc:11.1:12.9] [keggfc:14.2] [sgdfc:3.3.0.9.1.0] [db:gtc-saccharomyces cerevisiae]
b2x16511.y	19800668_c3_3	6099	20202	645	215	YNR044W	124	1.6(10)-5	Saccharomyces cerevisiae	[ui:ynr044w] [pn:a-agglutinin anchor subunit:a-agglutinin attachment subunit precursor] [gn:agal:n343l] [gtcfc:11.1:12.9] [keggfc:14.2] [sgdfc:3.3.0.9.1.0] [db:gtc-saccharomyces cerevisiae]
b1x11922.y	12225262_f3_2	6100	20203	213	71	YOL103W	125	4.5(10)-7	Saccharomyces cerevisiae	[ui:yol103w] [pn:myo-inositol permease, minor:myo-inositol transporter2] [gn:itr2:hrb612] [gtcfc:12.2:11.1:8.2] [keggfc:14.2] [sgdfc:1.5.3:7.3.0:8.7.0.9.1.0.17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5391	22269681_f2_7	6101	20204	1365	455	YOL030W	727	5.5(10)-72	Saccharomyces cerevisiae	[ui:yol030w] [pn:strong similarity to glycoprotein gas1] [gtcfc:11.1] [keggfc:14.2] [sgdfc:9.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5798	14082032_c1_28	6102	20205	1458	486	YOL030W	1139	1.2(10)-115	Saccharomyces cerevisiae	[ui:yol030w] [pn:strong similarity to glycoprotein gas1] [gtcfc:11.1] [keggfc:14.2] [sgdfc:9.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1804	2165682_f3_1	6103	20206	357	119	YOR153W	231	7.0(10)-18	Saccharomyces cerevisiae	[ui:yor153w] [pn:pleiotropic drug resistance protein:suppressor of toxicity of sporidesmin] [gn:pdr5:sts1:ydr1:lem1] [gtcfc:11.1:12.12:12.6] [keggfc:14.2] [sgdfc:7.9.0:9.1.0:11.3.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2003	19730018_c2_1	6104	20207	1476	492	YOR153W	1295	3.5(10)-132	Saccharomyces cerevisiae	[ui:yor153w] [pn:pleiotropic drug resistance protein:suppressor of toxicity of sporidesmin] [gn:pdr5:sts1:ydr1:lem1] [gtcfc:11.1:12.12.12.6] [keggfc:14.2] [sgdfc:7.9.0:9.1.0:11.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3893	3912700_c1_4	6105	20208	213	71	YOR153W	136	9.1(10)-8	Saccharomyces cerevisiae	[ui:yor153w] [pn:pleiotropic drug resistance protein:suppressor of toxicity of sporidesmin] [gn:pdr5:sts1:ydr1:lem1] [gtcfc:11.1:12.12.12.6] [keggfc:14.2] [sgdfc:7.9.0:9.1.0:11.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3893	24409837_c3_5	6106	20209	1182	394	YOR153W	1064	2.2(10)-107	Saccharomyces cerevisiae	[ui:yor153w] [pn:pleiotropic drug resistance protein:suppressor of toxicity of sporidesmin] [gn:pdr5:sts1:ydr1:lem1] [gtcfc:11.1:12.12.12.6] [keggfc:14.2] [sgdfc:7.9.0:9.1.0:11.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4325	10944062_c2_4	6107	20210	2085	695	YOR153W	1839	7.9(10)-190	Saccharomyces cerevisiae	[ui:yor153w] [pn:pleiotropic drug resistance protein:suppressor of toxicity of sporidesmin] [gn:pdr5:sts1:ydr1:lem1] [gtcfc:11.1:12.12.12.6] [keggfc:14.2] [sgdfc:7.9.0:9.1.0:11.3.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4513	9776886_c2_10	6108	20211	1878	626	YOR153W	1513	2.7(10)-155	Saccharomyces cerevisiae	[ui:yor153w] [pn:pleiotropic drug resistance protein:suppressor of toxicity of sporidesmin] [gn:pdr5:sts1:ydr1:lem1] [gtcfc:11.1:12.12.12.6] [keggfc:14.2] [sgdfc:7.9.0:9.1.0:11.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5733	3440 7687_f3_14	6109	20212	2223	741	YOR153W	1927	3.7(10)-199	Saccharomyces cerevisiae	[ui:yor153w] [pn:pleiotropic drug resistance protein:suppressor of toxicity of sporidesmin] [gn:pdr5:sts1:ydr1:lem1] [gtcfc:11.1:12.12.12.6] [keggfc:14.2] [sgdfc:7.9.0:9.1.0:11.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3215	1056349_c1_4	6110	20213	723	241	YOR153W	180	1.8(10)-12	Saccharomyces cerevisiae	[ui:yor153w] [pn:pleiotropic drug resistance protein:suppressor of toxicity of sporidesmin] [gn:pdr5:sts1:ydr1:lem1] [gtcfc:11.1:12.12.12.6] [keggfc:14.2] [sgdfc:7.9.0:9.1.0:11.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4724	2353769_c1_5	6111	20214	1809	603	YOR153W	1786	3.2(10)-184	Saccharomyces cerevisiae	[ui:yor153w] [pn:pleiotropic drug resistance protein:suppressor of toxicity of sporidesmin] [gn:pdr5:sts1:ydr1:lem1] [gtcfc:11.1:12.12.12.6] [keggfc:14.2] [sgdfc:7.9.0:9.1.0:11.3.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5164	30548253_f3_4	6112	20215	1215	405	YOR212W	371	1.8(10)-68	Saccharomyces cerevisiae	[ui:yor212w] [pn:gtp-binding protein beta subunit of the pheromone pathway:guanine nucleotide-binding protein beta subunit] [gn:ste4:yor50-2] [gtcfc:11.1:11.3:12.13:12.8:12.9] [keggfc:13.1] [sgdfc:3.3.0:9.1.0:10.1.2] [db:gtc-saccharom
CONTIG5164	20157626_f1_2	6113	20216	303	101	YOR212W	212	8.3(10)-17	Saccharomyces cerevisiae	[ui:yor212w] [pn:gtp-binding protein beta subunit of the pheromone pathway:guanine nucleotide-binding protein beta subunit] [gn:ste4:yor50-2] [gtcfc:11.1:11.3:12.13:12.8:12.9] [keggfc:13.1] [sgdfc:3.3.0:9.1.0:10.1.2] [db:gtc-saccharom
CONTIG1479	10437713_f1_1	6114	20217	867	289	YOR328W	627	4.5(10)-60	Saccharomyces cerevisiae	[ui:yor328w] [pn:strong similarity to abc transporter proteins:atp-dependent permease] [gn:pdr10] [gtcfc:12.6:11.1] [keggfc:14.2] [sgdfc:7.9.0:9.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5548	962511_f3_7	6115	20218	1452	484	YOR348C	613	6.5(10)-60	Saccharomyces cerevisiae	[ui:yor348c] [pn:proline and gamma-aminobutyrate permease:proline-specific permease] [gn:put4:o63345] [gtcfc:11.1:12.11:12.6] [keggfc:14.2] [sgdfc:1.1.3:7.4.0:8.7.0:9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG	ID								Organism	Description
CONTIG1316	20706716_f1_1	6116	20219	1185	395	YPL176C	520	1.1(10)-49	Saccharomyces cerevisiae	[ui:ypl176c] [pn:similarity to chinese hamster transferrin receptor protein] [gtcfc:11.1.14.3] [keggfc:14.2] [sgdfc:9.1.0:13.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2272	11172192_f2_1	6117	20220	183	61	YPL036W	207	1.3(10)-15	Saccharomyces cerevisiae	[ui:ypl036w] [pn:h+-transporting p-type atpase 2:plasma membrane atpase 2:proton pump] [gn:pma2] [gtcfc:12.5:11.1] [ec:3.6.1.35] [keggfc:14.1] [sgdfc:1.8.2:7.2.2:7.8.0:9.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4917	3941881_c3_7	6118	20221	765	255	YPR124W	155	1.3(10)-10	Saccharomyces cerevisiae	[ui:ypr124w] [pn:copper transport protein:copper tranport protein ctr1:copper transporter 1] [gn:ctr1:p9642] [gtcfc:12.6:11.1] [keggfc:14.2] [sgdfc:1.8.1:7.2.1:8.7.0:9.1.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3371	3917188_c2_6	6119	20222	1317	439	YGR217W	696	3.5(10)-67	Saccharomyces cerevisiae	[ui:ygr217w] [pn:calcium channel protein:hypothetical 234.6 kd protein in gpl1-crm1 intergenic region] [gn:cch1:g8501] [gtcfc:11.3:12.6] [keggfc:14.2] [sgdfc:1.8.2:7.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG977	3380130_f1_1	6120	20223	1158	386	YGR217W	769	5.7(10)-75	Saccharomyces cerevisiae	[ui:ygr217w] [pn:calcium channel protein:hypothetical 234.6 kd protein in gpl1-crm1 intergenic region] [gn:cch1:g8501] [gtcfc:11.3:12.6] [keggfc:14.2] [sgdfc:1.8.2:7.1.0] [db:gtc-saccharomyces cerevisiae]

b1x18140.x	22447143_f3_2	6121	20224	804	268	YGR217W	328	5.0(10)-28	Saccharomyces cerevisiae	[ui:ygr217w] [pn:calcium channel protein:hypothetical 234.6 kd protein in gpi1-crm1 intergenic region] [gn:cch1:g8501] [gtcfc:11.3:12.6] [keggfc:14.2] [sgdfc:1.8.2:7.1.0] [db:gtc-saccharomyces cerevisiae]
b1x18140.y	26348125_c3_3	6122	20225	699	233	YGR217W	99	0.1	Saccharomyces cerevisiae	[ui:ygr217w] [pn:calcium channel protein:hypothetical 234.6 kd protein in gpi1-crm1 intergenic region] [gn:cch1:g8501] [gtcfc:11.3:12.6] [keggfc:14.2] [sgdfc:1.8.2:7.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5158	13985377_f2_4	6123	20226	375	125	YLL053C	330	6.4(10)-30	Saccharomyces cerevisiae	[ui:yll053c] [pn:similarity to water channel proteins] [gtcfc:11.3:12.6] [keggfc:14.2] [sgdfc:7.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4438	9814667_c3_9	6124	20227	1134	378	YHR146W	145	3.0(10)-7	Saccharomyces cerevisiae	[ui:yhr146w] [pn:similarity to pheromone-response g-protein mdg1p:hypothetical 51.1 kd protein in dcd1-mrpl6 intergenic region] [gtcfc:11.3:12.13:12.9] [keggfc:14.2] [sgdfc:3.3.0:10.1.2] [db:gtc-saccharomyces cerevisiae]
CONTIG4396	406591_f3_7	6125	20228	1239	413	YNL173C	220	2.0(10)-16	Saccharomyces cerevisiae	[ui:ynl173c] [pn:gtp-binding protein of the pheromone-response pathway:hypothetical 40.3 kd protein in rps3-psd1 intergenic region] [gn:mdg1:n1673] [gtcfc:11.3:12.13:12.9] [keggfc:14.2] [sgdfc:3.3.0:10.1.2] [db:gtc-saccharomyces cerev

CONTIG3561	5994582_f3_2	6126	20229	1671	557	YCR032W	791	3.0(10)-77	Saccharomyces cerevisiae	[ui:ycr032w] [pn:similarity to human cdc4l protein:hypothetical 251.0 kd protein in cry1-gns1 intergenic region] [gn:ycr32w:ycr591:ycr601] [gtcfc:12.10] [keggfc:14.2] [sgdfc:8.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4746	892153_c3_14	6127	20230	2970	990	YCR032W	131	0.00032	Saccharomyces cerevisiae	[ui:ycr032w] [pn:similarity to human cdc4l protein:hypothetical 251.0 kd protein in cry1-gns1 intergenic region] [gn:ycr32w:ycr591:ycr601] [gtcfc:12.10] [keggfc:14.2] [sgdfc:8.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3820	22039002_f1_1	6128	20231	1134	378	YDR129C	1396	7.0(10)-143	Saccharomyces cerevisiae	[ui:ydr129c] [pn:actin filament bundling protein, fimbrin:fimbrin:abp67] [gn:sac6:yd9302] [gtcfc:12.10:12.16:12.6:12.8] [db:gtc-saccharomyces cerevisiae]
b9x12817.x	12206280_f3_2	6129	20232	552	184	YDR129C	511	4.2(10)-49	Saccharomyces cerevisiae	[ui:ydr129c] [pn:actin filament bundling protein, fimbrin:fimbrin:abp67] [gn:sac6:yd9302] [gtcfc:12.10:12.16:12.6:12.8] [keggfc:14.2] [sgdfc:3.2.0:8.6.0:8.7.0:9.3.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4074	593979l_f3_2	6130	20233	1323	441	YDR164C	404	5.7(10)-50	Saccharomyces cerevisiae	[ui:ydr164c] [pn:protein transport protein sec1] [gn:sec1:yd8358] [sgtcfc:12.6-12.10] [keggfc:14.2] [sgdfc:8.6.0:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5623	21675306_f2_3	6131	20234	2919	973	YDR166C	167	4.4(10)-13	Saccharomyces cerevisiae	[ui:ydr166c] [pn:required for exocytosis] [gn:sec5] [gtcfc:12.10] [keggfc:14.2] [sgdfc:8.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5659	12897311_f1_5	6132	20235	1596	532	YER006W	1169	7.0(10)-132	Saccharomyces cerevisiae	[ui:yer006w] [pn:similarity to p.polycephalum myosin-related protein mlpa:hypothetical gtp-binding protein in pmi40-pac2 intergenic region] [gtcfc:12.10] [keggfc:14.2] [sgdfc:8.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4180	23475013_f1_1	6133	20236	1008	336	YER008C	110	0.0082	Saccharomyces cerevisiae	[ui:yer008c] [pn:secretory pathway protein:sec3 protein:psl1 protein] [gn:sec3:psl1] [gtcfc:12.10] [keggfc:14.2] [sgdfc:8.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4682	4085302_c2_9	6134	20237	1971	657	YER008C	195	8.9(10)-14	Saccharomyces cerevisiae	[ui:yer008c] [pn:secretory pathway protein:sec3 protein:psl1 protein] [gn:sec3:psl1] [gtcfc:12.10] [keggfc:14.2] [sgdfc:8.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2338	10156251_f1_2	6135	20238	1269	423	YER136W	1450	1.3(10)-148	Saccharomyces cerevisiae	[ui:yer136w] [pn:gdp dissociation inhibitor:secretory pathway gdp dissociation inhibitor] [gn:gdi1:sec19] [gtcfc:12.10] [keggfc:14.2] [sgdfc:8.6.0:9.2.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3542	23835456_f3_5	6136	20239	240	80	YER136W	243	3.7(10)-20	Saccharomyces cerevisiae	[ui:yer136w] [pn:gdp dissociation inhibitor:secretory pathway gdp dissociation inhibitor] [gn:gdi1:sec19] [gtcfc:12.10] [keggfc:14.2] [sgdfc:8.6.0.9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1785	14219066_f2_4	6137	20240	513	171	YIL068C	134	7.0(10)-8	Saccharomyces cerevisiae	[ui:yil068c] [pn:protein transport protein] [gn:sec6] [gtcfc:12.6:12.10] [keggfc:14.2] [sgdfc:8.6.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG910	19697067_f2_1	6138	20241	1152	384	YIL068C	154	8.9(10)-8	Saccharomyces cerevisiae	[ui:yil068c] [pn:protein transport protein] [gn:sec6] [gtcfc:12.6:12.10] [keggfc:14.2] [sgdfc:8.6.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5737	33707175_f1_1	6139	20242	1839	613	YJL085W	206	1.8(10)-13	Saccharomyces cerevisiae	[ui:yjl085w] [pn:70 kda exocyst component protein:hypothetical 71.3 kd protein in trl1-act3 intergenic region] [gn:exo70:j0932] [gtcfc:14.1] [keggfc:14.2] [sgdfc:8.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4522	29382768_c3_7	6140	20243	1569	523	YJL044C	96	0.13	Saccharomyces cerevisiae	[ui:yjl044c] [pn:gtpase-activating protein:gtpase-activating protein of ypt6] [gn:gyp6;j1202] [gtcfc:12.10] [keggfc:14.2] [sgdfc:8.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2964	7070336_c3_1	6141	20244	1752	584	YKL212W	1297	2.2(10)-132	Saccharomyces cerevisiae	[ui:ykl212w] [pn:recessive suppressor of secretory defect] [gn:rsd1:sac1] [gtcfc:12.10:12.16] [keggfc:14.2] [sgdfc:8.6.0.9.4.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5676	12145181_f2_7	6142	20245	2385	795	580	1.6(10)-103	Saccharomyces cerevisiae	[ui:ylr166c] [pn:required for exocytosis] [gn:sec10] [gtcfc:12.10] [keggfc:14.2] [sgdfc:8.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2088	25657775_c1_4	6143	20246	387	129	209	4.2(10)-17	Saccharomyces cerevisiae	[ui:ylr250w] [pn:secretory protein:protein ssp120 precursor] [gn:ssp120:l9672] [keggfc:14.2] [sgdfc:8.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5628	35351442_f3_7	6144	20247	285	95	171	4.5(10)-13	Saccharomyces cerevisiae	[ui:ylr250w] [pn:secretory protein:protein ssp120 precursor] [gn:ssp120:l9672] [keggfc:14.2] [sgdfc:8.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1601	26692655_c3_4	6145	20248	576	192	286	6.2(10)-24	Saccharomyces cerevisiae	[ui:ymr308c] [pn:protein secretion enhancer:protein secretion enhancer 1] [gn:pse1:ym9952] [gtcfc:12.10] [keggfc:14.2] [sgdfc:8.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4469	20523407_c3_9	6146	20249	1710	570	1423	9.5(10)-146	Saccharomyces cerevisiae	[ui:ymr308c] [pn:protein secretion enhancer:protein secretion enhancer 1] [gn:pse1:ym9952] [gtcfc:12.10] [keggfc:14.2] [sgdfc:8.6.0] [db:gtc-saccharomyces cerevisiae]
b1x11465.y	5948958_f1_1	6147	20250	690	230	465	4.2(10)-43	Saccharomyces cerevisiae	[ui:ymr308c] [pn:protein secretion enhancer:protein secretion enhancer 1] [gn:pse1:ym9952] [gtcfc:12.10] [keggfc:14.2] [sgdfc:8.6.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2985	29298752_c2_6	6148	20251	924	308	YNL325C	112	0.00209	Saccharomyces cerevisiae	[ui:ynl325c] [pn:suppressor of sac1 mutation:hypothetical 101.7 kd protein in egt2-kre1 intergenic region] [gn:n0330] [gtcfc:14.2] [sgdfc:8.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2985	36114765_c1_5	6149	20252	954	318	YNL325C	917	4.0(10)-92	Saccharomyces cerevisiae	[ui:ynl325c] [pn:suppressor of sac1 mutation:hypothetical 101.7 kd protein in egt2-kre1 intergenic region] [gn:n0330] [gtcfc:14.1] [keggfc:14.2] [sgdfc:8.6.0] [db:gtc-saccharomyces cerevisiae]
b1x17759.y	36586066_c3_1	6150	20253	477	159	YNL325C	281	1.5(10)-23	Saccharomyces cerevisiae	[ui:ynl325c] [pn:suppressor of sac1 mutation:hypothetical 101.7 kd protein in egt2-kre1 intergenic region] [gn:n0330] [gtcfc:14.1] [keggfc:14.2] [sgdfc:8.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5643	10720437_f1_1	6151	20254	780	260	YNL036W	344	2.1(10)-31	Saccharomyces cerevisiae	[ui:ynl036w] [pn:involved in non-classical protein export pathway:non-classical protein export protein nce3] [gn:nce3:n2695] [gtcfc:12.10] [keggfc:14.2]
CONTIG5697	24097192_c1_16	6152	20255	552	184	YNR049C	114	8.1(10)-7	Saccharomyces cerevisiae	[ui:ynr049c] [pn:secretion protein, multicopy suppressor of sec1:mso1 protein] [gn:mso1:n3457] [gtcfc:12.10] [keggfc:14.2] [sgdfc:8.6.0:9.2.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5397	21650312_f1_2	6153	20256	1575	525	YOR307C	677	1.1(10)-66	Saccharomyces cerevisiae	[ui:yor307c] [pn:secretory pathway protein:sly41 protein] [gn:sly41:o5663] [gtcfc:12.10] [keggfc:14.2] [sgdfc:8.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4631	10603402_c2_9	6154	20257	567	189	YOR326W	654	6.0(10)-63	Saccharomyces cerevisiae	[ui:yor326w] [pn:myosin heavy chain:myosin-2 isoform] [gn:myo2:cdc66:o6167] [gtcfc:12.10:12.16:12.8] [keggfc:14.2] [sgdfc:3.2.0:8.3.0:8.6.0:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4823	23938942_c3_11	6155	20258	3783	1261	YOR326W	2317	1.8(10)-240	Saccharomyces cerevisiae	[ui:yor326w] [pn:myosin heavy chain:myosin-2 isoform] [gn:myo2:cdc66:o6167] [gtcfc:12.10:12.16:12.8] [keggfc:14.2] [sgdfc:3.2.0:8.3.0:8.6.0:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4917	1064138_f3_2	6156	20259	2439	813	YPR055W	180	9.5(10)-35	Saccharomyces cerevisiae	[ui:ypr055w] [pn:protein transport protein:protein transport protein sec8] [gn:sec8:yp9499] [gtcfc:12.6:12.10] [keggfc:14.2] [sgdfc:8.6.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4917	2350017_f3_3	6157	20260	378	126	YPR055W	143	1.1(10)-8	Saccharomyces cerevisiae	[ui:ypr055w] [pn:protein transport protein:protein transport protein sec8] [gn:sec8:yp9499] [gtcfc:12.6:12.10] [keggfc:14.2] [sgdfc:8.6.0:9.2.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3891	29393826_c1_6	6158	20261	444	YPR149W	165	2.0(10)-12	Saccharomyces cerevisiae	[ui:ypr149w] [pn:involved in non-classical protein export pathway] [gn:nce2] [gtcfc:12.10] [keggfc:14.2] [sgdfc:8.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5307	19531308_c2_8	6159	20262	918	YBL050W	582	1.3(10)-56	Saccharomyces cerevisiae	[ui:ybl050w] [pn:transport vesicle fusion protein:vesicular-fusion protein sec17] [gn:sec17:ybl0505] [gtcfc:12.6:12.10:12.16] [keggfc:14.2] [sgdfc:8.3.0:9.0] [db:gtc-saccharomyces cerevisiae]
b3x13161.x	11182317_f1_1	6160	20263	489	YDL195W	359	1.3(10)-31	Saccharomyces cerevisiae	[ui:ydl195w] [pn:component of the copii coat of er-golgi vesicles:web1 protein:protein transport protein sec31] [gn:web1:sec31:d1229] [gtcfc:12.6:12.10:12.16] [keggfc:14.2] [sgdfc:8.3.0:9.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5234	6674055_c2_14	6161	20264	558	YDL192W	764	6.5(10)-76	Saccharomyces cerevisiae	[ui:ydl192w] [pn:gtp-binding protein of the arf family:adp-ribosylation factor 1] [gn:arf1:d1244] [gtcfc:12.10:12.16] [keggfc:14.2] [db:gtc-saccharomyces cerevisiae]
CONTIG5563	36362925_c3_27	6162	20265	321	YDL192W	410	2.1(10)-38	Saccharomyces cerevisiae	[ui:ydl192w] [pn:gtp-binding protein of the arf family:adp-ribosylation factor 1] [gn:arf1:d1244] [gtcfc:12.10:12.16] [keggfc:14.2] [sgdfc:6.4.0:8.3.0:9.4.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2659	23439003_c2_2	6163	20266	1350	450	YDL145C	752	1.2(10)-85	Saccharomyces cerevisiae	[ui:ydl145c] [pn:coatomer complex alpha chain of secretory pathway vesicles:coatomer alpha subunit:alpha-coat protein:alpha-cop] [gn:ret1:d1578] [gtcfc:12.10:12.16] [keggfc:14.2] [sgdfc:8.3.0:9.9.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4447	4328801_f3_3	6164	20267	2187	729	YDL145C	2630	1.2(10)-273	Saccharomyces cerevisiae	[ui:ydl145c] [pn:coatomer complex alpha chain of secretory pathway vesicles:coatomer alpha subunit:alpha-coat protein:alpha-cop] [gn:ret1:d1578] [gtcfc:12.10:12.16] [keggfc:14.2] [sgdfc:8.3.0:9.9.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5563	4866425_c3_28	6165	20268	204	68	YDL137W	250	1.8(10)-21	Saccharomyces cerevisiae	[ui:ydl137w] [pn:gtp-binding protein of the arf family:adp-ribosylation factor 2] [gn:arf2:d2165] [gtcfc:12.10:12.16] [keggfc:14.2] [sgdfc:6.4.0:8.3.0:9.9.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2554	2156312_c1_2	6166	20269	1245	415	YDL058W	91	0.77	Saccharomyces cerevisiae	[ui:ydl058w] [pn:intracellular protein transport protein:intracellular protein transport protein uso1] [gn:uso1:int1] [gtcfc:12.6:12.10:12.16] [keggfc:14.2] [sgdfc:8.3.0:9.4.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2678	964037_c3_7	6167	20270	1548	516	YDL058W	132	6.5(10)-5	Saccharomyces cerevisiae	[ui:ydl058w] [pn:intracellular protein transport protein:intracellular protein transport protein usol] [gn:usol:intl] [gtcfc:12.6:12.10-12.16] [keggfc:14.2] [sgdfc:8.3.0-9.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4025	3944642_fl_1	6168	20271	1020	340	YDL058W	160	2.7(10)-9	Saccharomyces cerevisiae	[ui:ydl058w] [pn:intracellular protein transport protein:intracellular protein transport protein usol] [gn:usol:intl] [gtcfc:12.6:12.10-12.16] [keggfc:14.2] [sgdfc:8.3.0-9.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4561	19647768_c1_7	6169	20272	2535	845	YDL058W	157	1.3(10)-7	Saccharomyces cerevisiae	[ui:ydl058w] [pn:intracellular protein transport protein:intracellular protein transport protein usol] [gn:usol:intl] [gtcfc:12.6:12.10-12.16] [keggfc:14.2] [sgdfc:8.3.0-9.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4748	34554182_f3_6	6170	20273	480	160	YDL058W	435	1.7(10)-39	Saccharomyces cerevisiae	[ui:ydl058w] [pn:intracellular protein transport protein:intracellular protein transport protein usol] [gn:usol:intl] [gtcfc:12.6:12.10-12.16] [keggfc:14.2] [sgdfc:8.3.0-9.4.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4748	2212527_f3_7	6171	20274	723	241	YDL058W	421	5.2(10)-38	Saccharomyces cerevisiae	[ui:ydl058w] [pn:intracellular protein transport protein:intracellular protein transport protein usol] [gn:usol:int1] [gtcfc:12.6:12.10-12.16] [keggfc:14.2] [sgdfc:8.3.0-9.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4925	31463538_f2_2	6172	20275	1893	631	YDL058W	206	8.0(10)-13	Saccharomyces cerevisiae	[ui:ydl058w] [pn:intracellular protein transport protein:intracellular protein transport protein usol] [gn:usol:int1] [gtcfc:12.6:12.10-12.16] [keggfc:14.2] [sgdfc:8.3.0-9.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5390	860677_c3_18	6173	20276	2454	818	YDL058W	142	8.9(10)-6	Saccharomyces cerevisiae	[ui:ydl058w] [pn:intracellular protein transport protein:intracellular protein transport protein usol] [gn:usol:int1] [gtcfc:12.6:12.10-12.16] [keggfc:14.2] [sgdfc:8.3.0-9.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5559	50000_c1_15	6174	20277	1827	609	YDL058W	117	0.00459	Saccharomyces cerevisiae	[ui:ydl058w] [pn:intracellular protein transport protein:intracellular protein transport protein usol] [gn:usol:int1] [gtcfc:12.6:12.10-12.16] [keggfc:14.2] [sgdfc:8.3.0-9.4.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5652	33994130_f3_12	6175	20278	1977	659	YDL058W	179	1.2(10)-9	Saccharomyces cerevisiae	[ui:ydl058w] [pn:intracellular protein transport protein:intracellular protein transport protein uso1] [gn:uso1:int1] [gtcfc:12.6:12.10:12.16] [keggfc:14.2] [sgdfc:8.3.0:9.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5660	10425152_c1_17	6176	20279	1347	449	YDL058W	242	6.5(10)-17	Saccharomyces cerevisiae	[ui:ydl058w] [pn:intracellular protein transport protein:intracellular protein transport protein uso1] [gn:uso1:int1] [gtcfc:12.6:12.10:12.16] [keggfc:14.2] [sgdfc:8.3.0:9.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5700	36621337_f2_7	6177	20280	2241	747	YDL058W	110	0.024	Saccharomyces cerevisiae	[ui:ydl058w] [pn:intracellular protein transport protein:intracellular protein transport protein uso1] [gn:uso1:int1] [gtcfc:12.6:12.10:12.16] [keggfc:14.2] [sgdfc:8.3.0:9.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5758	32116327_c2_18	6178	20281	2433	811	YDL058W	298	2.1(10)-22	Saccharomyces cerevisiae	[ui:ydl058w] [pn:intracellular protein transport protein:intracellular protein transport protein uso1] [gn:uso1:int1] [gtcfc:12.6:12.10:12.16] [keggfc:14.2] [sgdfc:8.3.0:9.4.0] [db:gtc-saccharomyces cerevisiae]

b3x19231.y	22878150_f1_1	6179	20282	477	159	YDL058W	90	0.17	Saccharomyces cerevisiae	[ui:ydl058w] [pn:intracellular protein transport protein:intracellular protein transport protein uso1] [gn:uso1:int1] [gtcfc:12.6:12.10:12.16] [keggfc:14.2] [sgdfc:8.3.0:9.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1488	860799_c1_2	6180	20283	1152	384	YDL058W	93	0.60999	Saccharomyces cerevisiae	[ui:ydl058w] [pn:intracellular protein transport protein:intracellular protein transport protein uso1] [gn:uso1:int1] [gtcfc:12.6:12.10:12.16] [keggfc:14.2] [sgdfc:8.3.0:9.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5228	4385144_c2_8	6181	20284	3237	1079	YDL058W	766	1.8(10)-96	Saccharomyces cerevisiae	[ui:ydl058w] [pn:intracellular protein transport protein:intracellular protein transport protein uso1] [gn:uso1:int1] [gtcfc:12.6:12.10:12.16] [keggfc:14.2] [sgdfc:8.3.0:9.4.0] [db:gtc-saccharomyces cerevisiae]
b2x13809.x	26571937_c1_1	6182	20285	516	172	YDR107C	288	1.5(10)-24	Saccharomyces cerevisiae	[ui:ydr107c] [pn:strong similarity to emp70 protein] [gtcfc:12.10:12.16] [keggfc:14.2] [sgdfc:8.3.0:9.9.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4535	16048313_c1_5	6183	20286	1215	405	YDR170C	95	0.14	Saccharomyces cerevisiae	[ui:ydr170c] [pn:component of non-clathrin vesicle coat:protein transport protein] [gn:sec7] [gtcfc:12.6:12.10:12.16] [keggfc:14.2] [sgdfc:8.3.0:9.9.0] [db:gtc-saccharomyces cerevisiae]

b1x18043.x	23495188_c2_2	6184	20287	540	180	YDR170C	326	5.0(10)-29	Saccharomyces cerevisiae	[ui:ydr170c] [pn:component of non-clathrin vesicle coat:protein transport protein] [gn:sec7] [gtcfc:12.6:12.10:12.16] [keggfc:14.2] [sgdfc:8.3.0:9.9.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5794	10552186_c3_37	6185	20288	1938	646	YDR189W	1523	2.3(10)-156	Saccharomyces cerevisiae	[ui:ydr189w] [pn:hydrophilic suppressor of ypt1 and member of the sec1p family:sly1 protein] [gn:sly1:yd9395] [gtcfc:12.10:12.16] [keggfc:14.2] [sgdfc:8.3.0:9.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5526	23864032_f1_2	6186	20289	2889	963	YDR238C	2373	2.1(10)-246	Saccharomyces cerevisiae	[ui:ydr238c] [pn:coatomer complex beta chain of secretory pathway vesicles:coatomer beta subunit:beta-coat protein:beta-cop] [gn:sec26:yd8419] [gtcfc:12.10:12.16] [keggfc:14.2] [sgdfc:8.3.0:9.9.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5591	26250462_c1_9	6187	20290	1956	652	YEL022W	412	8.8(10)-43	Saccharomyces cerevisiae	[ui:yel022w] [pn:gdp/gtp exchange factor for arf:hypothetical 165.7 kd protein in rip1-ura3 intergenic region] [gn:gea2] [gtcfc:12.13] [keggfc:14.2] [sgdfc:8.3.0:9.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4437	20906375_f2_2	6188	20291	684	228	YFL038C	807	1.8(10)-80	Saccharomyces cerevisiae	[ui:yfl038c] [pn:gtp-binding protein of the rab family:gtp-binding protein ypt1] [gn:ypt1:yp2] [gtcfc:12.10:12.16] [keggfc:14.2] [sgdfc:8.3.0:9.4.0] [db:gtc-saccharomyces cerevisiae]

b3x12764.y	33363252_c3_2	6189	20292	504	168	YFL025C	243	2.2(10)-19	Saccharomyces cerevisiae	[ui:yfl025c] [pn:negative regulator of copii vesicle formation:hypothetical 117.8 kd protein in site2-frs2 intergenic region] [gn:bst1] [gtcfc:12.13] [keggfc:14.2] [sgdfc:8.3.0:9.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4023	4331311_c1_5	6190	20293	642	214	YFL005W	661	5.4(10)-65	Saccharomyces cerevisiae	[ui:yfl005w] [pn:gtp-binding protein of the ras superfamily:ras-related protein] [gn:sec4] [gtcfc:12.10:12.16] [keggfc:14.2] [sgdfc:8.3.0:9.9.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5218	6454378_c2_11	6191	20294	423	141	YFL005W	93	0.0015	Saccharomyces cerevisiae	[ui:yfl005w] [pn:gtp-binding protein of the ras superfamily:ras-related protein] [gn:sec4] [gtcfc:12.10:12.16] [keggfc:14.2] [sgdfc:8.3.0:9.9.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5633	19553200_c3_20	6192	20295	1767	589	YFR051C	451	4.7(10)-82	Saccharomyces cerevisiae	[ui:yfr051c] [pn:coatomer complex delta chain:coatomer delta subunit:delta-coat protein:delta-cop] [gn:ret2] [gtcfc:12.10:12.16] [keggfc:14.2] [sgdfc:8.3.0:9.9.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4965	11975878_c3_8	6193	20296	1359	453	YGL225W	861	3.3(10)-86	Saccharomyces cerevisiae	[ui:ygl225w] [pn:vanadate-resistance protein:vanadate resistance protein gog5/vrg4/van2] [gn:gog5:vrg4:van2] [gtcfc:12.10:12.16] [keggfc:14.2] [sgdfc:8.3.0:9.4.0] [db:gtc-saccharomyces cerevisiae]

CONTIG1396	33360718_f2_1	6194	20297	414	YGL210W	138	1.7(10)-38	Saccharomyces cerevisiae	[ui:ygl210w] [pn:small gtp-binding protein essential for golgi function:gtp-binding protein ypt32/ypt11] [gn:ypt32:ypt11] [gtcfc:12.10] [keggfc:14.2] [sgdfc:8.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1276	4382688_f1_1	6195	20298	639	YGL200C	598	2.5(10)-58	Saccharomyces cerevisiae	[ui:ygl200c] [pn:component of the copii-coated vesicles, 24 kda:endosomal p24b protein precursor:24 kd endomembrane protein:basic 24 kd late endocytic intermediate component] [gn:emp24:g1271] [gtcfc:12.10:12.16] [keggfc:14.2] [sgdfc:8
CONTIG379	33234688_f2_1	6196	20299	492	YGL167C	169	1.6(10)-11	Saccharomyces cerevisiae	[ui:ygl167c] [pn:ca2+-transporting p-type atpase:calcium-transporting atpase 1:golgi ca2+-atpase] [gn:pmr1:ssc1:bsd1:g1666] [gtcfc:12.5:12.10:12.16] [ec:3.6.1.38] [keggfc:14.1] [sgdfc:1.8.2:7.2.2:7.8.0:8.3.0.9.4.0] [db:gtc-saccharomyc
CONTIG3803	26609812_c3_7	6197	20300	1005	YGL167C	930	1.7(10)-93	Saccharomyces cerevisiae	[ui:ygl167c] [pn:ca2+-transporting p-type atpase:calcium-transporting atpase 1:golgi ca2+-atpase] [gn:pmr1:ssc1:bsd1:g1666] [gtcfc:12.5:12.10:12.16] [ec:3.6.1.38] [keggfc:14.1] [sgdfc:1.8.2:7.2.2:7.8.0:8.3.0:9.4.0] [db:gtc-saccharomyc

CONTIG4780	14167037_c2_9	6198	20301	225	75	YGL167C	110	3.2(10)-5	Saccharomyces cerevisiae	[ui:ygl167c] [pn:ca2+-transporting p-type atpase:calcium-transporting atpase 1:golgi ca2+-atpase] [gn:pmr1:sec1:bsd1:g1666] [ec:3.6.1.38] [keggfc:14.1] [sgdfc:1.8.2:7.2.2:7.8.0:8.3.0:9.4.0] [db:gtc-saccharomyc
CONTIG5017	32132212_c3_8	6199	20302	1158	386	YGL167C	836	1.5(10)-83	Saccharomyces cerevisiae	[ui:ygl167c] [pn:ca2+-transporting p-type atpase:calcium-transporting atpase 1:golgi ca2+-atpase] [gn:pmr1:sec1:bsd1:g1666] [ec:3.6.1.38] [keggfc:14.1] [sgdfc:1.8.2:7.2.2:7.8.0:8.3.0:9.4.0] [db:gtc-saccharomyc
CONTIG4235	20524127_c3_6	6200	20303	1443	481	YGL145W	121	0.00042	Saccharomyces cerevisiae	[ui:ygl145w] [pn:required for er to golgi transport:protein transport protein tip20] [gn:tip20:tip1] [gtcfc:12.6:12.10:12.16] [keggfc:14.2] [sgdfc:8.3.0:9.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3846	4884437_c3_2	6201	20304	1728	576	YGL137W	1848	8.8(10)-191	Saccharomyces cerevisiae	[ui:ygl137w] [pn:coatomer complex beta" chain:beta"-cop of secretory pathway vesicles:coatomer beta"-subunit:beta"-coat protein:beta"-cop] [gn:sec27:g2827] [gtcfc:12.10:12.16] [keggfc:14.2] [sgdfc:8.3.0:9.9.0] [db:gtc-saccharomyces c

CONTIG4593	7083401_c2_4	6202	20305	834	278	YGL137W	340	7.2(10)-30	Saccharomyces cerevisiae	[ui:ygl137w] [pn:coatomer complex beta" chain:beta"-cop of secretory pathway vesicles:coatomer beta" subunit:beta"-coat protein:beta"-cop] [gn:sec27:g2827] [gtcfc:12.10:12.16] [keggfc:14.2] [sgdfc:8.3.0:9.9.0] [db:gtc-saccharomyces c
CONTIG4500	21722675_f1_1	6203	20306	732	244	YGR167W	295	3.2(10)-26	Saccharomyces cerevisiae	[ui:ygr167w] [pn:clathrin light chain:clc] [gn:clc1] [gtcfc:12.10:12.6:12.8] [keggfc:14.2] [sgdfc:3.1.0:8.3.0:8.7.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4504	4862510_f2_1	6204	20307	483	161	YIL004C	129	1.3(10)-8	Saccharomyces cerevisiae	[ui:yil004c] [pn:protein transport protein:protein transport protein bet1:protein sly12] [gn:bet1:sly12:yia4c] [gtcfc:12.6:12.10:12.16] [keggfc:14.2] [sgdfc:8.3.0:9.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4702	25431318_c2_6	6205	20308	402	134	YKR068C	419	2.3(10)-39	Saccharomyces cerevisiae	[ui:ykr068c] [pn:involved in targeting and fusion of er to golgi transport vesicles:hypothetical 22.1 kd protein in ccp1-sis2 intergenic region] [gn:bet3] [gtcfc:12.6:12.10:12.16] [keggfc:14.2] [sgdfc:8.3.0] [db:gtc-saccharomyces cere
CONTIG3236	4151525_f1_1	6206	20309	570	190	YLR026C	280	1.3(10)-24	Saccharomyces cerevisiae	[ui:ylr026c] [pn:syntaxin:t-snare:integral membrane protein] [gn:sed5] [gtcfc:12.10:12.16] [keggfc:14.2] [sgdfc:8.3.0:9.4.0] [db:gtc-saccharomyces cerevisiae]

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CONTIG4698	10210151_c2_5	6207	20310	750	250	YLR078C	377	6.7(10)-35	Saccharomyces cerevisiae	[ui:ylr078c] [pn:weak similarity to synaptobrevin:v-snare:vesicular transport protein bos1] [gn:bos1:19449] [gtcfc:12.6.12.10:12.16] [keggfc:14.2] [sgdfc:8.3.0:9.9.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2154	398885_f2_3	6208	20311	726	242	YLR083C	656	1.8(10)-64	Saccharomyces cerevisiae	[ui:ylr083c] [pn:endosomal protein:endosomal p24a protein precursor:70 kd endomembrane protein:pheromone alpha-factor transporter:acidic 24 kd late endocytic intermediate component] [gn:emp70] [gtcfc:12.6:12.9:12.10-12.16] [keggfc:14.
b2x13809.x	15674131_c3_3	6209	20312	213	71	YLR083C	159	1.1(10)-10	Saccharomyces cerevisiae	[ui:ylr083c] [pn:endosomal protein:endosomal p24a protein precursor:70 kd endomembrane protein:pheromone alpha-factor transporter:acidic 24 kd late endocytic intermediate component] [gn:emp70] [gtcfc:12.6:12.9:12.10-12.16] [keggfc:14.
CONTIG5814	4412642_c3_63	6210	20313	843	281	YLR093C	149	9.1(10)-9	Saccharomyces cerevisiae	[ui:ylr093c] [pn:weak similarity to synaptobrevin] [gtcfc:12.10] [keggfc:14.2] [sgdfc:8.3.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5059	29345400_f2_2	6211	20314	912	304	YLR208W	798	1.6(10)-79	Saccharomyces cerevisiae	[ui:ylr208w] [pn:protein transport protein sec13] [gn:sec13:l8167] [gtcfc:12.6:12.10:12.16] [keggfc:14.2] [sgdfc:8.3.0:9.9.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5059	15735377_f2_3	6212	20315	228	76	YLR208W	291	8.6(10)-26	Saccharomyces cerevisiae	[ui:ylr208w] [pn:protein transport protein sec13] [gn:sec13:l8167] [gtcfc:12.6:12.10:12.16] [keggfc:14.2] [sgdfc:8.3.0:9.9.0] [db:gtc-saccharomyces cerevisiae]
b2x14395.y	12672062_f2_1	6213	20316	414	138	YLR262C	454	4.5(10)-43	Saccharomyces cerevisiae	[ui:ylr262c] [pn:gtp-binding protein of the rab family] [gn:ypt6] [gtcfc:12.10:12.16] [keggfc:14.2] [sgdfc:8.3.0:9.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5294	13084678_c1_9	6214	20317	345	115	YLR268W	198	6.2(10)-16	Saccharomyces cerevisiae	[ui:ylr268w] [pn:protein transport protein sec22:protein sly2] [gn:sec22:sly2:l8479] [gtcfc:12.6:12.10:12.13] [keggfc:14.2] [sgdfc:8.3.0:9.9.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5294	13865676_c3_13	6215	20318	378	126	YLR268W	280	1.3(10)-24	Saccharomyces cerevisiae	[ui:ylr268w] [pn:high copy suppressor of ypt1 null mutation:protein transport protein sec22:protein sly2] [gn:sec22:sly2:l8479] [gtcfc:12.6:12.10:12.13] [keggfc:14.2] [sgdfc:8.3.0:9.9.0] [db:gtc-saccharomyces cerevisiae]

CONTIG1382	9925053_c3_6	6216	20319	723	241	YML012W	539	4.5(10)-52	Saccharomyces cerevisiae	[ui:yml012w] [pn:component of the copii-coated vesicles, 25 kda:hypothetical 24.1 kd protein in ppz1-spt5 intergenic region precursor] [gn:erv25:ym9571] [gtcfc:12.10:12.16] [keggfc:14.2] [sgdfc:8.3.0:9.4.0] [db:gtc-saccharomyces cerev
CONTIG5218	4765925_c2_10	6217	20320	459	153	YML001W	123	6.7(10)-8	Saccharomyces cerevisiae	[ui:yml001w] [pn:gtp-binding protein of the rab family:gtp-binding protein ypt7] [gn:ypt7:vam4:ym8270] [gtcfc:12.10:12.16:12.6] [keggfc:14.2] [sgdfc:8.3.0:8.7.0:9.9.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5771	24414062_f1_4	6218	20321	1425	475	YNL287W	991	5.7(10)-100	Saccharomyces cerevisiae	[ui:ynl287w] [pn:coatomer complex gamma chain:gamma-cop of secretory pathway vesicles:coatomer gamma subunit:gamma-coat protein:gamma- cop] [gn:sec21:n0543] [gtcfc:12.10:12.16] [keggfc:14.2] [sgdfc:8.3.0:9.9.0] [db:gtc-saccharomyces c

CONTIG5771	34183137_f2_17	6219	20322	1209	403	YNL287W	765	5.0(10)-76	Saccharomyces cerevisiae	[ui:ynl287w] [pn:coatomer complex gamma chain:gamma-cop of secretory pathway vesicles:coatomer gamma subunit:gamma-coat protein:gamma- cop] [gn:sec21:n0543] [gtcfc:12.10:12.16] [keggfc:14.2] [sgdfc:8.3.0:9.0] [db:gtc-saccharomyces c
CONTIG4146	22837890_f2_3	6220	20323	561	187	YOR075W	152	1.8(10)-10	Saccharomyces cerevisiae	[ui:yor075w] [pn:syntaxin:t-snare of the er:protein] [gn:ufe1] [gtcfc:12.10:12.15:12.16:12.8] [keggfc:14.2] [sgdfc:3.1.0:3.4.0:8.3.0:9.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3096	789055_c2_3	6221	20324	513	171	YOR094W	502	3.7(10)-48	Saccharomyces cerevisiae	[ui:yor094w] [pn:adp-ribosylation factor 3] [gn:arf3:yor3172w] [gtcfc:12.10:12.16] [keggfc:14.2] [sgdfc:6.4.0:8.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4244	6750050_f3_5	6222	20325	564	188	YPL218W	682	3.2(10)-67	Saccharomyces cerevisiae	[ui:ypl218w] [pn:gtp-binding protein of the arf family:gtp-binding protein] [gn:sar1] [gtcfc:12.10:12.16] [keggfc:14.2] [sgdfc:8.3.0:9.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2371	20492010_f3_3	6223	20326	777	259	YPL085W	117	4.5(10)-8	Saccharomyces cerevisiae	[ui:ypl085w] [pn:multidomain vesicle coat protein] [gn:sec16] [gtcfc:12.10:12.16] [keggfc:14.2] [sgdfc:6.4.0:8.3.0:9.4.0:9.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5542	24632717_c1_14	6224	20327	570	190	YPL085W	141	4.0(10)-8	Saccharomyces cerevisiae	[ui:ypl085w] [pn:multidomain vesicle coat protein] [gn:sec16] [gtcfc:12.10:12.16] [keggfc:14.2] [sgdfc:6.4.0:8.3.0:9.4.0:9.9.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5542	203936_c2_18	6225	20328	2640	880	YPL085W	182	2.2(10)-11	Saccharomyces cerevisiae	[ui:ypl085w] [pn:multidomain vesicle coat protein] [gn:sec16] [gtcfc:12.10:12.16] [keggfc:14.2] [sgdfc:6.4.0:8.3.0:9.4.0:9.9.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3413	10585825_f3_3	6226	20329	354	118	YPL010W	212	2.0(10)-17	Saccharomyces cerevisiae	[ui:ypl010w] [pn:coatomer complex zeta chain:coatomer zeta subunit:zeta-coat protein:zeta-cop] [gn:ret3:lpa7w:yp8132] [gtcfc:12.10:12.16] [keggfc:14.2] [sgdfc:8.3.0:9.9.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3413	787757_f3_4	6227	20330	264	88	YPL010W	122	7.0(10)-8	Saccharomyces cerevisiae	[ui:ypl010w] [pn:coatomer complex zeta chain:coatomer zeta subunit:zeta-coat protein:zeta-cop] [gn:ret3:lpa7w:yp8132] [gtcfc:12.10:12.16] [keggfc:14.2] [sgdfc:8.3.0:9.9.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4477	23648437_f3_2	6228	20331	498	166	YPR017C	146	2.0(10)-10	Saccharomyces cerevisiae	[ui:ypr017c] [pn:gdp/gtp exchange factor for sec4p:protein] [gn:dss4] [gtcfc:12.10:12.16] [keggfc:14.2] [sgdfc:8.3.0:9.9.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3742	4766936_c1_8	6229	20332	864	288	YPR181C	759	2.2(10)-75	Saccharomyces cerevisiae	[ui:ypr181c] [pn:component of copii coat of er-golgi vesicles:protein transport protein sec23] [gn:sec23:p9705] [gtcfc:12.6:12.10.12.16] [keggfc:14.2] [sgdfc:8.3.0-9.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5369	14552287_f3_5	6230	20333	1956	652	YPR181C	407	7.2(10)-98	Saccharomyces cerevisiae	[ui:ypr181c] [pn:component of copii coat of er-golgi vesicles:protein transport protein sec23] [gn:sec23:p9705] [gtcfc:12.6:12.10.12.16] [keggfc:14.2] [sgdfc:8.3.0-9.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5369	20485688_f3_6	6231	20334	273	91	YPR181C	220	4.0(10)-17	Saccharomyces cerevisiae	[ui:ypr181c] [pn:component of copii coat of er-golgi vesicles:protein transport protein sec23] [gn:sec23:p9705] [gtcfc:12.6:12.10.12.16] [keggfc:14.2] [sgdfc:8.3.0-9.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5745	15835192_f3_7	6232	20335	1176	392	YPR181C	1256	4.7(10)-128	Saccharomyces cerevisiae	[ui:ypr181c] [pn:component of copii coat of er-golgi vesicles:protein transport protein sec23] [gn:sec23:p9705] [gtcfc:12.6:12.10.12.16] [keggfc:14.2] [sgdfc:8.3.0-9.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5811	16658452_f2_10	6233	20336	2586	862	YPR181C	395	2.7(10)-51	Saccharomyces cerevisiae	[ui:ypr181c] [pn:component of copii coat of er-golgi vesicles:protein transport protein sec23] [gn:sec23:p9705] [gtcfc:12.6:12.10.12.16] [keggfc:14.2] [sgdfc:8.3.0-9.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4077	16798577_c1_5	6234	20337	933	311	YJR005W	203	2.2(10)-15	Saccharomyces cerevisiae	[ui:yjr005w] [pn:clathrin-associated protein complex, beta chain:probable beta-adaptin:clathrin assembly protein large beta chain:clathrin assembly protein complex 2 beta large chain] [gn:ap1:yap80:j1422] [gtcfc:12.10:12.16:12.6] [ke
CONTIG3679	4066317_c3_5	6235	20338	864	288	YJR005W	416	2.0(10)-38	Saccharomyces cerevisiae	[ui:yjr005w] [pn:clathrin-associated protein complex, beta chain:probable beta-adaptin:clathrin assembly protein large beta chain:clathrin assembly protein complex 2 beta large chain] [gn:ap1:yap80:j1422] [gtcfc:12.10:12.16:12.6] [ke
CONTIG5482	957500_c2_20	6236	20339	507	169	YJR058C	469	1.2(10)-44	Saccharomyces cerevisiae	[ui:yjr058c] [pn:clathrin-associated protein 17, small subunit:clathrin coat assembly protein ap17:clathrin coat associated protein ap17:plasma membrane adaptor ap-2 17 kd protein:ha2 17 kd subunit:clathrin assembly protein 2 small cha
CONTIG1425	11739205_f1_1	6237	20340	807	269	YKL135C	144	5.2(10)-9	Saccharomyces cerevisiae	[ui:ykl135c] [pn:beta-adaptin:probable beta-adaptin:clathrin assembly protein large beta chain:clathrin assembly protein complex 2 beta large chain] [gn:ap2] [gtcfc:12.10:12.16:12.6] [keggfc:14.2] [sgdfc:6.4.0:8.7.0:9.9.0] [db:gtc-sa

CONTIG2023	23455050_f2_1	6238	20341	903	301	YKL135C	579	2.6(10)-56	Saccharomyces cerevisiae	[ui:ykl135c] [pn:beta-adaptin:probable beta-adaptin:clathrin assembly protein large beta chain:clathrin assembly protein complex 2 beta large chain] [gn:apl2] [gtcfc:12.10:12.16:12.6] [keggfc:14.2] [sgdfc:6.4.0:8.7.0:9.9.0] [db:gtc-sa
CONTIG2271	10972806_fl_3	6239	20342	372	124	YKL135C	345	1.3(10)-30	Saccharomyces cerevisiae	[ui:ykl135c] [pn:beta-adaptin:probable beta-adaptin:clathrin assembly protein large beta chain:clathrin assembly protein complex 2 beta large chain] [gn:apl2] [gtcfc:12.10:12.16:12.6] [keggfc:14.2] [sgdfc:6.4.0:8.7.0:9.9.0] [db:gtc-sa
CONTIG5783	14728343_f2_12	6240	20343	552	184	YLR080W	162	2.7(10)-11	Saccharomyces cerevisiae	[ui:ylr080w] [pn:strong similarity to emp47p] [gtcfc:12.10:12.16] [keggfc:14.2] [sgdfc:9.9.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3030	6756938_fl_1	6241	20344	390	130	YLR170C	390	2.7(10)-36	Saccharomyces cerevisiae	[ui:ylr170c] [pn:clathrin-associated protein:ap complex, small subunit ap19:clathrin coat assembly protein ap19:clathrin coat associated protein ap19:golgi adaptor ap-1 19 kd adaptin:ha1 19 kd subunit:clathrin assembly protein complex

CONTIG5548	33767162_f2_5	6242	20345	324	108	YBR132C	125	4.2(10)-7	Saccharomyces cerevisiae	[ui:ybr132c] [pn:strong similarity to amino-acid permeases:hypothetical amino-acid permease in vma2-cks1 intergenic region] [gn:ybr1007] [gtcfc:12.1:12.6] [keggfc:14.2] [sgdfc:1.1.3:7.4.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5765	20320930_f2_12	6243	20346	855	285	YBR132C	397	1.1(10)-41	Saccharomyces cerevisiae	[ui:ybr132c] [pn:strong similarity to amino-acid permeases:hypothetical amino-acid permease in vma2-cks1 intergenic region] [gn:ybr1007] [gtcfc:12.1:12.6] [keggfc:14.2] [sgdfc:1.1.3:7.4.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5765	12588156_f2_13	6244	20347	873	291	YBR132C	457	2.2(10)-43	Saccharomyces cerevisiae	[ui:ybr132c] [pn:strong similarity to amino-acid permeases:hypothetical amino-acid permease in vma2-cks1 intergenic region] [gn:ybr1007] [gtcfc:12.1:12.6] [keggfc:14.2] [sgdfc:1.1.3:7.4.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3979	4801715_c1_8	6245	20348	225	75	YDR160W	151	1.2(10)-9	Saccharomyces cerevisiae	[ui:ydr160w] [pn:similarity to amino acid permeases lyp1p and dip5p] [gtcfc:12.1:12.6] [keggfc:14.2] [sgdfc:1.1.3:7.4.0:17.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG	Seq					YDR		E-value	Organism	Description
CONTIG3979	4018766_c2_10	6246	20349	1341	447	YDR160W	734	9.9(10)-73	Saccharomyces cerevisiae	[ui:ydr160w] [pn:similarity to amino acid permeases lyp1p and dip5p] [gtcfc:12.1:12.6] [keggfc:14.2] [sgdfc:1.1.3:7.4.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3979	23921887_c3_11	6247	20350	384	128	YDR160W	127	4.2(10)-7	Saccharomyces cerevisiae	[ui:ydr160w] [pn:similarity to amino acid permeases lyp1p and dip5p] [gtcfc:12.1:12.6] [keggfc:14.2] [sgdfc:1.1.3:7.4.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5410	234380_c1_12	6248	20351	1191	397	YDR508C	651	6.2(10)-64	Saccharomyces cerevisiae	[ui:ydr508c] [pn:high-affinity glutamine permease] [gn:gnp1:d9719] [gtcfc:12.1:12.6] [keggfc:14.2] [sgdfc:1.1.3:7.4.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5787	10265628_c3_35	6249	20352	1731	577	YDR508C	1233	1.3(10)-125	Saccharomyces cerevisiae	[ui:ydr508c] [pn:high-affinity glutamine permease] [gn:gnp1:d9719] [gtcfc:12.1:12.6] [keggfc:14.2] [sgdfc:1.1.3:7.4.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5787	24788890_c3_33	6250	20353	1728	576	YDR508C	966	2.6(10)-97	Saccharomyces cerevisiae	[ui:ydr508c] [pn:high-affinity glutamine permease] [gn:gnp1:d9719] [gtcfc:12.1:12.6] [keggfc:14.2] [sgdfc:1.1.3:7.4.0:17.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2473	3938462_f2_2	6251	20354	639	213	YFL055W	306	2.2(10)-31	Saccharomyces cerevisiae	[ui:yfl055w] [pn:similarity to gap1p and other amino acid permeases:hypothetical amino-acid permease in thi5-emp47 intergenic region] [gtcfc:12.1:12.6] [keggfc:14.2] [sgdfc:1.1.3:7.4.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
b9x13d75.x	12353513_c3_2	6252	20355	615	205	YFL055W	571	1.8(10)-55	Saccharomyces cerevisiae	[ui:yfl055w] [pn:similarity to gap1p and other amino acid permeases:hypothetical amino-acid permease in thi5-emp47 intergenic region] [gtcfc:12.1:12.6] [keggfc:14.2] [sgdfc:1.1.3:7.4.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3223	22385953_f1_1	6253	20356	1311	437	YHL036W	860	4.4(10)-86	Saccharomyces cerevisiae	[ui:yhl036w] [pn:methionine permease:hypothetical 60.6 kd protein in cbp2-ssbr1 intergenic region] [gn:mup3] [gtcfc:12.1:12.6] [keggfc:14.2] [sgdfc:1.1.3:7.4.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3098	34494828_c3_4	6254	20357	1455	485	YKL174C	678	8.5(10)-67	Saccharomyces cerevisiae	[ui:ykl174c] [pn:similarity to choline transport protein hnm1p:hypothetical amino-acid permease in ste3-gin10 intergenic region] [gn:ykl639] [gtcfc:12.2:11.1] [keggfc:14.2] [sgdfc:1.6.5:7.4.0:7.5.0:17.0.0] [db:gtc-saccharomyces cerevi

CONTIG411	4691002_c3_2	6255	20358	525	175	YPL274W	164	2.7(10)-11	Saccharomyces cerevisiae	[ui:ypl274w] [pn:strong similarity to amino-acid transport proteins] [gtcfc:12.1] [sgdfc:1.1.3;7.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1576	9782688_f1_1	6256	20359	765	255	YPL265W	376	2.5(10)-34	Saccharomyces cerevisiae	[ui:ypl265w] [pn:dicarboxylic amino acid permease] [gn:dip5] [gtcfc:12.1:12.6] [sgdfc:1.1.3;7.4.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2689	13690811_c2_4	6257	20360	381	127	YPL265W	146	2.5(10)-9	Saccharomyces cerevisiae	[ui:ypl265w] [pn:dicarboxylic amino acid permease] [gn:dip5] [gtcfc:12.1:12.6] [sgdfc:1.1.3;7.4.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3496	17205_f3_3	6258	20361	402	134	YPL265W	105	6.2(10)-5	Saccharomyces cerevisiae	[ui:ypl265w] [pn:dicarboxylic amino acid permease] [gn:dip5] [gtcfc:12.1:12.6] [sgdfc:1.1.3;7.4.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5548	35162952_f1_4	6259	20362	1044	348	YPL265W	622	7.2(10)-61	Saccharomyces cerevisiae	[ui:ypl265w] [pn:dicarboxylic amino acid permease] [gn:dip5] [gtcfc:12.1:12.6] [sgdfc:1.1.3;7.4.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
b3x11276.x	25672876_c3_1	6260	20363	564	188	YPL265W	358	2.5(10)-32	Saccharomyces cerevisiae	[ui:ypl265w] [pn:dicarboxylic amino acid permease] [gn:dip5] [gtcfc:12.1:12.6] [sgdfc:1.1.3;7.4.0:17.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3075	32210432_c3_5	6261	20364	1143	381	YNR031C	1109	4.0(10)-112	Saccharomyces cerevisiae	[ui:ynr031c] [pn:map kinase kinase kinase of the high osmolarity signal transduction pathway:serine/threonine protein kinase 2] [gn:ssk2:suppressor of sensor kinase 2] [gtcfc:12.11:12.13:11.3] [ec:2.7.--] [keggfc:14.1] [sgdf
CONTIG4286	2110885_f3_2	6262	20365	2619	873	YNR031C	784	7.4(10)-85	Saccharomyces cerevisiae	[ui:ynr031c] [pn:map kinase kinase kinase of the high osmolarity signal transduction pathway:serine/threonine protein kinase ssk2:suppressor of sensor kinase 2] [gn:ssk2:suppressor of sensor kinase 2] [gtcfc:12.11:12.13:11.3] [ec:2.7.--] [keggfc:14.1] [sgdf
CONTIG5729	24411529_c2_22	6263	20366	774	258	YBL064C	644	3.3(10)-63	Saccharomyces cerevisiae	[ui:ybl064c] [pn:strong similarity to thiol-specific antioxidant enzyme:hypothetical 29.5 kd protein in ubp13-kip1 intergenic region] [gn:ybl0503:ybl0524] [gtcfc:12.12] [keggfc:14.2] [sgdfc:11.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2019	16578517_f2_1	6264	20367	1359	453	YBR043C	663	1.5(10)-85	Saccharomyces cerevisiae	[ui:ybr043c] [pn:similarity to benomyl/methotrexate resistance protein:hypothetical 77.3 kd protein in fig1-gip1 intergenic region] [gn:ybr0413] [gtcfc:12.12:12.6:13.3] [keggfc:14.2] [sgdfc:7.10.0:11.3.0:17.0.0] [db:gtc-saccharomyces

CONTIG5647	1990642_c2_14	6265	20368	1560	520	YBR180W	470	2.8(10)-76	Saccharomyces cerevisiae	[ui:ybr180w] [pn:similarity to drug resistance proteins;hypothetical 63.4 kd protein in smy2-rps101 intergenic region] [gn:ybr1242] [gtcfc:12.12.6:13.3] [keggfc:14.2] [sgdfc:7.10.0:11.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
b3x16081.y	35836703_c3_8	6266	20369	378	126	YCL069W	91	0.0027	Saccharomyces cerevisiae	[ui:ycl069w] [pn:strong similarity to drug resistance protein sgc1:hypothetical 50.2 kd protein in hml 5"region] [gn:ycl69w] [gtcfc:12.12.6:13.3] [keggfc:14.2] [sgdfc:7.10.0:11.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3010	2131562_f2_3	6267	20370	1464	488	YCR023C	444	1.3(10)-86	Saccharomyces cerevisiae	[ui:ycr023c] [pn:member of major facilitator superfamily multidrug-resistance protein family 2:hypothetical 69.2 kd protein in hsp30-pmp1 intergenic region] [gn:ycr23c:ycr241] [gtcfc:12.12.6] [keggfc:14.2] [sgdfc:7.11.0:11.3.0:17.0
CONTIG4693	6760956_c3_5	6268	20371	918	306	YCR023C	546	1.7(10)-57	Saccharomyces cerevisiae	[ui:ycr023c] [pn:member of major facilitator superfamily multidrug-resistance protein family 2:hypothetical 69.2 kd protein in hsp30-pmp1 intergenic region] [gn:ycr23c:ycr241] [gtcfc:12.12.6] [keggfc:14.2] [sgdfc:7.11.0:11.3.0:17.0

CONTIG5644	21984453_f2_4	6269	20372	372	124	YCR023C	174	2.3(10)-12	Saccharomyces cerevisiae	[ui:ycr023c] [pn:member of major facilitator superfamily multidrug-resistance protein family 2:hypothetical 69.2 kd protein in hsp30-pmp1 intergenic region] [gn:ycr23c:ycr241] [gtcfc:12.12:12.6] [keggfc:14.2] [sgdfc:7.11.0:11.3.0:17.0
CONTIG1849	29531277_c2_7	6270	20373	942	314	YDL100C	782	8.0(10)-78	Saccharomyces cerevisiae	[ui:ydl100c] [pn:similarity to e.coli arsenical pump-driving atpase] [gtcfc:12.12] [keggfc:14.2] [sgdfc:11.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1433	666715_f1_1	6271	20374	849	283	YDR135C	707	1.2(10)-68	Saccharomyces cerevisiae	[ui:ydr135c] [pn:glutathione s-conjugate transporter, vacuolar:metal resistance protein:yeast cadmium factor 1] [gn:ycf1] [gtcfc:12.6:12.12:12.13] [keggfc:14.2] [sgdfc:7.9.0:8.5.0:9.10.0:11.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4113	22475090_c2_4	6272	20375	1716	572	YDR135C	1582	9.5(10)-202	Saccharomyces cerevisiae	[ui:ydr135c] [pn:glutathione s-conjugate transporter, vacuolar:metal resistance protein:yeast cadmium factor 1] [gn:ycf1] [gtcfc:12.6:12.12:12.13] [keggfc:14.2] [sgdfc:7.9.0:8.5.0:9.10.0:11.3.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4155	12537878_c1_3	6273	20376	2250	750	YDR135C	1716	8.5(10)-177	Saccharomyces cerevisiae	[ui:ydr135c] [pn:glutathione s-conjugate transporter, vacuolar:metal resistance protein:yeast cadmium resistance protein:yeast cadmium factor 1] [gn:ycf1] [gtcfc:12.6:12.12:12.13] [sgdfc:7.9.0:8.5.0:9.10.0:11.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG397	1995832_c3_3	6274	20377	1191	397	YDR135C	408	1.0(10)-36	Saccharomyces cerevisiae	[ui:ydr135c] [pn:glutathione s-conjugate transporter, vacuolar:metal resistance protein:yeast cadmium factor 1] [gn:ycf1] [gtcfc:12.6:12.12:12.13] [keggfc:14.2] [sgdfc:7.9.0:8.5.0:9.10.0:11.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3463	13722300_c3_3	6275	20378	1464	488	YFR022W	631	5.2(10)-81	Saccharomyces cerevisiae	[ui:yfr022w] [pn:similarity to rod1p:hypothetical 79.7 kd protein in fab1-pes4 intergenic region] [gtcfc:12.12] [keggfc:14.2] [sgdfc:11.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5613	19767203_c1_20	6276	20379	1773	591	YFR022W	231	9.0(10)-30	Saccharomyces cerevisiae	[ui:yfr022w] [pn:similarity to rod1p:hypothetical 79.7 kd protein in fab1-pes4 intergenic region] [gtcfc:12.12] [keggfc:14.2] [sgdfc:11.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5613	23628562_c3_24	6277	20380	249	83	YFR022W	106	6.2(10)-5	Saccharomyces cerevisiae	[ui:yfr022w] [pn:similarity to rod1p:hypothetical 79.7 kd protein in fab1-pes4 intergenic region] [gtcfc:11.3.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5814	24400437_c3_50	6278	20381	705	235	YGL016W	257	7.5(10)-21	Saccharomyces cerevisiae	[ui:ygl016w] [pn:pleiotropic drug resistance regulatory protein:pleiotropic drug resistance regulatory protein 6] [gn:pdr6] [gtcfc:12.12] [keggfc:14.2] [sgdfc:11.3.0] [db:gtc-saccharomyces cerevisiae]
b2x11126.x	6833390_c1_4	6279	20382	441	147	YGL016W	135	7.9(10)-8	Saccharomyces cerevisiae	[ui:ygl016w] [pn:pleiotropic drug resistance regulatory protein:pleiotropic drug resistance regulatory protein 6] [gn:pdr6] [gtcfc:12.12] [keggfc:14.2] [sgdfc:11.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4203	13101687_c1_5	6280	20383	774	258	YGR138C	782	8.0(10)-78	Saccharomyces cerevisiae	[ui:ygr138c] [pn:similarity to multidrug resistance proteins:hypothetical 67.6 kd protein in pas5-cbf2 intergenic region] [gtcfc:12.12.6:13.3] [keggfc:14.2] [sgdfc:7.10.0:11.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4751	5961700_c2_10	6281	20384	936	312	YGR138C	369	1.6(10)-33	Saccharomyces cerevisiae	[ui:ygr138c] [pn:similarity to multidrug resistance proteins:hypothetical 67.6 kd protein in pas5-cbf2 intergenic region] [gtcfc:12.12.6:13.3] [keggfc:14.2] [sgdfc:7.10.0:11.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3322	894762_f1_1	6282	20385	939	313	YGR197C	362	4.4(10)-33	Saccharomyces cerevisiae	[ui:ygr197c] [pn:involved in nitroguanidine resistance:nitrosoguanidine resistance protein sng1] [gn:sng1:g7591] [gtcfc:12.12.6:13.3] [keggfc:14.2] [sgdfc:7.10.0:11.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4771	11837837_c2_9	6283	20386	525	175	YGR197C	159	8.4(10)-11	Saccharomyces cerevisiae	[ui:ygr197c] [pn:involved in nitroguanidine resistance:nitrosoguanidine resistance protein sng1] [gn:sng1:g7591] [gtcfc:12.12.6:13.3] [keggfc:14.2] [sgdfc:7.10.0:11.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4771	2616401_c1_6	6284	20387	270	90	YGR197C	107	3.2(10)-5	Saccharomyces cerevisiae	[ui:ygr197c] [pn:involved in nitroguanidine resistance:nitrosoguanidine resistance protein sng1] [gn:sng1:g7591] [gtcfc:12.12.6:13.3] [keggfc:14.2] [sgdfc:7.10.0:11.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG635	14191067_f1_1	6285	20388	702	234	YGR197C	348	1.8(10)-31	Saccharomyces cerevisiae	[ui:ygr197c] [pn:involved in nitroguanidine resistance:nitrosoguanidine resistance protein sng1] [gn:sng1:g7591] [gtcfc:12.12.6:13.3] [sgdfc:7.10.0:11.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1618	7837_f1_1	6286	20389	1074	358	YGR224W	380	9.4(10)-35	Saccharomyces cerevisiae	[ui:ygr224w] [pn:strong similarity to drug resistance protein sge1:hypothetical 67.2 kd protein in pet54-die2 intergenic region] [gn:g8537] [gtcfc:12.12.6:13.3] [keggfc:14.2] [sgdfc:7.10.0:11.3.0:17.0.0] [db:gtc-saccharomyces cerev]
CONTIG66	11113175_f1_1	6287	20390	630	210	YGR224W	308	8.0(10)-27	Saccharomyces cerevisiae	[ui:ygr224w] [pn:strong similarity to drug resistance protein sge1:hypothetical 67.2 kd protein in pet54-die2 intergenic region] [gn:g8537] [gtcfc:12.12.6:13.3] [keggfc:14.2] [sgdfc:7.10.0:11.3.0:17.0.0] [db:gtc-saccharomyces cerev]
CONTIG906	901928_f1_1	6288	20391	540	180	YGR224W	146	2.5(10)-9	Saccharomyces cerevisiae	[ui:ygr224w] [pn:strong similarity to drug resistance protein sge1:hypothetical 67.2 kd protein in pet54-die2 intergenic region] [gn:g8537] [gtcfc:12.12.6:13.3] [keggfc:14.2] [sgdfc:7.10.0:11.3.0:17.0.0] [db:gtc-saccharomyces cerev]

CONTIG1647	31926000_c2_4	6289	20392	1014	338	YHL040C	693	2.2(10)-68	Saccharomyces cerevisiae	[ui:yhl040c] [pn:similarity to c.carbonum toxin pump:hypothetical 70.9 kd protein in cbp2 5"region] [gtcfc:12.12.6.13.3] [keggfc:14.2] [sgdfc:7.10.0:11.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2318	16853432_f1_1	6290	20393	426	142	YHL040C	92	0.027	Saccharomyces cerevisiae	[ui:yhl040c] [pn:similarity to c.carbonum toxin pump:hypothetical 70.9 kd protein in cbp2 5"region] [gtcfc:12.12.6.13.3] [keggfc:14.2] [sgdfc:7.10.0:11.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3837	4954407_c2_7	6291	20394	378	126	YHL040C	223	1.3(10)-17	Saccharomyces cerevisiae	[ui:yhl040c] [pn:similarity to c.carbonum toxin pump:hypothetical 70.9 kd protein in cbp2 5"region] [gtcfc:12.12.6.13.3] [keggfc:14.2] [sgdfc:7.10.0:11.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3105	25658443_c3_9	6292	20395	1494	498	YHR032W	855	1.5(10)-85	Saccharomyces cerevisiae	[ui:yhr032w] [pn:ethionine resistance protein:hypothetical 64.2 kd protein in slt2-put2 intergenic region] [gn:erc1] [gtcfc:12.12.6.13.3] [keggfc:14.2] [sgdfc:7.10.0:11.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3187	578126_f2_3	6293	20396	1074	358	YHR032W	497	3.0(10)-56	Saccharomyces cerevisiae	[ui:yhr032w] [pn:ethionine resistance protein:hypothetical 64.2 kd protein in slt2-put2 intergenic region] [gn:erc1] [gtcfc:12.12:12.6.13.3] [keggfc:14.2] [sgdfc:7.10.0:11.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3200	4175067_f1_1	6294	20397	720	240	YHR032W	419	2.3(10)-39	Saccharomyces cerevisiae	[ui:yhr032w] [pn:ethionine resistance protein:hypothetical 64.2 kd protein in slt2-put2 intergenic region] [gn:erc1] [gtcfc:12.12:12.6.13.3] [keggfc:14.2] [sgdfc:7.10.0:11.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3246	4379637_c3_2	6295	20398	1023	341	YHR032W	600	1.6(10)-58	Saccharomyces cerevisiae	[ui:yhr032w] [pn:ethionine resistance protein:hypothetical 64.2 kd protein in slt2-put2 intergenic region] [gn:erc1] [gtcfc:12.12:12.6.13.3] [keggfc:14.2] [sgdfc:7.10.0:11.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5342	2347062_c3_23	6296	20399	1452	484	YHR032W	750	2.0(10)-74	Saccharomyces cerevisiae	[ui:yhr032w] [pn:ethionine resistance protein:hypothetical 64.2 kd protein in slt2-put2 intergenic region] [gn:erc1] [gtcfc:12.12:12.6.13.3] [keggfc:14.2] [sgdfc:7.10.0:11.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5707	21601512_f3_13	6297	20400	531	YHR048W	1073	1.2(10)-108	Saccharomyces cerevisiae	[ui:yhr048w] [pn:similarity to multidrug resistance proteins:hypothetical 57.8 kd protein in aap1-smf2 intergenic region] [gtcfc:12.12:12.6:13.3] [keggfc:14.2] [sgdfc:7.10.0:11.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4670	1464556_c3_10	6298	20401	372	YJR015W	186	9.0(10)-14	Saccharomyces cerevisiae	[ui:yjr015w] [pn:strong similarity to sng1p:hypothetical 58.1 kd protein in spc1-ilv3 intergenic region] [gn:j1448] [gtcfc:12.12] [keggfc:14.2] [sgdfc:11.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4865	12526586_f3_7	6299	20402	1188	YJR015W	224	5.9(10)-16	Saccharomyces cerevisiae	[ui:yjr015w] [pn:strong similarity to sng1p:hypothetical 58.1 kd protein in spc1-ilv3 intergenic region] [gn:j1448] [gtcfc:12.12] [keggfc:14.2] [sgdfc:11.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2879	5985002_f2_1	6300	20403	97	YJR104C	315	2.5(10)-28	Saccharomyces cerevisiae	[ui:yjr104c] [pn:copper-zinc superoxide dismutase:superoxide dismutase:cu-zn] [gn:sod1:j1968] [gtcfc:12.12:14.1] [ec:1.15.1.1] [keggfc:14.1] [sgdfc:9.2.0:11.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3171	12687761_f2_1	6301	20404	480	YJR104C	554	1.2(10)-53	Saccharomyces cerevisiae	[ui:yjr104c] [pn:copper-zinc superoxide dismutase:superoxide dismutase:cu-zn] [gn:sod1:j1968] [gtcfc:12.12:14.1] [ec:1.15.1.1] [keggfc:14.1] [sgdfc:9.2.0:11.3.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5673	25015_f3_17	6302	20405	2445	815	YKL064W	964	2.2(10)-135	Saccharomyces cerevisiae	[ui:ykl064w] [pn:overexpression overcomes manganese toxicity:hypothetical 109.7 kd protein in nup100-msn4 intergenic region] [gn:mnr2] [gtcfc:12.12.12.6] [keggfc:14.2] [sgdfc:1.8.1:11.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2972	5906632_c3_1	6303	20406	1455	485	YKL004W	314	1.7(10)-32	Saccharomyces cerevisiae	[ui:ykl004w] [pn:aureobasidin-resistance protein:hypothetical 45.2 kd protein rpl14a-mrp17 intergenic region] [gn:aur1] [gtcfc:12.12] [keggfc:14.2] [sgdfc:11.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5664	5947586_c3_23	6304	20407	1902	634	YKR105C	361	2.8(10)-61	Saccharomyces cerevisiae	[ui:ykr105c] [pn:strong similarity to sge1p and hypothetical protein ycl069w:hypothetical 63.4 kd protein in sir1 3"region] [gtcfc:12.12.6:13.3] [keggfc:14.2] [sgdfc:7.10.0:11.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2718	13929502_f2_2	6305	20408	1323	441	YLL028W	486	1.8(10)-46	Saccharomyces cerevisiae	[ui:yll028w] [pn:similarity to multidrug resistance proteins] [gtcfc:12.12.6:13.3] [keggfc:14.2] [sgdfc:7.10.0:11.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4898	5111008_c3_7	6306	20409	1266	422	YLL028W	988	1.2(10)-99	Saccharomyces cerevisiae	[ui:yll028w] [pn:similarity to multidrug resistance proteins] [gtcfc:12.12.6:13.3] [keggfc:14.2] [sgdfc:7.10.0:11.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG48844	14720377_f2_3	6307	20410	585	195	YLL028W	122	8.0(10)-6	Saccharomyces cerevisiae	[ui:yll028w] [pn:similarity to multidrug resistance proteins] [gtcfc:12.12.12.6.13.3] [keggfc:14.2] [sgdfc:7.10.0:11.3.0-17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5254	4413176_c2_19	6308	20411	1701	567	YLL028W	1116	3.2(10)-113	Saccharomyces cerevisiae	[ui:yll028w] [pn:similarity to multidrug resistance proteins] [gtcfc:12.12.12.6.13.3] [keggfc:14.2] [sgdfc:7.10.0:11.3.0-17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1371	26360662_f3_1	6309	20412	909	303	YLL028W	554	1.2(10)-58	Saccharomyces cerevisiae	[ui:yll015w] [pn:similarity to metal resistance proteins] [gtcfc:12.12.12.6] [keggfc:14.2] [sgdfc:7.9.0:11.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2696	1203503_c2_7	6310	20413	2019	673	YLL015W	1050	1.3(10)-105	Saccharomyces cerevisiae	[ui:yll015w] [pn:similarity to metal resistance proteins] [gtcfc:12.12.12.6] [keggfc:14.2] [sgdfc:7.9.0:11.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5211	13829562_f3_8	6311	20414	207	69	YLL015W	211	9.9(10)-16	Saccharomyces cerevisiae	[ui:yll015w] [pn:similarity to metal resistance proteins] [gtcfc:12.12.12.6] [keggfc:14.2] [sgdfc:7.9.0:11.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5591	2068753_f1_2	6312	20415	489	163	YLL015W	457	6.2(10)-42	Saccharomyces cerevisiae	[ui:yll015w] [pn:similarity to metal resistance proteins] [gtcfc:12.12.12.6] [keggfc:14.2] [sgdfc:7.9.0:11.3.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5744	217550300_f1_1	6313	20416	627	209	YML028W	766	4.0(10)-76	Saccharomyces cerevisiae	[ui:yml028w] [pn:thiol-specific antioxidant:thiol-specific antioxidant protein:prp] [gn:tsa1:tsa] [gtcfc:12.12] [keggfc:14.2] [sgdfc:9.2.0:11.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG763	34017686_cl_2	6314	20417	252	84	YNL259C	147	1.6(10)-10	Saccharomyces cerevisiae	[ui:ynl259c] [pn:antioxidant protein and metal homeostasis factor:metal homeostasis factor atx1] [gn:atx1:n0840] [gtcfc:12.12.12.6] [keggfc:14.2] [sgdfc:1.8.1:11.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4821	14537702_cl_10	6315	20418	1515	505	YNL065W	750	2.0(10)-74	Saccharomyces cerevisiae	[ui:ynl065w] [pn:similarity to resistance proteins:hypothetical 65.3 kd protein in sun4-mas5 intergenic region] [gn:n2417:ynl2417w] [gtcfc:12.12:12.6:13.3] [keggfc:14.2] [sgdfc:7.10.0:11.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5691	24414132_f1_1	6316	20419	1194	398	YNL065W	634	3.8(10)-62	Saccharomyces cerevisiae	[ui:ynl065w] [pn:similarity to resistance proteins:hypothetical 65.3 kd protein in sun4-mas5 intergenic region] [gn:n2417:ynl2417w] [gtcfc:12.12.12.6.13.3] [keggfc:14.2] [sgdfc:7.10.0:11.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2305	12673131_c2_4	6317	20420	360	120	YNR055C	120	1.5(10)-6	Saccharomyces cerevisiae	[ui:ynr055c] [pn:member of major facilitator superfamily multidrug-resistance protein subfamily 1:ho11 protein] [gn:ho11:n3494] [gtcfc:12.12:12.6:13.3] [keggfc:14.2] [sgdfc:7.10.0:11.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2809	31400_c1_6	6318	20421	798	266	YNR055C	161	5.9(10)-15	Saccharomyces cerevisiae	[ui:ynr055c] [pn:member of major facilitator superfamily multidrug-resistance protein subfamily 1:ho11 protein] [gn:ho11:n3494] [gtcfc:12.12:12.6:13.3] [keggfc:14.2] [sgdfc:7.10.0:11.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2809	23640702_c1_5	6319	20422	615	205	YNR055C	208	4.9(10)-16	Saccharomyces cerevisiae	[ui:ynr055c] [pn:member of major facilitator superfamily multidrug-resistance protein subfamily 1:ho11 protein] [gn:ho11:n3494] [gtcfc:12.12:12.6:13.3] [keggfc:14.2] [sgdfc:7.10.0:11.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5052	11726562_c2_4	6320	20423	1788	596	YNR055C	1514	2.2(10)-155	Saccharomyces cerevisiae	[ui:ynr055c] [pn:member of major facilitator superfamily multidrug-resistance protein subfamily 1:ho11 protein] [gn:ho11:n3494] [gtcfc:12.12:12.6:13.3] [keggfc:14.2] [sgdfc:7.10.0:11.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5216	502290_f3_8	6321	20424	1353	451	YNR055C	730	2.6(10)-72	Saccharomyces cerevisiae	[ui:ynr055c] [pn:member of major facilitator superfamily multidrug-resistance protein subfamily 1:ho11 protein] [gn:ho11:n3494] [gtcfc:12.12.6.13.3] [keggfc:14.2] [sgdfc:7.10.0:11.3.0:17.0.0] [db-gtc-saccharomyces cerevisiae]
CONTIG5307	24254561_f3_6	6322	20425	1329	443	YNR055C	177	1.2(10)-20	Saccharomyces cerevisiae	[ui:ynr055c] [pn:member of major facilitator superfamily multidrug-resistance protein subfamily 1:ho11 protein] [gn:ho11:n3494] [gtcfc:12.12.6.13.3] [keggfc:14.2] [sgdfc:7.10.0:11.3.0:17.0.0] [db-gtc-saccharomyces cerevisiae]
CONTIG5307	3947553_f2_3	6323	20426	438	146	YNR055C	143	4.9(10)-9	Saccharomyces cerevisiae	[ui:ynr055c] [pn:member of major facilitator superfamily multidrug-resistance protein subfamily 1:ho11 protein] [gn:ho11:n3494] [gtcfc:12.12.6.13.3] [keggfc:14.2] [sgdfc:7.10.0:11.3.0:17.0.0] [db-gtc-saccharomyces cerevisiae]
CONTIG5644	35369200_c3_20	6324	20427	795	265	YNR055C	248	2.2(10)-20	Saccharomyces cerevisiae	[ui:ynr055c] [pn:member of major facilitator superfamily multidrug-resistance protein subfamily 1:ho11 protein] [gn:ho11:n3494] [gtcfc:12.12.6.13.3] [keggfc:14.2] [sgdfc:7.10.0:11.3.0:17.0.0] [db-gtc-saccharomyces cerevisiae]

CONTIG	ID								Organism	Description
CONTIG5644	1370781_c1_14	6325	20428	1197	399	YNR055C	222	1.2(10)-15	Saccharomyces cerevisiae	[ui:ynr055c] [pn:member of major facilitator superfamily multidrug-resistance protein subfamily 1:hol1 protein] [gn:hol1:n3494] [gtcfc:12.12.6.13.3] [keggfc:14.2] [sgdfc:7.10.0:11.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG8	24254561_c1_1	6326	20429	249	83	YNR055C	94	0.00089	Saccharomyces cerevisiae	[ui:ynr055c] [pn:member of major facilitator superfamily multidrug-resistance protein subfamily 1:hol1 protein] [gn:hol1:n3494] [gtcfc:12.12.6.13.3] [keggfc:14.2] [sgdfc:7.10.0:11.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1524	16042580_f2_1	6327	20430	507	169	YOL130W	312	6.7(10)-27	Saccharomyces cerevisiae	[ui:yol130w] [pn:aluminium resistance protein] [gn:alr1] [gtcfc:12.12] [keggfc:14.2] [sgdfc:11.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3482	4720302_f1_1	6328	20431	2358	786	YOL130W	1002	3.8(10)-101	Saccharomyces cerevisiae	[ui:yol130w] [pn:aluminium resistance protein] [gn:alr1] [gtcfc:12.12] [keggfc:14.2] [sgdfc:11.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4240	20337552_c2_2	6329	20432	927	309	YOR273C	255	5.2(10)-21	Saccharomyces cerevisiae	[ui:yor273c] [pn:similarity to resistance proteins] [gtcfc:12.12.6.13.3] [keggfc:14.2] [sgdfc:7.10.0:11.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5024	34178918_f2_1	6330	20433	1083	361	YOR273C	719	3.7(10)-71	Saccharomyces cerevisiae	[ui:yor273c] [pn:similarity to resistance proteins] [gtcfc:12.12.12.6:13.3] [keggfc:14.2] [sgdfc:7.10.0:11.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3194	35832152_f1_1	6331	20434	1191	397	YOR378W	634	3.8(10)-62	Saccharomyces cerevisiae	[ui:yor378w] [pn:strong similarity to aminotriazole resistance protein] [gtcfc:12.12.12.6:13.3] [keggfc:14.2] [sgdfc:7.10.0:11.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3610	3994386_c1_7	6332	20435	426	142	YOR378W	127	2.1(10)-7	Saccharomyces cerevisiae	[ui:yor378w] [pn:strong similarity to aminotriazole resistance protein] [gtcfc:12.12.12.6:13.3] [keggfc:14.2] [sgdfc:7.10.0:11.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4609	14645400_f1_1	6333	20436	1650	550	YOR378W	963	5.2(10)-97	Saccharomyces cerevisiae	[ui:yor378w] [pn:strong similarity to aminotriazole resistance protein] [gtcfc:12.12.12.6:13.3] [keggfc:14.2] [sgdfc:7.10.0:11.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4928	2908412_f3_4	6334	20437	1554	518	YPL092W	285	4.5(10)-43	Saccharomyces cerevisiae	[ui:ypl092w] [pn:sulfite sensitivity protein:sulfite sensitivity protein ssu1] [gn:ssu1:lpg16w] [gtcfc:12.12] [keggfc:14.2] [sgdfc:11.3.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4203	5328252_c3_7	6335	20438	948	316	YPR156C	673	1.5(10)-85	Saccharomyces cerevisiae	[ui:ypr156c] [pn:similarity to multidrug resistance proteins] [gtcfc:12.12:12.6:13.3] [keggfc:14.2] [sgdfc:7.10.0:11.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5501	12111067_f2_8	6336	20439	1788	596	YPR156C	795	3.3(10)-79	Saccharomyces cerevisiae	[ui:ypr156c] [pn:similarity to multidrug resistance proteins] [gtcfc:12.12:12.6:13.3] [keggfc:14.2] [sgdfc:7.10.0:11.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5501	4569426_f1_5	6337	20440	1173	391	YPR156C	355	6.0(10)-32	Saccharomyces cerevisiae	[ui:ypr156c] [pn:similarity to multidrug resistance proteins] [gtcfc:12.12:12.6:13.3] [keggfc:14.2] [sgdfc:7.10.0:11.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4433	23728188_f3_4	6338	20441	582	194	YBL061C	467	3.6(10)-44	Saccharomyces cerevisiae	[ui:ybl061c] [pn:protoplast regeneration and killer toxin resistance protein:skt5 protein] [gn:skt5:ybl0506:ybl0519] [gtcfc:12.13] [keggfc:14.2] [sgdfc:1.5.2] [db:gtc-saccharomyces cerevisiae]
CONTIG1471	860932_f3_4	6339	20442	555	185	YCR002C	95	0.00119	Saccharomyces cerevisiae	[ui:ycr002c] [pn:cell division control protein:cell division control protein 10] [gn:cdc10:ycr2c:ycr022] [gtcfc:12.13:12.16:12.8:12.9] [keggfc:14.2] [sgdfc:1.5.2:3.0:3.8.0:3.9.0:9.3.0] [db:gtc-saccharomyces cerevisiae]

CONTIG	Identifier					Gene		E-value	Organism	Description
CONTIG4404	14625325_c2_8	6340	20443	1122	374	YCR002C	1147	1.7(10)-116	Saccharomyces cerevisiae	[ui:ycr002c] [pn:cell division control protein:cell division control protein 10] [gn:cdc10:ycr2c:ycr022] [gtcfc:12.13:12.16:12.8:12.9] [keggfc:14.2] [sgdfc:1.5.2:3.3.0.3.8.0.3.9.0-9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2588	14100915_c3_4	6341	20444	687	229	YCR010C	262	1.0(10)-22	Saccharomyces cerevisiae	[ui:ycr010c] [pn:strong similarity to y.lipolytica gpr1 protein and fun34p:hypothetical 30.7 kd protein in rvs161-adp1 intergenic region] [gn:ycr10c] [gtcfc:12.13] [keggfc:14.2] [sgdfc:1.5.2] [db:gtc-saccharomyces cerevisiae]
CONTIG2588	10603428_c1_3	6342	20445	408	136	YCR010C	203	1.8(10)-16	Saccharomyces cerevisiae	[ui:ycr010c] [pn:strong similarity to y.lipolytica gpr1 protein and fun34p:hypothetical 30.7 kd protein in rvs161-adp1 intergenic region] [gn:ycr10c] [gtcfc:12.13] [keggfc:14.2] [sgdfc:1.5.2] [db:gtc-saccharomyces cerevisiae]
CONTIG2876	20491558_f2_3	6343	20446	330	110	YCR010C	168	1.5(10)-12	Saccharomyces cerevisiae	[ui:ycr010c] [pn:strong similarity to y.lipolytica gpr1 protein and fun34p:hypothetical 30.7 kd protein in rvs161-adp1 intergenic region] [gn:ycr10c] [gtcfc:12.13] [keggfc:14.2] [sgdfc:1.5.2] [db:gtc-saccharomyces cerevisiae]

CONTIG2876	4718926_f3_4	6344	20447	192	64	YCR010C	95	0.00024	Saccharomyces cerevisiae	[ui:ycr010c] [pn:strong similarity to y.lipolytica gpr1 protein and fun34p:hypothetical 30.7 kd protein in rvs161-adp1 intergenic region] [gn:ycr010c] [gtcfc:12.13] [keggfc:14.2] [sgdfc:1.5.2] [db:gtc-saccharomyces cerevisiae]
CONTIG2876	4722625_f1_2	6345	20448	528	176	YCR010C	207	6.9(10)-17	Saccharomyces cerevisiae	[ui:ycr010c] [pn:strong similarity to y.lipolytica gpr1 protein and fun34p:hypothetical 30.7 kd protein in rvs161-adp1 intergenic region] [gn:ycr010c] [gtcfc:12.13] [keggfc:14.2] [sgdfc:1.5.2] [db:gtc-saccharomyces cerevisiae]
CONTIG2978	4041535_c2_7	6346	20449	927	309	YCR010C	585	6.0(10)-57	Saccharomyces cerevisiae	[ui:ycr010c] [pn:strong similarity to y.lipolytica gpr1 protein and fun34p:hypothetical 30.7 kd protein in rvs161-adp1 intergenic region] [gn:ycr010c] [gtcfc:12.13] [keggfc:14.2] [sgdfc:1.5.2] [db:gtc-saccharomyces cerevisiae]
CONTIG3805	800962_f2_3	6347	20450	735	245	YCR010C	477	1.7(10)-45	Saccharomyces cerevisiae	[ui:ycr010c] [pn:strong similarity to y.lipolytica gpr1 protein and fun34p:hypothetical 30.7 kd protein in rvs161-adp1 intergenic region] [gn:ycr010c] [gtcfc:12.13] [keggfc:14.2] [sgdfc:1.5.2] [db:gtc-saccharomyces cerevisiae]
CONTIG450	20110302_c2_3	6348	20451	948	316	YCR010C	682	3.2(10)-67	Saccharomyces cerevisiae	[ui:ycr010c] [pn:strong similarity to y.lipolytica gpr1 protein and fun34p:hypothetical 30.7 kd protein in rvs161-adp1 intergenic region] [gn:ycr010c] [gtcfc:12.13] [keggfc:14.2] [sgdfc:1.5.2] [db:gtc-saccharomyces cerevisiae]

CONTIG5652	33407503_f3_15	6349	20452	963	321	YCR010C	697	8.1(10)-69	Saccharomyces cerevisiae	[ui:ycr010c] [pn:strong similarity to y.lipolytica gpr1 protein and fun34p:hypothetical 30.7 kd protein in rvs161-adp1 intergenic region] [gn:ycr10c] [gtcfc:12.13] [keggfc:14.2] [sgdfc:1.5.2] [db:gtc-saccharomyces cerevisiae]
CONTIG1471	2362586_f2_3	6350	20453	279	93	YDL225W	106	4.2(10)-5	Saccharomyces cerevisiae	[ui:ydl225w] [pn:similarity to cdc11p, cdc3p and human cdc10 protein] [gtcfc:12.13:12.8:12.9] [keggfc:14.2] [sgdfc:1.5.2:3.2.0:3.3.0:3.8.0:3.9.0] [db:gtc-saccharomyces cerevisiae]
b1x13266.y	24016950_f1_1	6351	20454	558	186	YDL225W	283	3.1(10)-24	Saccharomyces cerevisiae	[ui:ydl225w] [pn:similarity to cdc11p, cdc3p and human cdc10 protein] [gtcfc:12.13:12.8:12.9] [keggfc:14.2] [sgdfc:1.5.2:3.2.0:3.3.0:3.8.0:3.9.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4815	10833337_f3_4	6352	20455	1611	537	YDL203C	146	6.7(10)-7	Saccharomyces cerevisiae	[ui:ydl203c] [pn:similarity to skt5p] [gtcfc:12.13] [keggfc:14.2] [sgdfc:1.5.2] [db:gtc-saccharomyces cerevisiae]
CONTIG5450	22681442_c3_13	6353	20456	840	280	YDR277C	142	2.2(10)-7	Saccharomyces cerevisiae	[ui:ydr277c] [pn:repressor of hexose transport genes:mth1 protein] [gn:mth1:d99954] [gtcfc:12.13] [keggfc:14.2] [sgdfc:1.5.2] [db:gtc-saccharomyces cerevisiae]

CONTIG5694	2451145 3_c2_19	6354	20457	2121	707	YGR070W	136	3.2(10)-5	Saccharomyces cerevisiae	[ui:ygr070w] [pn:gdp/gtp exchange protein for rho1p:rho1 gdp-gtp exchange protein 1:protein kinase c suppressor skc1] [gn:rom1:skc1] [gtcfc:12.13:12.8] [sgdfc:1.5.2:3.2.0:10.2.4] [db:gtc-saccharomyces cerevisiae]
CONTIG1831	6928402_f1_1	6355	20458	336	112	YGR227W	144	9.5(10)-17	Saccharomyces cerevisiae	[ui:ygr227w] [pn:itr1 expression promoting protein:die2 protein] [gn:die2:g8547] [gtcfc:12.13] [keggfc:14.2] [sgdfc:1.5.2] [db:gtc-saccharomyces cerevisiae]
CONTIG4081	1425467 7_f2_1	6356	20459	786	262	YGR227W	160	2.0(10)-24	Saccharomyces cerevisiae	[ui:ygr227w] [pn:itr1 expression promoting protein:die2 protein] [gn:die2:g8547] [gtcfc:12.13] [keggfc:14.2] [sgdfc:1.5.2] [db:gtc-saccharomyces cerevisiae]
CONTIG5556	29944799_c1_13	6357	20460	945	315	YHR107C	942	9.0(10)-95	Saccharomyces cerevisiae	[ui:yhr107c] [pn:cell division control protein 12:septin] [gn:cdc12:cla10:psl7] [gtcfc:12.13:12.16:12.8:12.9] [keggfc:14.2] [sgdfc:1.5.2:3.2.0:3.3.03.8.0:3.9.0:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2842	6814032_f3_1	6358	20461	858	286	YHR155W	102	5.0(10)-5	Saccharomyces cerevisiae	[ui:yhr155w] [pn:strong similarity to snf1p-interacting protein sip3p:hypothetical 143.6 kd protein in spo16-rec104 intergenic region] [gn:spo16-rec104 intergenic region] [gtcfc:12.13] [keggfc:14.2] [sgdfc:1.5.2] [db:gtc-saccharomyces cerevisiae]

CONTIG5775	9850261_f3_17	6359	20462	1416	472	YIL033C	711	4.5(10)-84	Saccharomyces cerevisiae	[ui:yil033c] [pn:camp dependent protein kinase, regulatory subunit:camp-dependent protein kinase regulatory chain] [gn:reg1:bcy1:sra1] [gtcfc:12.13:12.15:13.2] [keggfc:14.2] [sgdfc:1.5.2:3.4.0:9.2.0:11.0-15.0.0] [db:gtc-saccharomyce
CONTIG2906	24022187_f3_3	6360	20463	1263	421	YJR076C	697	8.1(10)-69	Saccharomyces cerevisiae	[ui:yjr076c] [pn:septin:cell division control protein 11] [gn:cdc11:psl9:j1833] [gtcfc:12.13:12.16:12.8:12.9] [keggfc:14.2] [sgdfc:1.5.2:3.2.0:3.3.0:3.8.0:3.9.0-9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5020	26835776_c3_11	6361	20464	1440	480	YJR076C	298	1.6(10)-26	Saccharomyces cerevisiae	[ui:yjr076c] [pn:septin:cell division control protein 11] [gn:cdc11:psl9:j1833] [gtcfc:12.13:12.16:12.8:12.9] [keggfc:14.2] [sgdfc:1.5.2:3.2.0:3.3.0:3.8.0:3.9.0-9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2553	4695257_c2_1	6362	20465	780	260	YJR090C	100	0.032	Saccharomyces cerevisiae	[ui:yjr090c] [pn:required for glucose repression and for glucose and cation transport:grr1 protein] [gn:grr1:cot2:cat80:j1885] [gtcfc:12.13:12.2:12.8:13.2] [keggfc:14.2] [sgdfc:1.5.2:3.1.0:3.2.0:8.7.0-11.1.0] [db:gtc-saccharomyces cer

CONTIG3400	33673152_f3_3	6363	20466	1281	427	YJR090C	719	2.0(10)-70	Saccharomyces cerevisiae	[ui:yjr090c] [pn:required for glucose repression and for glucose and cation transport:grr1 protein] [gn:grr1:col2:cat80:j1885] [gtfc:12.13:12.2:12.8:13.2] [keggfc:14.2] [sgdfc:1.5.2:3.1.0:3.2.0:8.7.0:11.1.0] [db:gtc-saccharomyces cer
CONTIG3779	1063l500_c1_6	6364	20467	807	269	YJR090C	279	3.7(10)-23	Saccharomyces cerevisiae	[ui:yjr090c] [pn:required for glucose repression and for glucose and cation transport:grr1 protein] [gn:grr1:col2:cat80:j1885] [gtfc:12.13:12.2:12.8:13.2] [keggfc:14.2] [sgdfc:1.5.2:3.1.0:3.2.0:8.7.0:11.1.0] [db:gtc-saccharomyces cer
CONTIG3784	159563_c2_4	6365	20468	1458	486	YJR090C	167	6.7(10)-9	Saccharomyces cerevisiae	[ui:yjr090c] [pn:required for glucose repression and for glucose and cation transport:grr1 protein] [gn:grr1:col2:cat80:j1885] [gtfc:12.13:12.2:12.8:13.2] [keggfc:14.2] [sgdfc:1.5.2:3.1.0:3.2.0:8.7.0:11.1.0] [db:gtc-saccharomyces cer
CONTIG4576	14725937_f1_3	6366	20469	444	148	YLR150W	105	1.7(10)-5	Saccharomyces cerevisiae	[ui:ylr150w] [pn:specific affinity for guanine-rich quadruplex nucleic acids:suppressor protein mpt4:stm1 protein:gu4 nucleic-binding protein 2:g4p2 protein] [gn:mpt4:stm1:sto1:i9634] [gtfc:12.13] [keggfc:14.2] [sgdfc:1.5.2] [db:gtc-

CONTIG3241	14625928_f2_1	6367	20470	1431	477	YLR330W	517	9.8(10)-50	Saccharomyces cerevisiae	[ui:ylr330w] [pn:chitin synthesis protein] [gn:chs5] [gtcfc:11.4:7.2] [sgdfc:1.5.2:3.2.0:3.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3811	4063801_f2_1	6368	20471	1665	555	YLR371W	313	1.1(10)-26	Saccharomyces cerevisiae	[ui:ylr371w] [pn:gdp/gtp exchange factor for rho1p:rho1 gdp-gtp exchange protein 2] [gn:rom2:i8039] [gtcfc:12.13:12.8] [keggfc:14.2] [sgdfc:1.5.2:3.2.0:10.2.4] [db:gtc-saccharomyces cerevisiae]
CONTIG5358	13750326_c1_8	6369	20472	2046	682	YLR371W	1006	1.5(10)-101	Saccharomyces cerevisiae	[ui:ylr371w] [pn:gdp/gtp exchange factor for rho1p:rho1 gdp-gtp exchange protein 2] [gn:rom2:i8039] [gtcfc:12.13:12.8] [keggfc:14.2] [sgdfc:1.5.2:3.2.0:10.2.4] [db:gtc-saccharomyces cerevisiae]
CONTIG5358	25587508_c3_13	6370	20473	549	183	YLR371W	342	9.1(10)-30	Saccharomyces cerevisiae	[ui:ylr371w] [pn:gdp/gtp exchange factor for rho1p:rho1 gdp-gtp exchange protein 2] [gn:rom2:i8039] [gtcfc:12.13:12.8] [keggfc:14.2] [sgdfc:1.5.2:3.2.0:10.2.4] [db:gtc-saccharomyces cerevisiae]
CONTIG5795	24335958_c2_34	6371	20474	420	140	YML048W	94	0.00054	Saccharomyces cerevisiae	[ui:yml048w] [pn:involved in glucose repression] [gn:eft2] [gtcfc:12.13] [keggfc:14.2] [sgdfc:1.5.2] [db:gtc-saccharomyces cerevisiae]

b2x10461.y	21898302_f3_1	6372	20475	696	232	YML048W	338	9.0(10)-31	Saccharomyces cerevisiae	[ui:yml048w] [pn:involved in glucose repression] [gn:eff2] [gtcfc:12.13] [sgdfc:1.5.2] [db:gtc-saccharomyces cerevisiae]
CONTIG2086	6737932_c1_2	6373	20476	1110	370	YNL257C	398	8.1(10)-36	Saccharomyces cerevisiae	[ui:ynl257c] [pn:snf1p protein kinase interacting protein:sip3 protein] [gn:sip3:n0844] [gtcfc:12.13] [keggfc:14.2] [sgdfc:1.5.2] [db:gtc-saccharomyces cerevisiae]
b3x17312.x	213252_f1_1	6374	20477	729	243	YNL257C	215	2.7(10)-16	Saccharomyces cerevisiae	[ui:ynl257c] [pn:snf1p protein kinase interacting protein:sip3 protein] [gn:sip3:n0844] [gtcfc:12.13] [keggfc:14.2] [sgdfc:1.5.2] [db:gtc-saccharomyces cerevisiae]
CONTIG2147	24414068_c1_2	6375	20478	447	149	YNL201C	308	1.8(10)-26	Saccharomyces cerevisiae	[ui:ynl201c] [pn:involved in regulation of carbon metabolism:hypothetical 98.1 kd protein in spx19-gcr2 intergenic region] [gn:n1366] [gtcfc:12.13] [keggfc:14.2] [sgdfc:1.5.2] [db:gtc-saccharomyces cerevisiae]
CONTIG3791	25594427_f1_1	6376	20479	1212	404	YNL201C	170	3.6(10)-19	Saccharomyces cerevisiae	[ui:ynl201c] [pn:involved in regulation of carbon metabolism:hypothetical 98.1 kd protein in spx19-gcr2 intergenic region] [gn:n1366] [gtcfc:14.2] [sgdfc:1.5.2] [keggfc:12.13] [db:gtc-saccharomyces cerevisiae]

b3x15662.y	7260150_f1_1	6377	20480	528	176	YNL201C	283	8.6(10)-24	Saccharomyces cerevisiae	[ui:ynl201c] [pn:involved in regulation of carbon metabolism:hypothetical 98.1 kd protein in spx19-gcr2 intergenic region] [gn:n1366] [gtcfc:12.13] [keggfc:14.2] [sgdfc:1.5.2] [db:gtc-saccharomyces cerevisiae]
CONTIG5747	10756952_c2_40	6378	20481	564	188	YNL090W	621	9.3(10)-61	Saccharomyces cerevisiae	[ui:ynl090w] [pn:gtp-binding protein of the rho subfamily of ras-like proteins:rho2 protein] [gn:rho2:n22371] [gtcfc:12.13:12.16:12.8] [keggfc:14.2] [sgdfc:1.5.2:3.2.0:9.4.0:10.2.3] [db:gtc-saccharomyces cerevisiae]
CONTIG1952	14187550_f2_2	6379	20482	207	69	YNR002C	130	3.1(10)-8	Saccharomyces cerevisiae	[ui:ynr002c] [pn:strong similarity to y.lipolytica glyoxylate pathway regulator gpr1:fun34 protein] [gn:fun34:n2029] [gtcfc:12.13] [keggfc:14.2] [sgdfc:1.5.2] [db:gtc-saccharomyces cerevisiae]
CONTIG3471	6413176_c1_5	6380	20483	876	292	YNR002C	538	5.7(10)-52	Saccharomyces cerevisiae	[ui:ynr002c] [pn:strong similarity to y.lipolytica glyoxylate pathway regulator gpr1:fun34 protein] [gn:fun34:n2029] [gtcfc:12.13] [keggfc:14.2] [sgdfc:1.5.2] [db:gtc-saccharomyces cerevisiae]

CONTIG598	14570462_c2_4	6381	20484	768	256	YNR002C	535	1.2(10)-51	Saccharomyces cerevisiae	[ui:ynr002c] [pn:strong similarity to y.lipolytica glyoxylate pathway regulator gpr1:fun34 protein] [gn:fun34:n2029] [gtcfc:12.13] [keggfc:14.2] [sgdfc:1.5.2] [db:gtc-saccharomyces cerevisiae]
CONTIG1152	1250000_f3_4	6382	20485	843	281	YOR125C	691	3.6(10)-68	Saccharomyces cerevisiae	[ui:yor125c] [pn:involved in glucose repression:cat5 protein:ubiquinone biosynthesis protein coq7] [gn:cat5:coq7:o3284:yor3284c] [gtcfc:12.13:9.12] [keggfc:14.2] [sgdfc:1.5.2:1.7.3] [db:gtc-saccharomyces cerevisiae]
CONTIG4461	6924017_c2_4	6383	20486	1734	578	YPL026C	259	4.0(10)-42	Saccharomyces cerevisiae	[ui:ypl026c] [pn:suppressor kinase of snf3] [gn:sks1] [gtcfc:12.13] [keggfc:14.2] [sgdfc:1.5.2] [db:gtc-saccharomyces cerevisiae]
CONTIG3974	1956881_c2_3	6384	20487	858	286	YPL002C	299	1.3(10)-38	Saccharomyces cerevisiae	[ui:ypl002c] [pn:involved in glucose derepression] [gn:snf8] [gtcfc:12.13] [keggfc:14.2] [sgdfc:1.5.2] [db:gtc-saccharomyces cerevisiae]
CONTIG4717	34156676_f1_1	6385	20488	606	202	YPR165W	548	5.0(10)-53	Saccharomyces cerevisiae	[ui:ypr165w] [pn:gtp-binding protein of the rho subfamily of ras-like proteins:rho1 protein] [gn:rho1:p9325] [gtcfc:12.13:12.16:12.8] [keggfc:13.3] [sgdfc:1.5.2:3.2.0:9.4.0:10.2.3] [db:gtc-saccharomyces cerevisiae]

CONTIG4819	4723132_f1_1	6386	20489	606	202	YPR165W	737	4.7(10)-73	Saccharomyces cerevisiae	[ui:ypr165w] [pn:gtp-binding protein of the rho subfamily of ras-like proteins:rho1 protein] [gn:rho1:p9325] [gtcfc:12.13:12.16:12.8] [keggfc:13.3] [sgdfc:1.5.2:3.2.0:9.4.0:10.2.3] [db:gtc-saccharomyces cerevisiae]
CONTIG4082	11022577_f2_1	6387	20490	1239	413	YHL003C	1089	2.3(10)-110	Saccharomyces cerevisiae	[ui:yhl003c] [pn:longevity-assurance protein:longevity-assurance protein 1] [gn:lag1] [gtcfc:12.13:12.8] [keggfc:14.2] [sgdfc:3.10.0:11.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3085	34413175_c2_5	6388	20491	1263	421	YIL123W	1009	7.0(10)-102	Saccharomyces cerevisiae	[ui:yil123w] [pn:strong similarity to sun4p, uth1p, nca3p and c.wickerhamii beta-glucosidase:hypothetical 48.1 kd protein in kgd1-rpi1 intergenic region] [gtcfc:12.13] [keggfc:14.2] [sgdfc:11.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4489	14459376_f1_2	6389	20492	534	178	YIL123W	235	3.5(10)-19	Saccharomyces cerevisiae	[ui:yil123w] [pn:strong similarity to sun4p, uth1p, nca3p and c.wickerhamii beta-glucosidase:hypothetical 48.1 kd protein in kgd1-rpi1 intergenic region] [gtcfc:12.13] [keggfc:14.2] [sgdfc:11.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG	ID								Organism	Description
CONTIG2528	395426_f3_1	6390	20493	1302	434	YKL008C	336	1.5(10)-30	Saccharomyces cerevisiae	[ui:ykl008c] [pn:strong similarity to lag1p:hypothetical 49.0 kd protein ufd4-cap1 intergenic region] [gn:ykl156] [gtcfc:12.13] [keggfc:14.2] [sgdfc:11.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5207	10198557_f2_3	6391	20494	984	328	YDL025C	329	4.2(10)-29	Saccharomyces cerevisiae	[ui:ydl025c] [pn:ser/thr protein kinase of the dead/deah box family] [gtcfc:12.13:13.2] [keggfc:14.2] [sgdfc:11.1.0:15.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5780	20345001_c2_28	6392	20495	2706	902	YDR466W	755	2.2(10)-78	Saccharomyces cerevisiae	[ui:ydr466w] [pn:similarity to ser/thr protein kinase] [gtcfc:12.13:14.3] [keggfc:14.2] [sgdfc:15.0.0:13.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4588	4959626_c3_8	6393	20496	810	270	YDR490C	113	0.00084	Saccharomyces cerevisiae	[ui:ydr490c] [pn:similarity to ser/thr protein kinases] [gtcfc:12.13:14.3] [keggfc:14.2] [sgdfc:15.0.0:13.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1369	3914057_c3_4	6394	20497	1080	360	YDR507C	1088	3.0(10)-110	Saccharomyces cerevisiae	[ui:ydr507c] [pn:ser/thr-protein kinase] [gn:gin4] [gtcfc:12.13:14.3] [keggfc:14.2] [sgdfc:15.0.0:13.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1896	31688383_f1_1	6395	20498	1575	525	YDR507C	177	1.2(10)-20	Saccharomyces cerevisiae	[ui:ydr507c] [pn:ser/thr-protein kinase] [gn:gin4] [gtcfc:12.13:14.3] [keggfc:14.2] [sgdfc:15.0.0:13.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2418	13930402_c3_4	6396	20499	951	317	YDR507C	207	1.8(10)-15	Saccharomyces cerevisiae	[ui:ydr507c] [pn:ser/thr-protein kinase] [gn:gin4] [gtcfc:12.13:14.3] [keggfc:14.2] [sgdfc:15.0.0:13.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1440	23600192_f2_1	6397	20500	771	257	YFR014C	308	1.3(10)-27	Saccharomyces cerevisiae	[ui:yfr014c] [pn:ca2+/calmodulin-dependent ser/thr protein kinase type i:calcium/calmodulin-dependent protein kinase type i] [gn:cmk1] [gtcfc:12.13:12.8:14.1] [ec:2.7.1.123] [keggfc:14.1] [sgdfc:3.1.0:9.2.0:15.0.0] [db:gtc-saccharomyc
CONTIG4006	14540907_f1_2	6398	20501	687	229	YGR080W	153	1.3(10)-10	Saccharomyces cerevisiae	[ui:ygr080w] [pn:weak similarity to human tyrosine kinase a6:hypothetical 37.1 kd protein in pac10-tom20 intergenic region] [gtcfc:12.13:14.3] [sgdfc:15.0.0:13.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4006	22363752_f3_4	6399	20502	573	191	YGR080W	148	4.9(10)-10	Saccharomyces cerevisiae	[ui:ygr080w] [pn:weak similarity to human tyrosine kinase a6:hypothetical 37.1 kd protein in pac10-tom20 intergenic region] [gtcfc:12.13:14.3] [sgdfc:15.0.0:13.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4652	23859655_c3_8	6400	20503	909	303	YGR262C	336	1.5(10)-30	Saccharomyces cerevisiae	[ui:ygr262c] [pn:weak similarity to protein kinases:hypothetical 29.9 kd protein in apl6-mes1 intergenic region] [gtcfc:12.13:14.3] [sgdfc:15.0.0:13.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5520	4093775_f1_3	6401	20504	1263	421	YHR205W	248	1.0(10)-18	Saccharomyces cerevisiae	[ui:yhr205w] [pn:strong similarity to s.pombe sck1 protein kinase:camp-dependent protein kinase sch9] [gn:sch9:kom1] [gtcfc:12.13:12.8] [ec:2.7.1.37] [keggfc:14.1] [sgdfc:3.8.0:15.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5520	23539062_f1_4	6402	20505	1131	377	YHR205W	1351	4.0(10)-138	Saccharomyces cerevisiae	[ui:yhr205w] [pn:strong similarity to s.pombe sck1 protein kinase:camp-dependent protein kinase sch9] [gn:sch9:kom1] [gtcfc:12.13:12.8] [ec:2.7.1.37] [keggfc:14.1] [sgdfc:3.8.0:15.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5619	29782012_c3_20	6403	20506	4140	1380	YJL095W	1086	1.7(10)-137	Saccharomyces cerevisiae	[ui:yjl095w] [pn:ser/thr protein kinase of the mekk family:serine/threonine protein kinase bck1/slk1/ssp31] [gn:bck1:slk1:ssp31:las3:j0906] [gtcfc:12.13:12.8:13.2:14.1] [ec:2.7.--] [keggfc:14.1] [sgdfc:3.1.0:3.2.0:3.8.0:9.2.0:10.2.5:
CONTIG5276	23832527_c1_11	6404	20507	972	324	YLR063W	489	9.0(10)-47	Saccharomyces cerevisiae	[ui:ylr063w] [pn:ser/thr protein kinase] [gtcfc:12.13:14.3] [keggfc:14.2] [sgdfc:15.0.0:13.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1192	433325_f2_1	6405	20508	519	173	YMR216C	281	1.1(10)-23	Saccharomyces cerevisiae	[ui:ymr216c] [pn:similarity to ser/thr protein kinases] [gtcfc:12.13:14.3] [keggfc:14.2] [sgdfc:15.0.0:13.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4234	683784l_f2_1	6406	20509	1731	577	YMR216C	688	4.5(10)-107	Saccharomyces cerevisiae	[ui:ymr216c] [pn:similarity to ser/thr protein kinases] [gtcfc:12.13:14.3] [keggfc:14.2] saccharomyces cerevisiae]
b3x16065.y	12632160_c1_5	6407	20510	186	62	YMR216C	119	2.5(10)-6	Saccharomyces cerevisiae	[ui:ymr216c] [pn:similarity to ser/thr protein kinases] [gtcfc:12.13:14.3] [keggfc:14.2] [sgdfc:15.0.0:13.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3370	22866412_c1_6	6408	20511	2367	789	YOL100W	545	1.1(10)-51	Saccharomyces cerevisiae	[ui:yol100w] [pn:similarity to ser/thr protein kinases] [gtcfc:12.13:14.3] [keggfc:14.2] [sgdfc:15.0.0:13.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3118	1178827_c1_1	6409	20512	846	282	YOL045W	938	2.3(10)-94	Saccharomyces cerevisiae	[ui:yol045w] [pn:similarity to ser/thr protein kinase] [gtcfc:12.13:14.3] [keggfc:14.2] [sgdfc:15.0.0:13.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4637	15819388_f2_1	6410	20513	2799	933	YOL045W	334	2.3(10)-62	Saccharomyces cerevisiae	[ui:yol045w] [pn:similarity to ser/thr protein kinase] [gtcfc:12.13:14.3] [keggfc:14.2] [sgdfc:15.0.0:13.0.0] saccharomyces cerevisiae]
CONTIG1179	547030_f3_1	6411	20514	1086	362	YOL016C	1065	8.3(10)-108	Saccharomyces cerevisiae	[ui:yol016c] [pn:ca2+/calmodulin-dependent ser/thr protein kinase, type ii:calcium/calmodulin-dependent protein kinase type ii] [gn:cmk2] [gtcfc:12.13:14.1] [ec:2.7.1.123] [keggfc:14.1] [sgdfc:9.2.0:15.0.0] [db:gtc-saccharomyces cerev

CONTIG2469	20343800_f2_1	6412	20515	1458	486	YOR267C	587	3.7(10)-57	Saccharomyces cerevisiae	[ui:yor267c] [pn:similarity to ser/thr protein kinases] [gtcfc:12.13:14.3] [keggfc:14.2] [sgdfc:15.0.0:13.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3562	11797027_f3_4	6413	20516	1401	467	YOR267C	869	4.9(10)-87	Saccharomyces cerevisiae	[ui:yor267c] [pn:similarity to ser/thr protein kinases] [gtcfc:12.13:14.3] [keggfc:14.2] [sgdfc:15.0.0:13.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2806	10161442_f2_1	6414	20517	858	286	YPL236C	233	1.7(10)-19	Saccharomyces cerevisiae	[ui:ypl236c] [pn:similarity to s.pombe hypothetical protein spac3h1.13] [gtcfc:12.13:14.1] [keggfc:14.2] [sgdfc:15.0.0:13.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5023	4070138_c2_9	6415	20518	1317	439	YPL203W	1355	1.5(10)-138	Saccharomyces cerevisiae	[ui:ypl203w] [pn:camp-dependent protein kinase 2, catalytic chain:camp-dependent protein kinase type 2:pka 2] [gn:tpk2:ykr1:pka2] [gtcfc:12.13:12.8] [ec:2.7.1.37] [keggfc:13.1] [sgdfc:9.2.0:15.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5056	488131_f1_4	6416	20519	1212	404	YPL203W	1302	6.4(10)-133	Saccharomyces cerevisiae	[ui:ypl203w] [pn:camp-dependent protein kinase 2, catalytic chain:camp-dependent protein kinase type 2:pka 2] [gn:tpk2:ykr1:pka2] [gtcfc:12.13:12.8] [ec:2.7.1.37] [keggfc:13.1] [sgdfc:9.2.0:15.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5114	192076_f1_1	6417	20520	2856	952	YPL150W	695	1.3(10)-68	Saccharomyces cerevisiae	[ui:ypl150w] [pn:similarity to ser/thr kinases] [gtcfc:12.13:14.3] [keggfc:14.2] [sgdfc:15.0.0:13.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG728	25976513_c2_2	6418	20521	546	182	YPL141C	486	1.2(10)-45	Saccharomyces cerevisiae	[ui:ypl141c] [pn:strong similarity to protein kinase kin4p] [gtcfc:12.13:14.3] [keggfc:14.2] [sgdfc:15.0.0:13.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5628	863912_f3_8	6419	20522	2574	858	YAL041W	853	7.0(10)-98	Saccharomyces cerevisiae	[ui:yal041w] [pn:gtp/gdp exchange factor for cdc42p:cell division control protein 24:calcium regulatory protein] [gn:cdc24:cls4] [gtcfc:12.13:12.9] [keggfc:13.1:13.3] [sgdfc:3.2.0:3.3.0:3.8.0:9.2.0:10.1.3:10.2.4] [db:gtc-saccharo
CONTIG4077	25835202_c3_7	6420	20523	408	136	YDL135C	158	1.1(10)-11	Saccharomyces cerevisiae	[ui:ydl135c] [pn:rho gdp dissociation inhibitor with activity toward rho1p] [gn:rdi1] [gtcfc:12.13:12.8] [keggfc:14.2] [sgdfc:3.2.0:10.2.4] [db:gtc-saccharomyces cerevisiae]
CONTIG4319	5273502_c1_8	6421	20524	621	207	YDL135C	515	1.6(10)-49	Saccharomyces cerevisiae	[ui:ydl135c] [pn:rho gdp dissociation inhibitor with activity toward rho1p] [gn:rdi1] [gtcfc:12.13:12.8] [keggfc:14.2] [sgdfc:3.2.0:10.2.4] [db:gtc-saccharomyces cerevisiae]
CONTIG5749	24665635_c2_23	6422	20525	600	200	YDL135C	113	4.2(10)-5	Saccharomyces cerevisiae	[ui:ydl135c] [pn:rho gdp dissociation inhibitor with activity toward rho1p] [gn:rdi1] [gtcfc:12.13:12.8] [keggfc:14.2] [sgdfc:3.2.0:10.2.4] [db:gtc-saccharomyces cerevisiae]

CONTIG2879	34573406_c1_3	6423	20526	915	305	YPL115C	295	7.0(10)-25	Saccharomyces cerevisiae	[ui:ypl115c] [pn:gtpase-activating protein for cdc42p and rho1p:protein] [gn:bem3] [gtcfc:12.13:12.8:12.9] [sgdfc:3.2.0:3.3.0:9.2.0:10.2.4] [db:gtc-saccharomyces cerevisiae]
CONTIG3171	23626442_c1_4	6424	20527	825	275	YPL115C	295	7.0(10)-25	Saccharomyces cerevisiae	[ui:ypl115c] [pn:gtpase-activating protein for cdc42p and rho1p:protein] [gn:bem3] [gtcfc:12.13:12.8:12.9] [keggfc:13.3] [sgdfc:3.2.0:3.3.0:9.2.0:10.2.4] [db:gtc-saccharomyces cerevisiae]
b9x10d83.y	29329385_c2_1	6425	20528	453	151	YPL115C	111	3.0(10)-5	Saccharomyces cerevisiae	[ui:ypl115c] [pn:gtpase-activating protein for cdc42p and rho1p:protein] [gn:bem3] [gtcfc:12.13:12.8:12.9] [keggfc:13.3] [sgdfc:3.2.0:3.3.0:9.2.0:10.2.4] [db:gtc-saccharomyces cerevisiae]
CONTIG5809	4296926_f1_6	6426	20529	564	188	YBR109C	470	9.3(10)-45	Saccharomyces cerevisiae	[ui:ybr109c] [pn:calmodulin] [gn:cmd1:ybr0904] [gtcfc:12.13:12.16:12.6:12.8:12.9] [keggfc:14.2] [sgdfc:3.1.0:3.2.0:3.3.0:3.8.0:8.7.0:9.3.0:10.2.7] [db:gtc-saccharomyces cerevisiae]

CONTIG4093	19695760_c2_5	6427	20530	924	308	YBR200W	271	1.8(10)-29	Saccharomyces cerevisiae	[ui:ybr200w] [pn:bud emergence mediator:bem1 protein] [gn:bem1:sro1:ybr1412] [gtcfc:12.13:12.16:12.8:12.9] [sgdfc:3.2.0:3.3.0:3.8.0:9.3.0:10.2.7] [db:gtc-saccharomyces cerevisiae]
CONTIG4093	23478436_c2_4	6428	20531	978	326	YBR200W	370	5.4(10)-34	Saccharomyces cerevisiae	[ui:ybr200w] [pn:bud emergence mediator:bem1 protein] [gn:bem1:sro1:ybr1412] [gtcfc:12.13:12.16:12.8:12.9] [keggfc:13.1] [sgdfc:3.2.0:3.3.0:3.8.0:9.3.0:10.2.7] [db:gtc-saccharomyces cerevisiae]
CONTIG2864	26386562_c1_5	6429	20532	1113	371	YBR200W	153	2.7(10)-8	Saccharomyces cerevisiae	[ui:ybr200w] [pn:bud emergence mediator:bem1 protein] [gn:bem1:sro1:ybr1412] [gtcfc:12.13:12.16:12.8:12.9] [keggfc:13.1] [sgdfc:3.2.0:3.3.0:3.8.0:9.3.0:10.2.7] [db:gtc-saccharomyces cerevisiae]
CONTIG2881	25410625_c3_8	6430	20533	465	155	YOR149C	100	0.0015	Saccharomyces cerevisiae	[ui:yor149c] [pn:protein kinase c pathway protein:protein] [gn:smp3] [gtcfc:12.13:12.8] [keggfc:14.2] [sgdfc:3.1.0:3.2.0:3.8.0:10.2.7] [db:gtc-saccharomyces cerevisiae]

CONTIG2881	4334458_c2_7	6431	20534	582	194	232	YOR149C	9.4(10)-19	Saccharomyces cerevisiae	[ui:yor149c] [pn:protein kinase c pathway protein:protein] [gn:smp3] [gtcfc:12.13:12.8] [keggfc:14.2] [sgdfc:3.1.0:3.2.0:3.8.0:10.2.7] [db:gtc-saccharomyces cerevisiae]
CONTIG1696	3994012_f1_1	6432	20535	810	270	927	YPL106C	3.5(10)-93	Saccharomyces cerevisiae	[ui:ypl106c] [pn:heat shock protein of hsp70 family:heat shock protein homolog sse1] [gn:sse1:msi3:lpg3c] [gtcfc:12.7:13.2] [keggfc:14.2] [sgdfc:10.2.7:10.4.8:11.1.0] [db:gtc-saccharomyces cerevisiae]
b2x11950.y	34617300_c1_1	6433	20536	510	170	354	YDL128W	1.8(10)-32	Saccharomyces cerevisiae	[ui:ydl128w] [pn:ca2+-transport:h+/ca2+ exchange protein, vacuolar] [gn:vcx1] [gtcfc:12.5:12.13:12.16] [keggfc:14.2] [sgdfc:1.8.2:7.2.2:8.5.0:9.10.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2355	2740682_c1_3	6434	20537	1365	455	699	YGL006W	3.3(10)-68	Saccharomyces cerevisiae	[ui:ygl006w] [pn:ca2+-transporting p-type atpase:calcium-transporting atpase 2:vacuolar ca2+-atpase] [gn:pca1:pmc1] [gtcfc:12.5:12.13:12.16] [ec:3.6.1.38] [keggfc:14.1] [sgdfc:1.8.2:7.2.2:7.8.0:8.5.0:9.10.0] [db:gtc-saccharomyces cere

CONTIG3119	35392812_f2_1	6435	20538	1350	450	YGL006W	574	9.1(10)-79	Saccharomyces cerevisiae	[ui:ygl006w] [pn:ca2+-transporting p-type atpase:calcium-transporting atpase 2:vacuolar ca2+-atpase] [gn:pca1:pmc1] [gtcfc:12.5:12.13:12.16] [sgdfc:1.8.2:7.2.2.7.8.0:8.5.0:9.10.0] [db:gtc-saccharomyces cere
CONTIG3371	9922150_c2_6	6436	20539	225	75	YPL234C	279	1.6(10)-24	Saccharomyces cerevisiae	[ui:ypl234c] [pn:h+-atpase v0 domain 17 kd subunit, vacuolar:proteolipid protein vma11] [gn:vma11:tfp3:cls9:p1064] [gtcfc:12.13:12.16:12.5:12.6] [keggfc:14.2] [sgdfc:1.8.2:6.4.0:7.2.2.7.8.0:8.5.0:9 .10.0] [db:gtc-saccharomyces cerevisi
CONTIG5387	21490702_f3_13	6437	20540	1380	460	YPL066W	126	6.0(10)-5	Saccharomyces cerevisiae	[ui:ypl066w] [pn:involved in vacuolar traffic] [gn:vps28] [gtcfc:12.13] [keggfc:14.2] [sgdfc:8.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4730	14641882_c1_9	6438	20541	1344	448	YPR173C	1338	1.1(10)-163	Saccharomyces cerevisiae	[ui:ypr173c] [pn:vacuolar sorting protein:end13 protein] [gn:end13:vps4:grd13:p9705] [gtcfc:12.13:12.16] [keggfc:14.2] [sgdfc:8.5.0:9.10.0] [db:gtc-saccharomyces cerevisiae]

b3x13880.x	32628752_f1_1	6439	20542	264	88	YJR069C	192	2.7(10)-15	Saccharomyces cerevisiae	[ui:yjr069c] [pn:controls 6-n-hydroxylaminopurine sensitivity and mutagenesis:ham1 protein] [gn:ham1:jl811] [gtcfc:12.14] [keggfc:14.2] [sgdfc:11.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4456	9960763_c3_8	6440	20543	789	263	YKL110C	432	1.0(10)-53	Saccharomyces cerevisiae	[ui:ykl110c] [pn:involved in resistance to k.lactis killer toxin:kti12 protein] [gn:kti12:ykl500-ykl446] [gtcfc:12.14] [keggfc:14.2]
CONTIG5797	23628301_f3_12	6441	20544	1695	565	YAL009W	384	1.2(10)-35	Saccharomyces cerevisiae	[ui:yal009w] [pn:meiotic protein:sporulation protein] [gn:spo7] [gtcfc:12.15:12.8] [keggfc:14.2] [sgdfc:3.4.0:3.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5531	39038_f2_13	6442	20545	747	249	YBR057C	128	5.0(10)-6	Saccharomyces cerevisiae	[ui:ybr057c] [pn:meiotic protein:hypothetical 41.4 kd protein in prp6-ubp14 intergenic region] [gn:mum2:ybr0514] [gtcfc:12.15:12.8] [keggfc:14.2] [sgdfc:3.4.0:3.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1924	23560953_c3_4	6443	20546	297	99	YCL048W	168	6.5(10)-12	Saccharomyces cerevisiae	[ui:ycl048w] [pn:strong similarity to sporulation-specific protein sps2:p:hypothetical sps2-like 52.0 kd protein in apa1/dtp-pdi1 intergenic region] [gn:ycl48w] [gtcfc:12.15:12.8] [keggfc:14.2] [sgdfc:3.4.0:3.5.0] [db:gtc-saccharomyces

CONTIG	Identifier								Organism	Description
CONTIG499	24406692_f3_1	6444	20547	603	201	YCL048W	342	3.3(10)-31	Saccharomyces cerevisiae	[ui:ycl048w] [pn:strong similarity to sporulation-specific protein sps2p:hypothetical sps2-like 52.0 kd protein in apa1/dtp-pdi1 intergenic region] [gn:ycl048w] [gtcfc:12.15:12.8] [keggfc:14.2] [sgdfc:3.4.0:3.5.0] [db:gtc-saccharomyces
CONTIG4150	30757692_f2_2	6445	20548	1542	514	YDL240W	341	1.1(10)-28	Saccharomyces cerevisiae	[ui:ydl240w] [pn:gtpase-activating protein of the rho/rac family:protein] [gn:lrg1] [gtcfc:12.15] [keggfc:14.2] [sgdfc:3.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4150	23910752_f3_6	6446	20549	1164	388	YDL240W	580	8.6(10)-63	Saccharomyces cerevisiae	[ui:ydl240w] [pn:gtpase-activating protein of the rho/rac family:protein] [gn:lrg1] [gtcfc:12.15] [keggfc:14.2] [sgdfc:3.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4150	187761_f2_3	6447	20550	411	137	YDL240W	92	0.0028	Saccharomyces cerevisiae	[ui:ydl240w] [pn:gtpase-activating protein of the rho/rac family:protein] [gn:lrg1] [gtcfc:12.15] [keggfc:14.2] [sgdfc:3.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4282	10212586_f2_2	6448	20551	903	301	YDR055W	362	2.6(10)-33	Saccharomyces cerevisiae	[ui:ydr055w] [pn:strong similarity to sps2 protein] [gtcfc:12.15:12.8] [keggfc:14.2] [sgdfc:3.4.0:3.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5756	13835750_f3_11	6449	20552	1239	413	YDR055W	399	3.1(10)-37	Saccharomyces cerevisiae	[ui:ydr055w] [pn:strong similarity to sps2 protein] [gtcfc:12.15:12.8] [keggfc:14.2] [sgdfc:3.4.0:3.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG	Seq								Organism	Description
CONTIG2124	29879577_c3_3	6450	20553	1431	477	YDR108W	178	5.4(10)-19	Saccharomyces cerevisiae	[ui:ydr108w] [pn:sporulation specific protein:sporulation protein] [gn:gsg1] [gtcfc:12.15:12.8] [keggfc:14.2] [sgdfc:3.4.0:3.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1087	1048281_f1_1	6451	20554	504	168	YDR218C	215	3.8(10)-17	Saccharomyces cerevisiae	[ui:ydr218c] [pn:septin-related sporulation protein] [gn:spr28] [gtcfc:12.15:12.16-12.8] [keggfc:14.2]
CONTIG5162	1953125_c2_7	6452	20555	1557	519	YDR403W	918	3.1(10)-92	Saccharomyces cerevisiae	[ui:ydr403w] [pn:spore wall maturation protein:spore wall maturation protein dit1] [gn:dit1:d9509] [gtcfc:12.15] [keggfc:14.2] [sgdfc:3.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5776	4472215_f1_4	6453	20556	1140	380	YGR059W	473	4.5(10)-45	Saccharomyces cerevisiae	[ui:ygr059w] [pn:sporulation-specific septin] [gn:spr3] [gtcfc:12.15:12.16] [keggfc:14.2] [sgdfc:3.4.0:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2552	34064625_f3_2	6454	20557	627	209	YKL165C	464	3.5(10)-43	Saccharomyces cerevisiae	[ui:ykl165c] [pn:sporulation protein:hypothetical 105.7 kd protein in tpk3-pir1 intergenic region] [gn:ykl619] [gtcfc:12.15] [keggfc:3.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2552	976502_f3_3	6455	20558	270	90	YKL165C	213	3.0(10)-16	Saccharomyces cerevisiae	[ui:ykl165c] [pn:sporulation protein:hypothetical 105.7 kd protein in tpk3-pir1 intergenic region] [gn:ykl619] [gtcfc:12.15] [keggfc:3.4.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2870	839555_c3_2	6456	20559	852	284	YKL165C	404	1.0(10)-36	Saccharomyces cerevisiae	[ui:ykl165c] [pn:sporulation protein:hypothetical 105.7 kd protein in tpk3-pir1 intergenic region] [gn:ykl619] [gtcfc:3.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5472	9953437_f2_4	6457	20560	1722	574	YKL165C	1240	2.3(10)-126	Saccharomyces cerevisiae	[ui:ykl165c] [pn:sporulation protein:hypothetical 105.7 kd protein in tpk3-pir1 intergenic region] [gn:ykl619] [gtcfc:12.15] [keggfc:14.2] [sgdfc:3.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3459	6281875_f2_2	6458	20561	1311	437	YML115C	126	5.5(10)-5	Saccharomyces cerevisiae	[ui:yml115c] [pn:vanadate resistance protein] [gn:van1:vrg7:ym8339] [gtcfc:12.15:12.8] [keggfc:14.2] [sgdfc:3.4.0:3.8.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5090	550678_c3_10	6459	20562	318	106	YML115C	399	3.1(10)-37	Saccharomyces cerevisiae	[ui:yml115c] [pn:vanadate resistance protein] [gn:van1:vrg7:ym8339] [gtcfc:12.15:12.8] [keggfc:14.2] [sgdfc:3.4.0:3.8.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4018	6723775_f1_1	6460	20563	933	311	YML110C	934	6.2(10)-94	Saccharomyces cerevisiae	[ui:yml110c] [pn:dbf2 interacting protein:hypothetical 34.7 kd protein in ctk3-zds2 intergenic region] [gn:dbi56:ym8339] [gtcfc:12.15] [keggfc:14.2] [sgdfc:3.4.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2174	1285131_f1_1	6461	20564	780	260	YMR063W	119	2.3(10)-5	Saccharomyces cerevisiae	[ui:ymr063w] [pn:regulator for sporulation and invasive growth] [gn:rtim9] [gtcfc:12.15:12.8] [keggfc:14.2] [sgdfc:3.2.0:3.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3791	9798180_f1_2	6462	20565	471	157	YNL202W	319	9.4(10)-29	Saccharomyces cerevisiae	[ui:ynl202w] [pn:sporulation-specific protein:sporulation protein sps19] [gn:sps19:spx19:n1362] [gtcfc:12.15:12.6:12.8] [keggfc:14.2] [sgdfc:3.4.0:3.5.0:9.8.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3945	9922137_c3_5	6463	20566	936	312	YNL202W	926	4.5(10)-93	Saccharomyces cerevisiae	[ui:ynl202w] [pn:sporulation-specific protein:sporulation protein sps19] [gn:sps19:spx19:n1362] [gtcfc:12.15:12.6:12.8] [keggfc:14.2] [sgdfc:3.4.0:3.5.0:9.8.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5353	12929652_c3_15	6464	20567	879	293	YNL202W	881	2.6(10)-88	Saccharomyces cerevisiae	[ui:ynl202w] [pn:sporulation-specific protein:sporulation protein sps19] [gn:sps19:spx19:n1362] [gtcfc:12.15:12.6:12.8] [keggfc:14.2] [sgdfc:3.4.0:3.5.0:9.8.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5787	10548250_c3_37	6465	20568	954	318	YOR313C	167	4.0(10)-12	Saccharomyces cerevisiae	[ui:yor313c] [pn:sporulation-specific protein:sporulation-specific protein 4] [gn:sps4:o6120] [keggfc:12.15] [sgdfc:3.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1919	24391380_f2_3	6466	20569	1167	389	YAL047C	114	0.0014	Saccharomyces cerevisiae	[ui:yal047c] [pn:stu2p interactant:hypothetical 72.1 kd protein in acs1-gcv3 intergenic region] [gn:spi6:fun42] [gtcfc:12.16] [keggfc:14.2] [sgdfc:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4316	10625306_c3_9	6467	20570	705	235	YAL047C	96	0.041	Saccharomyces cerevisiae	[ui:yal047c] [pn:stu2p interactant:hypothetical 72.1 kd protein in acs1-gcv3 intergenic region] [gn:spi6:fun42] [gtcfc:12.16] [keggfc:14.2] [sgdfc:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG713	2222013_c2_3	6468	20571	429	143	YAL020C	201	5.4(10)-16	Saccharomyces cerevisiae	[ui:yal020c] [pn:alpha-tubulin suppressor:ats1 protein:alpha-tubulin suppressor 1] [gn:ats1:yal006:fun28] [gtcfc:12.16] [keggfc:14.2] [sgdfc:9.3.0] [db:gtc-saccharomyces cerevisiae]
b9x13524.x	24319792_c2_6	6469	20572	318	106	YAL020C	109	9.3(10)-6	Saccharomyces cerevisiae	[ui:yal020c] [pn:alpha-tubulin suppressor:ats1 protein:alpha-tubulin suppressor 1] [gn:ats1:yal006:fun28] [gtcfc:12.16] [keggfc:14.2] [sgdfc:9.3.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4778	36456301_c3_8	6470	20573	3078	1026	YBL034C	212	5.4(10)-13	Saccharomyces cerevisiae	[ui:ybl034c] [pn:mitotic spindle protein:mitotic spindle protein stu1] [gn:stu1:ybl0416] [gtcfc:12.16] [keggfc:14.2] [sgdfc:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4097	32675441_f1_1	6471	20574	2652	884	YBL007C	617	1.3(10)-115	Saccharomyces cerevisiae	[ui:ybl007c] [pn:cytoskeleton assembly control protein:cytoskeleton assembly control protein sla1] [gn:sla1:ybl0321] [keggfc:14.2] [sgdfc:3.1.0:6.4.0:9.3.0] [gtcfc:12.16:12.8] [db:gtc-saccharomyces cerevisiae]
CONTIG3731	21660187_c1_12	6472	20575	1113	371	YBL007C	99	0.078	Saccharomyces cerevisiae	[ui:ybl007c] [pn:cytoskeleton assembly control protein:cytoskeleton assembly control protein sla1] [gn:sla1:ybl0321] [gtcfc:12.16:12.8] [sgdfc:3.1.0:6.4.0:9.3.0] [db:gtc-saccharomyces cerevisiae]
b1x16816.x	110301_c3_2	6473	20576	345	115	YBL007C	279	4.2(10)-23	Saccharomyces cerevisiae	[ui:ybl007c] [pn:cytoskeleton assembly control protein:cytoskeleton assembly control protein sla1] [gn:sla1:ybl0321] [keggfc:14.2] [sgdfc:3.1.0:6.4.0:9.3.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5011	10833254_c2_9	6474	20577	822	274	YBL007C	124	1.2(10)-7	Saccharomyces cerevisiae	[ui:ybl007c] [pn:cytoskeleton assembly control protein:cytoskeleton assembly control protein sla1] [gn:sla1:ybl0321] [gtcfc:12.16:12.8] [keggfc:14.2] [sgdfc:3.1.0:6.4.0:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2549	3181267_c3_5	6475	20578	1257	419	YBR130C	94	0.11	Saccharomyces cerevisiae	[ui:ybr130c] [pn:required for mother cell-specific expression of ho:hypothetical 47.4 kd protein in vma2-cks1 intergenic region] [gn:she3:ybr1005] [keggfc:14.2] [sgdfc:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4178	14881552_f2_5	6476	20579	309	103	YBR130C	123	4.2(10)-7	Saccharomyces cerevisiae	[ui:ybr130c] [pn:required for mother cell-specific expression of ho:hypothetical 47.4 kd protein in vma2-cks1 intergenic region] [gn:she3:ybr1005] [keggfc:14.2] [sgdfc:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4178	24391051_f3_7	6477	20580	1152	384	YBR130C	96	0.055	Saccharomyces cerevisiae	[ui:ybr130c] [pn:required for mother cell-specific expression of ho:hypothetical 47.4 kd protein in vma2-cks1 intergenic region] [gn:she3:ybr1005] [keggfc:14.2] [sgdfc:9.3.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5321	2345083_c1_21	6478	20581	1482	494	YBR130C	103	0.017	Saccharomyces cerevisiae	[ui:ybr130c] [pn:required for mother cell-specific expression of ho:hypothetical 47.4 kd protein in vma2-cks1 intergenic region] [gn:she3:ybr1005] [gtcfc:12.16] [keggfc:14.2] [sgdfc:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2094	26682963_f1_1	6479	20582	1284	428	YBR172C	101	0.03599	Saccharomyces cerevisiae	[ui:ybr172c] [pn:kinesin-related protein:smy2 protein] [gn:smy2:ybr1233] [gtcfc:12.16] [keggfc:14.2] [sgdfc:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG571	35957706_f3_16	6480	20583	1920	640	YBR172C	221	7.7(10)-15	Saccharomyces cerevisiae	[ui:ybr172c] [pn:kinesin-related protein:smy2 protein] [gn:smy2:ybr1233] [gtcfc:12.16] [keggfc:14.2] [sgdfc:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2508	20426386_f2_1	6481	20584	1071	357	YCR009C	218	1.5(10)-33	Saccharomyces cerevisiae	[ui:ycr009c] [pn:similarity to human amphiphysin and rvs167p:reduced viability upon starvation protein 161] [gn:rvs161:spe161:ycr9c] [gtcfc:12.16:12.6:12.8] [keggfc:14.2] [sgdfc:3.2.0:8.7.0:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4424	13010953_f3_4	6482	20585	1395	465	YCR088W	136	2.7(10)-15	Saccharomyces cerevisiae	[ui:ycr088w] [pn:actin-binding protein:actin binding protein] [gn:abp1:ycr88w] [gtcfc:12.16:12.8] [keggfc:14.2] [sgdfc:3.1.0:3.2.0:9.3.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5731	21879562_f2_10	6483	20586	363	121	YCR088W	226	5.7(10)-18	Saccharomyces cerevisiae	[ui:ycr088w] [pn:actin-binding protein:actin binding protein] [gn:abp1:ycr88w] [gtcfc:12.16:12.8] [keggfc:14.2] [sgdfc:3.1.0:3.2.0:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5733	2773275_f2_8	6484	20587	876	292	YCR088W	119	0.00011	Saccharomyces cerevisiae	[ui:ycr088w] [pn:actin-binding protein:actin binding protein] [gn:abp1:ycr88w] [gtcfc:12.16:12.8] [keggfc:14.2] [sgdfc:3.1.0:3.2.0:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5061	15628377_c3_13	6485	20588	837	279	YDL178W	646	2.1(10)-63	Saccharomyces cerevisiae	[ui:ydl178w] [pn:actin interacting protein 2] [gn:aip2] [keggfc:14.2] [sgdfc:9.3.0] [gtcfc:12.16] [db:gtc-saccharomyces cerevisiae]
CONTIG5541	34100078_c3_21	6486	20589	393	131	YDL178W	284	2.1(10)-24	Saccharomyces cerevisiae	[ui:ydl178w] [pn:actin interacting protein 2] [gn:aip2] [keggfc:14.2] [sgdfc:9.3.0] [gtcfc:12.16] [db:gtc-saccharomyces cerevisiae]
CONTIG5587	30272567_f2_5	6487	20590	816	272	YDR085C	96	0.069	Saccharomyces cerevisiae	[ui:ydr085c] [pn:involved in morphogenesis of the mating projection:afr1 protein] [gn:afr1:d4471] [gtcfc:12.16:12.8:12.9] [keggfc:14.2] [sgdfc:3.2.0:3.3.0:9.3.0] [db:gtc-saccharomyces cerevisiae]

CONTIG1278	25390933_f3_3	6488	20591	555	185	YDR388W	127	1.8(10)-7	Saccharomyces cerevisiae	[ui:ydr388w] [pn:reduced viability upon starvation protein:reduced viability upon starvation protein 167] [gn:rvs167:d9509] [gtcfc:12.16:12.8] [keggfc:14.2] [sgdfc:3.2.0:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4621	10040878_c2_5	6489	20592	1068	356	YDR388W	129	1.8(10)-5	Saccharomyces cerevisiae	[ui:ydr388w] [pn:reduced viability upon starvation protein:reduced viability upon starvation protein 167] [gn:rvs167:d9509] [gtcfc:12.16:12.8] [keggfc:14.2] [sgdfc:3.2.0:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5180	24398876_c3_15	6490	20593	1440	480	YDR388W	1148	1.3(10)-116	Saccharomyces cerevisiae	[ui:ydr388w] [pn:reduced viability upon starvation protein:reduced viability upon starvation protein 167] [gn:rvs167:d9509] [gtcfc:12.16:12.8] [keggfc:14.2] [sgdfc:3.2.0:9.3.0] [db:gtc-saccharomyces cerevisiae]
b9x10802.x	188410_f2_1	6491	20594	210	70	YDR388W	122	6.7(10)-7	Saccharomyces cerevisiae	[ui:ydr388w] [pn:reduced viability upon starvation protein:reduced viability upon starvation protein 167] [gn:rvs167:d9509] [gtcfc:12.16:12.8] [keggfc:14.2] [sgdfc:3.2.0:9.3.0] [db:gtc-saccharomyces cerevisiae]

CONTIG	ID				Gene		E-value	Organism	Description
CONTIG3405	6350826_f2_3	6492	20595	1020	340	YDR389W	290	1.3(10)-32	Saccharomyces cerevisiae	[ui:ydr389w] [pn:suppressor of actin mutation:protein] [gn:sac7] [gtcfc:12.16] [keggfc:14.2] [sgdfc:6.4.0:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3884	10192052_f1_1	6493	20596	849	283	YDR389W	147	4.9(10)-8	Saccharomyces cerevisiae	[ui:ydr389w] [pn:suppressor of actin mutation:protein] [gn:sac7] [gtcfc:12.16] [keggfc:14.2] [sgdfc:6.4.0:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5417	503288_c3_20	6494	20597	684	228	YDR484W	137	7.4(10)-7	Saccharomyces cerevisiae	[ui:ydr484w] [pn:suppressor of actin mutation:protein] [gn:sac2] [gtcfc:12.16] [keggfc:14.2] [sgdfc:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3725	10032590_c1_4	6495	20598	903	301	YER007W	188	1.7(10)-12	Saccharomyces cerevisiae	[ui:yer007w] [pn:required in the absence of cin8p:protein] [gn:pac2] [gtcfc:12.16] [keggfc:14.2] [sgdfc:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2273	2910900_c2_7	6496	20599	975	325	YER016W	371	1.8(10)-40	Saccharomyces cerevisiae	[ui:yer016w] [pn:binding to microtubules:hypothetical 38.4 kd protein in faa2-afg3 intergenic region] [gn:bim1] [gtcfc:12.16] [keggfc:14.2] [sgdfc:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3189	21883361_f3_2	6497	20600	960	320	YFL037W	1371	3.1(10)-140	Saccharomyces cerevisiae	[ui:yfl037w] [pn:beta-tubulin:tubulin beta chain] [gn:tub2] [gtcfc:12.16:12.8] [keggfc:14.2] [sgdfc:3.5.0:3.8.0:9.3.0] [db:gtc-saccharomyces cerevisiae]

CONTIG1599	19956502_c2_3	6498	20601	1101	367	YGL216W	397	4.0(10)-36	Saccharomyces cerevisiae	[ui:ygl216w] [pn:similarity to mouse kinesin-related protein kif3:putative kinesin-like protein ygl216w] [gtcfc:12.16] [keggfc:14.2] [sgdfc:8.8.0:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3758	23630067_f1_1	6499	20602	2148	716	YGL216W	477	8.0(10)-45	Saccharomyces cerevisiae	[ui:ygl216w] [pn:similarity to mouse kinesin-related protein kif3:putative kinesin-like protein ygl216w] [gtcfc:12.16] [keggfc:14.2] [sgdfc:8.8.0:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5733	9766885_f1_2	6500	20603	987	329	YGL116W	142	5.2(10)-7	Saccharomyces cerevisiae	[ui:ygl116w] [pn:cell division control protein:cell division control protein 20] [gn:cdc20] [gtcfc:12.16.12.8] [keggfc:14.2] [sgdfc:3.8.0:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5733	2241512_f2_7	6501	20604	609	203	YGL116W	228	3.7(10)-18	Saccharomyces cerevisiae	[ui:ygl116w] [pn:cell division control protein:cell division control protein 20] [gn:cdc20] [gtcfc:12.16.12.8] [keggfc:14.2] [sgdfc:3.8.0:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG585	1191505_f1_1	6502	20605	1053	351	YGL116W	632	6.4(10)-62	Saccharomyces cerevisiae	[ui:ygl116w] [pn:cell division control protein:cell division control protein 20] [gn:cdc20] [gtcfc:12.16.12.8] [keggfc:14.2] [sgdfc:3.8.0:9.3.0] [db:gtc-saccharomyces cerevisiae]

b9x13f58.x	960191_c2_1	6503	20606	492	YGL116W	151	7.2(10)-10	Saccharomyces cerevisiae	[ui:ygl116w] [pn:cell division control protein:cell division control protein 20] [gn:cdc20] [gtcfc:12.16.12.8] [keggfc:14.2] [sgdfc:3.8.0:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5814	25445930_f2_9	6504	20607	1242	YGL003C	472	7.0(10)-55	Saccharomyces cerevisiae	[ui:ygl003c] [pn:similarity to cdc20p and human p55cdc:hypothetical trp-asp repeats containing protein in pmc1-tfg2 intergenic region] [gtcfc:12.16:12.8] [keggfc:14.2] [sgdfc:3.8.0:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5814	5275063_f1_1	6505	20608	588	YGL003C	595	5.2(10)-58	Saccharomyces cerevisiae	[ui:ygl003c] [pn:similarity to cdc20p and human p55cdc:hypothetical trp-asp repeats containing protein in pmc1-tfg2 intergenic region] [gtcfc:12.16:12.8] [keggfc:14.2] [sgdfc:3.8.0:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5521	23539626_c1_24	6506	20609	546	YGR078C	182	7.5(10)-43	Saccharomyces cerevisiae	[ui:ygr078c] [pn:required in the absence of cin8p:protein] [gn:pac10] [gtcfc:12.16:12.8] [keggfc:14.2] [sgdfc:3.8.0:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4045	13866715_c3_10	6507	20610	834	YHR023W	94	0.28	Saccharomyces cerevisiae	[ui:yhr023w] [pn:type ii myosin heavy chain:myosin-1 isoform:type ii myosin] [gn:myo1] [gtcfc:12.16:12.8] [keggfc:14.2] [sgdfc:3.2.0:3.9.0:9.3.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4494	4773286_f2_3	6508	20611	1419	473	YHR023W	129	0.00018	Saccharomyces cerevisiae	[ui:yhr023w] [pn:type ii myosin heavy chain:myosin-1 isoform:type ii myosin] [gn:myo1] [gtcfc:12.16:12.8] [sgdfc:3.2.0:3.9.0:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4627	978506_c2_3	6509	20612	2592	864	YHR023W	1731	2.2(10)-178	Saccharomyces cerevisiae	[ui:yhr023w] [pn:type ii myosin heavy chain:myosin-1 isoform:type ii myosin] [gn:myo1] [gtcfc:12.16:12.8] [sgdfc:3.2.0:3.9.0:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5325	12673188_f2_4	6510	20613	2169	723	YHR023W	228	6.0(10)-18	Saccharomyces cerevisiae	[ui:yhr023w] [pn:type ii myosin heavy chain:myosin-1 isoform:type ii myosin] [gn:myo1] [gtcfc:12.16:12.8] [sgdfc:3.2.0:3.9.0:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5335	20391000_f3_5	6511	20614	1884	628	YHR023W	135	6.0(10)-5	Saccharomyces cerevisiae	[ui:yhr023w] [pn:type ii myosin heavy chain:myosin-1 isoform:type ii myosin] [gn:myo1] [gtcfc:12.16:12.8] [sgdfc:3.2.0:3.9.0:9.3.0] [db:gtc-saccharomyces cerevisiae]
b9x13n32.x	1167285_f3_1	6512	20615	492	164	YHR023W	93	0.05299	Saccharomyces cerevisiae	[ui:yhr023w] [pn:type ii myosin heavy chain:myosin-1 isoform:type ii myosin] [gn:myo1] [gtcfc:12.16:12.8] [sgdfc:3.2.0:3.9.0:9.3.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3220	10656511_c3_6	6513	20616	648	216	556	7.2(10)-54	Saccharomyces cerevisiae	[ui:yil034c] [pn:f-actin capping protein, beta subunit:f-actin capping protein beta subunit] [gn:cap2] [gtcfc:12.16:12.8:12.9] [keggfc:14.2] [sgdfc:3.2.0:3.3.0:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4003	12538962_f1_1	6514	20617	1941	647	529	4.0(10)-53	Saccharomyces cerevisiae	[ui:yjl042w] [pn:microtubule-associated protein:map-homologous protein 1] [gn:mhp1:j1206] [gtcfc:12.16] [keggfc:14.2] [sgdfc:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5634	2116682_f2_7	6515	20618	2085	695	469	5.7(10)-42	Saccharomyces cerevisiae	[ui:yjl042w] [pn:microtubule-associated protein:map-homologous protein 1] [gn:mhp1:j1206] [gtcfc:12.16] [keggfc:14.2] [sgdfc:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5230	3906252_c1_15	6516	20619	1095	365	1112	2.5(10)-125	Saccharomyces cerevisiae	[ui:yjr065c] [pn:actin related protein:actin-like protein act4] [gn:arp3:act4:j1760] [gtcfc:12.16] [keggfc:14.2] [sgdfc:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1877	308_f3_6	6517	20620	606	202	110	2.2(10)-5	Saccharomyces cerevisiae	[ui:yjr134c] [pn:similarity to paramyosin, myosin:hypothetical 81.2 kd protein in nmd5-hom6 intergenic region] [gn:j2120] [gtcfc:12.16] [keggfc:14.2] [sgdfc:9.3.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4822	11837806_c2_13	6518	20621	564	YJR134C	96	0.029	Saccharomyces cerevisiae	[ui:yjr134c] [pn:similarity to paramyosin, myosin:hypothetical 81.2 kd protein in nmd5-hom6 intergenic region] [gn:j2120] [gtcfc:12.16] [keggfc:14.2] [sgdfc:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2827	15801_c2_5	6519	20622	636	YKL179C	391	9.8(10)-36	Saccharomyces cerevisiae	[ui:ykl179c] [pn:similarity to nuf1p:hypothetical 77.5 kd protein in prp1-ste3 intergenic region] [gtcfc:12.16:12.8] [keggfc:14.2] [sgdfc:3.8.0.9.3.0] [db:gtc-saccharomyces cerevisiae]
b9x11927.x	22776681_f3_2	6520	20623	411	YKL179C	176	1.8(10)-12	Saccharomyces cerevisiae	[ui:ykl179c] [pn:similarity to nuf1p:hypothetical 77.5 kd protein in prp1-ste3 intergenic region] [gtcfc:12.16:12.8] [keggfc:14.2] [sgdfc:3.8.0.9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5295	33407052_f1_1	6521	20624	1017	YKL079W	107	0.00579	Saccharomyces cerevisiae	[ui:ykl079w] [pn:kinesin-related protein:kinesin-related protein smy1:suppressor protein smy1] [gn:smy1:ykl409] [gtcfc:12.16:12.8] [keggfc:14.2] [sgdfc:3.2.0.9.3.0] [db:gtc-saccharomyces cerevisiae]
b2x17273.x	13959792_f3_1	6522	20625	525	YKL079W	192	3.2(10)-14	Saccharomyces cerevisiae	[ui:ykl079w] [pn:kinesin-related protein:kinesin-related protein smy1:suppressor protein smy1] [gn:smy1:ykl409] [gtcfc:12.16:12.8] [sgdfc:3.2.0.9.3.0] [db:gtc-saccharomyces cerevisiae]

CONTIG	ID									
CONTIG4510	1257680_c2_3	6523	20626	771	257	YKL007W	321	5.7(10)-29	Saccharomyces cerevisiae	[ui:ykl007w] [pn:f-actin capping protein alpha subunit] [gn:cap1:ykl155] [gtcfc:12.16:12.8:12.9] [keggfc:14.2] [sgdfc:3.2.0:3.3.0:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4813	10984801_f1_3	6524	20627	441	147	YLL050C	552	1.8(10)-53	Saccharomyces cerevisiae	[ui:yll050c] [pn:cofilin, actin binding and severing protein:cofilin] [gn:cof1] [gtcfc:12.16:12.8] [keggfc:14.2] [sgdfc:3.2.0:3.3.0:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5622	1173287_c3_18	6525	20628	2949	983	YLL021W	521	6.5(10)-54	Saccharomyces cerevisiae	[ui:yll021w] [pn:involved in cell polarity:spa2 protein] [gn:spa2:pea1:11209] [gtcfc:12.16:12.8:12.9] [sgdfc:3.2.0:3.3.0:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5622	4084632_c2_16	6526	20629	1515	505	YLL021W	339	7.2(10)-34	Saccharomyces cerevisiae	[ui:yll021w] [pn:involved in cell polarity:spa2 protein] [gn:spa2:pea1:11209] [gtcfc:12.16:12.8:12.9] [keggfc:14.2] [sgdfc:3.2.0:3.3.0:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1715	1259628_c3_9	6527	20630	183	61	YLL001W	214	1.8(10)-16	Saccharomyces cerevisiae	[ui:yll001w] [pn:dynamin-related protein:dynamin-related protein dnm1] [gn:dnm1:11381] [gtcfc:12.16:12.6] [keggfc:14.2] [sgdfc:8.7.0:9.3.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3452	23613381_fl_1	6528	20631	498	166	YLL001W	466	9.3(10)-44	Saccharomyces cerevisiae	[ui:yll001w] [pn:dynamin-related protein:dynamin-related protein dnm1] [gn:dnm1:11381] [gtcfc:12.16:12.6] [keggfc:14.2] [sgdfc:8.7.0:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3452	26345338_fl_2	6529	20632	807	269	YLL001W	327	1.2(10)-28	Saccharomyces cerevisiae	[ui:yll001w] [pn:dynamin-related protein:dynamin-related protein dnm1] [gn:dnm1:11381] [gtcfc:12.16:12.6] [keggfc:14.2] [sgdfc:8.7.0:9.3.0] [db:gtc-saccharomyces cerevisiae]
b9x11d54.y	1196938_c1_2	6530	20633	762	254	YLL001W	814	3.2(10)-81	Saccharomyces cerevisiae	[ui:yll001w] [pn:dynamin-related protein:dynamin-related protein dnm1] [gn:dnm1:11381] [gtcfc:12.16:12.6] [keggfc:14.2] [sgdfc:8.7.0:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2156	24256265_c1_3	6531	20634	951	317	YLR045C	208	2.7(10)-29	Saccharomyces cerevisiae	[ui:ylr045c] [pn:suppressor of a cs tubulin mutation:suppressor of tubulin stu2] [gn:stu2:12108] [gtcfc:12.16] [keggfc:14.2] [sgdfc:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3576	2907812_c2_6	6532	20635	1164	388	YLR085C	314	5.9(10)-51	Saccharomyces cerevisiae	[ui:ylr085c] [pn:actin-related protein] [gn:arp6] [gtcfc:12.16] [keggfc:14.2] [sgdfc:9.3.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4625	4197192_c3_8	6533	20636	333	111 ·	YLR314C	284	1.8(10)-24	Saccharomyces cerevisiae	[ui:ylr314c] [pn:cell division control protein:cell division control protein 31] [gn:cdc3:i8543] [gtcfc:12.16:12.8:12.9] [keggfc:14.2] [sgdfc:3.2.0:3.3.0:3.8.0:3.9.0-9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2878	473526_c3_5	6534	20637	1230	410	YLR319C	244	2.0(10)-49	Saccharomyces cerevisiae	[ui:ylr319c] [pn:bud site selection protein:bud site selection protein bud6:actin interacting protein 3] [gn:bud6:aip3:i8543] [gtcfc:12.16:12.8] [keggfc:14.2] [sgdfc:3.2.0:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG949	4183150_c1_5	6535	20638	732	244	YLR319C	439	1.0(10)-40	Saccharomyces cerevisiae	[ui:ylr319c] [pn:bud site selection protein:bud site selection protein bud6:actin interacting protein 3] [gn:bud6:aip3:i8543] [gtcfc:12.16:12.8] [keggfc:14.2] [sgdfc:3.2.0:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4214	22037713_f2_4	6536	20639	855	285	YLR337W	170	1.0(10)-11	Saccharomyces cerevisiae	[ui:ylr337w] [pn:verprolin] [gn:vrp1] [gtcfc:12.16:12.6:12.8] [keggfc:14.2] [sgdfc:3.1.0:3.2.0:8.7.0:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5761	898500_f3_16	6537	20640	294	98	YLR337W	125	6.5(10)-7	Saccharomyces cerevisiae	[ui:ylr337w] [pn:verprolin] [gn:vrp1] [gtcfc:12.16:12.6:12.8] [keggfc:14.2] [sgdfc:3.1.0:3.2.0:8.7.0:9.3.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5403	34642778_f1_2	6538	20641	1950	650	YLR429W	94	0.35999	Saccharomyces cerevisiae	[ui:ylr429w] [pn:similarity to actin binding protein coronin] [gtcfc:12.16] [keggfc:14.2] [sgdfc:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5759	957936_c1_17	6539	20642	1515	505	YLR429W	1505	2.0(10)-154	Saccharomyces cerevisiae	[ui:ylr429w] [pn:similarity to actin binding protein coronin] [gtcfc:12.16] [keggfc:14.2] [sgdfc:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5739	24804528_c3_33	6540	20643	1182	394	YML104C	392	1.7(10)-36	Saccharomyces cerevisiae	[ui:yml104c] [pn:intermediate filament protein:structural protein mdm1] [gn:mdm1:ym8339] [gtcfc:12.16:12.8] [keggfc:14.2] [sgdfc:3.8.0:9.3.0] [db:gtc-saccharomyces cerevisiae]
b3x14621.y	21955093_f1_1	6541	20644	528	176	YML085C	647	1.6(10)-63	Saccharomyces cerevisiae	[ui:yml085c] [pn:alpha-1 tubulin:tubulin alpha-1 chain] [gn:tub1] [gtcfc:12.16] [keggfc:14.2] [sgdfc:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5543	4772652_c3_19	6542	20645	1359	453	YMR033W	389	3.6(10)-36	Saccharomyces cerevisiae	[ui:ymr033w] [pn:actin-related protein] [gn:arp9] [gtcfc:12.16] [keggfc:14.2] [sgdfc:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4982	22298162_f1_4	6543	20646	1863	621	YMR092C	914	8.3(10)-92	Saccharomyces cerevisiae	[ui:ymr092c] [pn:actin cytoskeleton component:actin interacting protein 1] [gn:aip1:ym9582] [gtcfc:14.2] [sgdfc:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3926	5897562_f2_2	6544	20647	1413	471	YMR109W	1572	1.6(10)-161	Saccharomyces cerevisiae	[ui:ymr109w] [pn:myosin i] [gn:myo5] [gtcfc:12.16:12.8] [keggfc:14.2] [sgdfc:3.2.0:9.3.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5038	15727137_c3_7	6545	20648	612	204	YMR109W	104	0.00018	Saccharomyces cerevisiae	[ui:ymr109w] [pn:myosin i] [gn:myo5] [gtcfc:12.16:12.8] [keggfc:14.2] [sgdfc:3.2.0:9.3.0] [db:gtc-saccharomyces cerevisiae]
blx19775.y	5319525_f3_2	6546	20649	474	158	YMR109W	303	1.1(10)-25	Saccharomyces cerevisiae	[ui:ymr109w] [pn:myosin i] [gn:myo5] [gtcfc:12.16:12.8] [keggfc:14.2] [sgdfc:3.2.0:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1080	34408180_c3_5	6547	20650	423	141	YMR138W	200	3.7(10)-16	Saccharomyces cerevisiae	[ui:ymr138w] [pn:gtp-binding protein:gtp-binding protein cin4] [gn:cin4-gtp1:ugx1:ym9375] [gtcfc:12.16:12.8] [keggfc:14.2] [sgdfc:3.8.0:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3524	34236641_f2_1	6548	20651	1980	660	YNL271C	420	9.0(10)-50	Saccharomyces cerevisiae	[ui:ynl271c] [pn:budding protein:bni1 protein:synthetic lethal 39] [gn:bni1:she5:n0646] [gtcfc:12.16:12.8] [keggfc:14.2] [sgdfc:3.2.0:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4299	11760912_c1_3	6549	20652	1815	605	YNL271C	1201	3.1(10)-121	Saccharomyces cerevisiae	[ui:ynl271c] [pn:budding protein:bni1 protein:synthetic lethal 39] [gn:bni1:she5:n0646] [gtcfc:12.16:12.8] [keggfc:14.2] [sgdfc:3.2.0:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5680	10797577_c3_46	6550	20653	699	233	YNL271C	219	1.8(10)-16	Saccharomyces cerevisiae	[ui:ynl271c] [pn:budding protein:bni1 protein:synthetic lethal 39] [gn:bni1:she5:n0646] [gtcfc:12.16:12.8] [keggfc:14.2] [sgdfc:3.2.0:9.3.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5680	12890627_c3_45	6551	20654	3873	1291	YNL271C	687	4.4(10)-78	Saccharomyces cerevisiae	[ui:ynl271c] [pn:budding protein:bni1 protein:synthetic lethal 39] [gn:bni1 :she5:n06646] [gtcfc:12.16:12.8] [keggfc:14.2] [sgdfc:3.2.0:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4986	36522702_c3_11	6552	20655	1002	334	YNL243W	439	2.0(10)-40	Saccharomyces cerevisiae	[ui:ynl243w] [pn:cytoskeleton assembly control protein:sla2 protein:transmembrane protein mop2] [gn:sla2:end4:mop2:ufg1:n1102] [gtcfc:12.16:12.6:12.8:12.9] [keggfc:14.2] [sgdfc:3.2.0:3.3.0:6.4.0:8.7.0:9.3.0] [db:gtc-saccharomyces cere
CONTIG4986	20509442_c2_9	6553	20656	2001	667	YNL243W	377	3.3(10)-58	Saccharomyces cerevisiae	[ui:ynl243w] [pn:cytoskeleton assembly control protein:sla2 protein:transmembrane protein mop2] [gn:sla2:end4:mop2:ufg1:n1102] [gtcfc:12.16:12.6:12.8:12.9] [keggfc:14.2] [sgdfc:3.2.0:3.3.0:6.4.0:8.7.0:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5691	23605000_c3_32	6554	20657	1746	582	YNL138W	1039	4.7(10)-105	Saccharomyces cerevisiae	[ui:ynl138w] [pn:adenylate cyclase-associated protein, 70kda:adenylyl cyclase-associated protein:cap] [gn:srv2:cap1:n1210:n1838] [gtcfc:12.16:12.8] [keggfc:14.2] [sgdfc:3.1.0:3.2.0:9.3.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5591	13828377_f3_8	6555	20658	1227	409	YNL084C	473	1.8(10)-52	Saccharomyces cerevisiae	[ui:ynl084c] [pn:required for endocytosis and cytoskeletal organization:end3 protein] [gn:end3:n2307] [gtfc:12.16:12.6:12.8:12.9] [sgdfc:3.2.0:3.3.0:8.7.0:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2630	7062807_f3_3	6556	20659	1137	379	YNL079C	181	1.3(10)-13	Saccharomyces cerevisiae	[ui:ynl079c] [pn:tropomyosin 1] [gn:tpm1:n2332] [gtfc:12.16:12.8:12.9] [keggfc:14.2] [sgdfc:3.1.0:3.2.0:3.3.0:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3587	24017307_f2_2	6557	20660	987	329	YNL079C	92	0.029	Saccharomyces cerevisiae	[ui:ynl079c] [pn:tropomyosin 1] [gn:tpm1:n2332] [gtfc:12.16:12.8:12.9] [keggfc:14.2] [sgdfc:3.1.0:3.2.0:3.3.0:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5652	14657183_f3_13	6558	20661	390	130	YNL079C	96	8.1(10)-5	Saccharomyces cerevisiae	[ui:ynl079c] [pn:tropomyosin 1] [gn:tpm1:n2332] [gtfc:12.16:12.8:12.9] [keggfc:14.2] [sgdfc:3.1.0:3.2.0:3.3.0:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4290	33785677_c3_11	6559	20662	420	140	YOR122C	492	4.4(10)-47	Saccharomyces cerevisiae	[ui:yor122c] [pn:profilin] [gn:pfy1:pfy:prf1:o3275:yor3275c] [gtfc:12.16:12.8] [keggfc:14.2] [sgdfc:3.2.0:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1543	16579002_c3_2	6560	20663	984	328	YOR141C	494	1.7(10)-46	Saccharomyces cerevisiae	[ui:yor141c] [pn:actin-related protein] [gn:arp8] [gtfc:12.16] [keggfc:14.2] [sgdfc:9.3.0] [db:gtc-saccharomyces cerevisiae]

b3x14418.y	10119075_c1_6	6561	20664	789	263	YOR141C	149	2.0(10)-9	Saccharomyces cerevisiae	[ui:yor141c] [pn:actin-related protein] [gn:arp8] [gtcfc:12.16] [keggfc:14.2] [sgdfc:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2891	798311_c3_6	6562	20665	573	191	YOR156C	104	0.005	Saccharomyces cerevisiae	[ui:yor156c] [pn:interacts with cdc12p in 2-hybrid assay] [gn:nfi1] [gtcfc:12.16:12.8] [sgdfc:3.2.0:3.8.0:3.9.0:9.3.0] [db:gtc-saccharomyces cerevisiae]
b9x13h02.x	31879280_f3_1	6563	20666	495	165	YOR156C	179	9.3(10)-13	Saccharomyces cerevisiae	[ui:yor156c] [pn:interacts with cdc12p in 2-hybrid assay] [gn:nfi1] [gtcfc:12.16:12.8] [keggfc:14.2] [sgdfc:3.2.0:3.8.0:3.9.0:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2589	1017269l_f3_2	6564	20667	1563	521	YOR349W	147	3.7(10)-16	Saccharomyces cerevisiae	[ui:yor349w] [pn:chromosome segregation protein:cin1 protein] [gn:cin1:o6350] [gtcfc:12.16:12.8] [keggfc:14.2] [sgdfc:3.8.0:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5212	4725882_f3_10	6565	20668	594	198	YOR367W	170	5.7(10)-13	Saccharomyces cerevisiae	[ui:yor367w] [pn:similarity to mammalian smooth muscle protein sm22] [gtcfc:12.16] [keggfc:14.2] [sgdfc:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5571	24406687_f2_10	6566	20669	1212	404	YPL105C	105	0.01499	Saccharomyces cerevisiae	[ui:ypl105c] [pn:similarity to smy2p] [gtcfc:12.16] [keggfc:14.2] [sgdfc:9.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4430	4351557_c1_6	6567	20670	810	270	YPR034W	290	2.7(10)-25	Saccharomyces cerevisiae	[ui:ypr034w] [pn:similarity to actins] [gn:arp7] [gtcfc:12.16] [keggfc:14.2] [sgdfc:9.3.0] [db:gtc-saccharomyces cerevisiae]

b2x16596.x	471041_f3_1	6568	20671	651	217	YAL058W	327	2.2(10)-29	Saccharomyces cerevisiae	[ui:yal058w] [pn:similarity to calnexin:calnexin homolog precursor] [gn:cne1:fun48] [gtcfc:12.16] [keggfc:14.2] [sgdfc:9.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4324	10586087_f1_2	6569	20672	768	256	YBL102W	257	3.5(10)-22	Saccharomyces cerevisiae	[ui:ybl102w] [pn:suppressor of sed5 ts mutants:sft2 protein] [gn:sft2:ybl0812] [gtcfc:12.16] [keggfc:14.2] [sgdfc:9.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5516	2112580_f2_4	6570	20673	351	117	YBL102W	138	1.3(10)-9	Saccharomyces cerevisiae	[ui:ybl102w] [pn:suppressor of sed5 ts mutants:sft2 protein] [gn:sft2:ybl0812] [gtcfc:12.16] [keggfc:14.2] [sgdfc:9.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5516	16679015_f1_1	6571	20674	342	114	YBL102W	116	5.2(10)-7	Saccharomyces cerevisiae	[ui:ybl102w] [pn:suppressor of sed5 ts mutants:sft2 protein] [gn:sft2:ybl0812] [gtcfc:12.16] [keggfc:14.2] [sgdfc:9.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2210	33759380_c2_5	6572	20675	510	170	YDR297W	531	3.2(10)-51	Saccharomyces cerevisiae	[ui:ydr297w] [pn:suppressor of rvs161 and rvs167 mutations:sur2 protein:syringomycin response protein 2] [gn:sur2:syr2:d9740] [gtcfc:12.16:12.8] [keggfc:14.2] [sgdfc:3.2.0:9.4.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5308	4329537_f1_3	6573	20676	765	255	YEL036C	908	3.6(10)-91	Saccharomyces cerevisiae	[ui:yel036c] [pn:protein of the endoplasmatic reticulum:aminonitrophenyl propanediol resistance protein] [gn:anp1:gem3:sygp-orf28] [gtcfc:12.16] [keggfc:14.2] [sgdfc:9.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4573	15631461_f1_5	6574	20677	306	102	YGR105W	192	2.7(10)-15	Saccharomyces cerevisiae	[ui:ygr105w] [pn:atpase assembly integral membrane protein, vacuolar:vacuolar atpase assembly integral membrane protein] [gn:vma21] [gtcfc:12.16] [keggfc:14.2] [sgdfc:6.4.0-9.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4999	4332936_c1_8	6575	20678	579	193	YKL065C	176	1.3(10)-13	Saccharomyces cerevisiae	[ui:ykl065c] [pn:yeast endoplasmic reticulum 25 kda transmembrane protein:hypothetical 23.4 kd protein in nup100-msn4 intergenic region] [gn:yet1:ykl331] [keggfc:14.2] [sgdfc:9.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5673	33765927_f1_4	6576	20679	723	241	YKL065C	136	5.2(10)-8	Saccharomyces cerevisiae	[ui:ykl065c] [pn:yeast endoplasmic reticulum 25 kda transmembrane protein:hypothetical 23.4 kd protein in nup100-msn4 intergenic region] [gn:yet1:ykl331] [gtcfc:12.16] [keggfc:14.2] [sgdfc:9.4.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4257	22460061_f2_1	6577	20680	972	324	YLR220W	674	2.2(10)-66	Saccharomyces cerevisiae	[ui:ylr220w] [pn:involved in calcium regulation:ccc1 protein] [gn:ccc1:l8083] [gtcfc:14.2:16:12.6] [sgdfc:1.8.2:9.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3782	23439035_c1_3	6578	20681	1236	412	YDR080W	418	3.8(10)-38	Saccharomyces cerevisiae	[ui:ydr080w] [pn:required for the vacuolar assembly:hypothetical 113.4 kd protein in sed1-pdc2 intergenic region] [gn:vam2:d4446] [gtcfc:12.16] [keggfc:14.2] [sgdfc:6.4.0:9.10.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5593	23484375_f3_11	6579	20682	663	221	YDR080W	404	1.2(10)-36	Saccharomyces cerevisiae	[ui:ydr080w] [pn:required for the vacuolar assembly:hypothetical 113.4 kd protein in sed1-pdc2 intergenic region] [gn:vam2:d4446] [gtcfc:12.16] [keggfc:14.2] [sgdfc:6.4.0:9.10.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2592	14540931_f1_2	6580	20683	897	299	YGL212W	173	2.2(10)-11	Saccharomyces cerevisiae	[ui:ygl212w] [pn:vacuolar morphogenesis protein:protein] [gn:vam7] [gtcfc:12.16] [keggfc:14.2] [sgdfc:9.10.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5635	801000_f3_9	6581	20684	861	287	YGL212W	114	0.00021	Saccharomyces cerevisiae	[ui:ygl212w] [pn:vacuolar morphogenesis protein:protein] [gn:vam7] [keggfc:14.2] [sgdfc:9.10.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2568	4022782_c3_3	6582	20685	636	212	YHR026W	582	1.3(10)-56	Saccharomyces cerevisiae	[ui:yhr026w] [pn:h+-atpase 23 kd subunit, vacuolar:proteolipid protein] [gn:vma16:ppa1] [gtcfc:12.16:12.5:12.6] [keggfc:14.2] [sgdfc:7.2.2:7.8.0:9.10.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4735	16423305_c3_9	6583	20686	675	225	YKL119C	194	1.6(10)-15	Saccharomyces cerevisiae	[ui:ykl119c] [pn:h+-atpase assembly protein, vacuolar:vacuolar atpase assembly integral membrane protein vma12:protein vph2] [gn:vma12:yph2:cls10:ykl520] [gtcfc:12.16] [keggfc:14.2] [sgdfc:6.4.0:9.10.0] [db:gtc-saccharomyces cerevisia]
CONTIG1187	9853437_f3_3	6584	20687	714	238	YMR231W	222	1.3(10)-33	Saccharomyces cerevisiae	[ui:ym231w] [pn:vacuolar biogenesis protein:vacuolar biogenesis protein end1:pep5 protein] [gn:end1:pep5:vps11:ym9959] [gtcfc:12.16:12.6] [keggfc:14.2] [sgdfc:8.7.0:9.10.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1517	26444458_c3_1	6585	20688	828	276	YMR231W	233	7.2(10)-23	Saccharomyces cerevisiae	[ui:ym231w] [pn:vacuolar biogenesis protein:vacuolar biogenesis protein end1:pep5 protein] [gn:end1:pep5:vps11:ym9959] [gtcfc:12.16:12.6] [keggfc:14.2] [sgdfc:8.7.0:9.10.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2609	915643_c2_3	6586	20689	534	178	YER060W	330	1.5(10)-29	Saccharomyces cerevisiae	[ui:yer060w] [pn:purine-cytosine permease:hypothetical 58.1 kd protein in pet117-cem1 intergenic region] [gn:fcy21:fcyy] [gtcfc:12.16:12.3:12.6] [keggfc:14.2] [sgdfc:1.3.7:7.6.0:8.8.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2609	1213556_c3_4	6587	20690	702	234	YER060W-A	499	7.9(10)-48	Saccharomyces cerevisiae	[ui:yer060w-a] [pn:strong similarity to fcy2p] [gn:fcy22] [gtcfc:12.16:12.3:12.6] [keggfc:14.2] [sgdfc:1.3.7:7.6.0:8.8.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2609	3441702_c1_2	6588	20691	414	138	YER060W-A	194	1.3(10)-14	Saccharomyces cerevisiae	[ui:yer060w-a] [pn:strong similarity to fcy2p] [gn:fcy22] [gtcfc:12.16:12.3:12.6] [keggfc:14.2] [sgdfc:1.3.7:7.6.0:8.8.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3872	4863500_f3_5	6589	20692	981	327	YOR100C	126	1.5(10)-5	Saccharomyces cerevisiae	[ui:yor100c] [pn:similarity to mitochondrial carrier protein ymc1] [gtcfc:12.16] [keggfc:14.2] [sgdfc:8.8.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4420	24037512_c2_7	6590	20693	876	292	YOR100C	747	4.0(10)-74	Saccharomyces cerevisiae	[ui:yor100c] [pn:similarity to mitochondrial carrier protein ymc1] [gtcfc:12.16] [keggfc:14.2] [sgdfc:8.8.0] [db:gtc-saccharomyces cerevisiae]

CONTIG1621	24485906_f3_1	6591	20694	723	241	YBL037W	356	5.5(10)-34	Saccharomyces cerevisiae	[ui:ybl037w] [pn:alpha-adaptin, large subunit of the clathrin-associated protein:ap complex:alpha-adaptin homolog in ura7-pol12 intergenic region] [gn:apl3:ybl0412] [gtcfc:12.16:12.6] [keggfc:14.2] [sgdfc:6.4.0:8.7.0] [db:gtc-saccharo
CONTIG4408	12191910_c3_10	6592	20695	756	252	YBL037W	185	3.3(10)-13	Saccharomyces cerevisiae	[ui:ybl037w] [pn:alpha-adaptin, large subunit of the clathrin-associated protein:ap complex:alpha-adaptin homolog in ura7-pol12 intergenic region] [gn:apl3:ybl0412] [gtcfc:12.16:12.6] [keggfc:14.2] [sgdfc:6.4.0:8.7.0] [db:gtc-saccharo
CONTIG2516	4706642_c2_2	6593	20696	954	318	YDR162C	182	3.1(10)-14	Saccharomyces cerevisiae	[ui:ydr162c] [pn:nap1p-binding protein] [gn:nbp2] [gtcfc:12.16] [keggfc:14.2] [sgdfc:6.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3342	23453211_f1_2	6594	20697	885	295	YDR265W	369	4.7(10)-34	Saccharomyces cerevisiae	[ui:ydr265w] [pn:peroxisomal assembly protein] [gn:pas4] [gtcfc:12.16:12.6] [keggfc:14.2] [sgdfc:6.4.0:9.8.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5372	484675_c2_14	6595	20698	2115	705	YGR261C	490	1.6(10)-49	Saccharomyces cerevisiae	[ui:ygr261c] [pn:beta-adaptin, large subunit of the clathrin-associated protein:ap complex:probable beta-adaptin:clathrin assembly protein large beta chain:clathrin assembly protein complex 2 beta large chain] [gn:apl6:ykss:g931] [gtc

CONTIG5670	13790932_f1_3	6596	20699	2028	676	YHR161C	447	2.2(10)-46	Saccharomyces cerevisiae	[ui:yhr161c] [pn:similarity to rat clathrin assembly protein ap180:hypothetical 71.7 kd protein in rec104-sol3 intergenic region] [gtcfc:12.16] [keggfc:14.2] [sgdfc:6.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3178	29470261_c2_3	6597	20700	306	102	YJL024C	291	8.6(10)-26	Saccharomyces cerevisiae	[ui:yjl024c] [pn:clathrin-associated protein:ap complex, small subunit:probable adaptin complex small chain homolog] [gn:aps3:yks7:j1274] [gtcfc:12.16:12.6] [keggfc:14.2] [sgdfc:6.4.0:8.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3802	2788942_c1_5	6598	20701	189	63	YJL024C	128	1.6(10)-8	Saccharomyces cerevisiae	[ui:yjl024c] [pn:clathrin-associated protein:ap complex, small subunit:probable adaptin complex small chain homolog] [gn:aps3:yks7:j1274] [gtcfc:12.16:12.6] [keggfc:14.2] [sgdfc:6.4.0:8.7.0] [db:gtc-saccharomyces cerevisiae]
b1x14032.y	10032016_c3_2	6599	20702	792	264	YKL197C	273	1.3(10)-22	Saccharomyces cerevisiae	[ui:ykl197c] [pn:peroxisomal assembly protein:peroxisome biosynthesis protein] [gn:pas1] [gtcfc:12.16] [keggfc:14.2] [sgdfc:6.4.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5167	4454376_f2_4	6600	20703	282	94	YLR327C	190	4.4(10)-15	Saccharomyces cerevisiae	[ui:ylr327c] [pn:strong similarity to stf2p] [gtcfc:12.16] [keggfc:14.2] [sgdfc:6.4.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2416	26751525_c3_6	6601	20704	1002	334	YNL329C	1003	3.1(10)-101	Saccharomyces cerevisiae	[ui:ynl329c] [pn:peroxisomal assembly protein:peroxisome biosynthesis protein pas8] [gn:pas8:n0310] [gtcfc:12.16:12.6] [keggfc:14.2] [sgdfc:6.4.0:9.8.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3028	4422750_c2_4	6602	20705	1608	536	YPL195W	635	6.5(10)-62	Saccharomyces cerevisiae	[ui:ypl195w] [pn:alpha- or gamma-adaptin, large subunit of the clathrin- associated protein:ap complex] [gn:yks4] [gtcfc:12.16:12.6] [keggfc:14.2] [sgdfc:6.4.0:8.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG788	2460010_f2_2	6603	20706	441	147	YPL195W	409	3.1(10)-37	Saccharomyces cerevisiae	[ui:ypl195w] [pn:alpha- or gamma-adaptin, large subunit of the clathrin- associated protein:ap complex] [gn:yks4] [gtcfc:12.16:12.6] [sgdfc:6.4.0:8.7.0] [db:gtc-saccharomyces cerevisiae]
b2x16287.x	23469002_c3_2	6604	20707	732	244	YPR029C	128	4.2(10)-6	Saccharomyces cerevisiae	[ui:ypr029c] [pn:gamma-adaptin, large subunit of the clathrin-associated protein:ap complex] [gn:apl4] [gtcfc:12.16:12.6] [keggfc:14.2] [sgdfc:6.4.0:8.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1553	7313775_f1_1	6605	20708	513	171	YBR241C	425	5.5(10)-40	Saccharomyces cerevisiae	[ui:ybr241c] [pn:similarity to glucose transport proteins:probable metabolite transport protein ybr241c] [gn:ybr1625] [gtcfc:12.2:12.6] [keggfc:14.2] [sgdfc:1.5.3:7.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2225	5212782_c2_3	6606	20709	633	211	YBR241C	510	5.4(10)-49	Saccharomyces cerevisiae	[ui:ybr241c] [pn:similarity to glucose transport proteins:probable metabolite transport protein ybr241c] [gn:ybr1625] [gtcfc:12.2:12.6] [keggfc:14.2] [sgdfc:1.5.3:7.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5819	23540907_c2_50	6607	20710	1515	505	YBR241C	701	3.1(10)-69	Saccharomyces cerevisiae	[ui:ybr241c] [pn:similarity to glucose transport proteins:probable metabolite transport protein ybr241c] [gn:ybr1625] [gtcfc:12.2:12.6] [keggfc:14.2] [sgdfc:1.5.3:7.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5144	24392002_f3_3	6608	20711	1068	356	YDL199C	362	1.5(10)-32	Saccharomyces cerevisiae	[ui:ydl199c] [pn:similarity to sugar transporter proteins] [gtcfc:12.2:12.6] [keggfc:14.2] [sgdfc:1.5.3:7.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5348	6047337_c1_11	6609	20712	609	203	YDL138W	430	8.6(10)-40	Saccharomyces cerevisiae	[ui:ydl138w] [pn:suppressor of snf3 mutant] [gn:rgt2] [gtcfc:12.2] [keggfc:14.2] [sgdfc:1.5.3:7.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5509	23652182_f1_2	6610	20713	1659	553	YDL138W	447	1.2(10)-41	Saccharomyces cerevisiae	[ui:ydl138w] [pn:suppressor of snf3 mutant] [gn:rgt2] [gtcfc:12.2] [keggfc:14.2] [sgdfc:1.5.3:7.3.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2140	972311_c3_5	6611	20714	915	305	YFL040W	112	0.00129	Saccharomyces cerevisiae	[ui:yfl040w] [pn:similarity to yeast glucose transport proteins;probable metabolite transport protein yfl040w] [gtcfc:12.2:12.6] [keggfc:14.2] [sgdfc:1.5.3:7.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4937	29381925_c2_8	6612	20715	1215	405	YFR045W	231	4.5(10)-19	Saccharomyces cerevisiae	[ui:yfr045w] [pn:similarity to mitochondrial citrate transport proteins;putative mitochondrial carrier yfr045w] [gtcfc:12.2] [keggfc:14.2] [sgdfc:7.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4958	35422157_c3_12	6613	20716	1353	451	YKL217W	673	2.8(10)-66	Saccharomyces cerevisiae	[ui:ykl217w] [pn:carboxylic acid transporter protein:carboxylic acid transporter protein homolog] [gn:jen1] [gtcfc:12.2:12.6] [keggfc:14.2] [sgdfc:1.5.3:7.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5497	7081302_c2_7	6614	20717	555	185	YKL217W	269	1.3(10)-22	Saccharomyces cerevisiae	[ui:ykl217w] [pn:carboxylic acid transporter protein:carboxylic acid transporter protein homolog] [gn:jen1] [gtcfc:12.2:12.6] [keggfc:14.2] [sgdfc:1.5.3:7.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG751	9942668_f3_1	6615	20718	645	215	YKL217W	316	1.1(10)-27	Saccharomyces cerevisiae	[ui:ykl217w] [pn:carboxylic acid transporter protein:carboxylic acid transporter protein homolog] [gn:jen1] [gtcfc:12.2:12.6] [keggfc:14.2] [sgdfc:1.5.3:7.3.0:17.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG1708	16835882_c2_10	6616	20719	930	310	YOR271C	1072	1.5(10)-108	Saccharomyces cerevisiae	[ui:yor271c] [pn:strong similarity to rattus tricarboxylate carrier] [gtcfc:12.2] [keggfc:14.2] [sgdfc:7.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1965	242312_f1_1	6617	20720	780	260	YOR271C	849	6.4(10)-85	Saccharomyces cerevisiae	[ui:yor271c] [pn:strong similarity to rattus tricarboxylate carrier] [gtcfc:12.2] [keggfc:14.2] [sgdfc:7.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG854	14257050_c2_4	6618	20721	540	180	YBR041W	500	6.2(10)-48	Saccharomyces cerevisiae	[ui:ybr041w] [pn:similarity to m.musculus fatty acid transport protein:hypothetical 71.7 kd protein in fig1-gip1 intergenic region] [gn:fat1:ybr0411] [keggfc:14.2] [sgdfc:1.6.5:7.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG854	26567212_c2_3	6619	20722	282	94	YBR041W	211	2.6(10)-16	Saccharomyces cerevisiae	[ui:ybr041w] [pn:similarity to m.musculus fatty acid transport protein:hypothetical 71.7 kd protein in fig1-gip1 intergenic region] [gn:fat1:ybr0411] [keggfc:14.2] [sgdfc:1.6.5:7.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4552	26369586_c2_14	6620	20723	1185	395	YKL188C	430	2.7(10)-75	Saccharomyces cerevisiae	[ui:ykl188c] [pn:long-chain fatty acid transporter:peroxisomal long-chain fatty acid import protein 1] [gn:pat1:ykl741] [keggfc:12.2:12.6] [keggfc:14.2] [sgdfc:1.6.5:7.5.0:7.9.0:8.4.0:9.8.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4552	510285_c1_12	6621	20724	1107	369	YPL147W	208	9.5(10)-16	Saccharomyces cerevisiae	[ui:ypl147w] [pn:long-chain fatty acid transporter:peroxisomal long-chain fatty acid import protein 2] [gn:pat2:pxa1:pal1:ssh2:lpi1w:p260 7] [gtcfc:12.2:12.6] [keggfc:14.2] [sgdfc:1.6.5:7.5.0:7.9.0:8.4.0:9.8.0] [db:gtc-saccharomyces ce
CONTIG5470	5085003_c3_9	6622	20725	2316	772	YPL147W	895	4.4(10)-166	Saccharomyces cerevisiae	[ui:ypl147w] [pn:long-chain fatty acid transporter:peroxisomal long-chain fatty acid import protein 2] [gn:pat2:pxa1:pal1:ssh2:lpi1w:p260 7] [gtcfc:12.2:12.6] [keggfc:14.2] [sgdfc:1.6.5:7.5.0:7.9.0:8.4.0:9.8.0] [db:gtc-saccharomyces ce
CONTIG1202	22666557_c1_2	6623	20726	492	164	YDR142C	361	3.2(10)-33	Saccharomyces cerevisiae	[ui:ydr142c] [pn:peroxisomal import protein:peroxisome import protein pas7:peroxin 7] [gn:pas7:peb1:pex7:yd2943] [gtcfc:12.2:12.6] [keggfc:14.2] [sgdfc:8.4.0:9.8.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3815	15038180_c3_7	6624	20727	282	94	YDR142C	277	2.6(10)-24	Saccharomyces cerevisiae	[ui:ydr142c] [pn:peroxisomal import protein:peroxisome import protein pas7:peroxin 7] [gn:pas7:peb1:pex7:yd2943] [gtcfc:12.2:12.6] [keggfc:14.2] [sgdfc:8.4.0:9.8.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2834	803312_c2_2	6625	20728	894	298	YGL186C	757	3.6(10)-75	Saccharomyces cerevisiae	[ui:ygl186c] [pn:similarity to hypothetical protein fcy21p and weak similarity to fcy2 protein:hypothetical 64.5 kd protein in cox4-gts1 intergenic region] [gn:gl370] [gtcfc:12.3:12.6] [keggfc:14.2] [sgdfc:1.3.7:7.6.0:17.0.0] [db:gtc-
CONTIG5642	12148577_f2_2	6626	20729	1587	529	YGL186C	1007	3.0(10)-118	Saccharomyces cerevisiae	[ui:ygl186c] [pn:similarity to hypothetical protein fcy21p and weak similarity to fcy2 protein:hypothetical 64.5 kd protein in cox4-gts1 intergenic region] [gn:gl370] [gtcfc:12.3:12.6] [keggfc:14.2] [sgdfc:1.3.7:7.6.0:17.0.0] [db:gtc-
b9x10393.y	4335156_c1_1	6627	20730	534	178	YGL186C	300	5.0(10)-26	Saccharomyces cerevisiae	[ui:ygl186c] [pn:similarity to hypothetical protein fcy21p and weak similarity to fcy2 protein:hypothetical 64.5 kd protein in cox4-gts1 intergenic region] [gn:gl370] [gtcfc:12.3:12.6] [keggfc:14.2] [sgdfc:1.3.7:7.6.0:17.0.0] [db:gtc-
CONTIG4416	23553827_f1_1	6628	20731	906	302	YGR096W	453	5.9(10)-43	Saccharomyces cerevisiae	[ui:ygr096w] [pn:similarity to bovine graves disease carrier protein:putative mitochondrial carrier ygr096w] [gtcfc:12.3] [keggfc:14.2] [sgdfc:1.3.7:7.6.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5156	21994017_c3_14	6629	20732	339	113	YHR002W	159	3.6(10)-11	Saccharomyces cerevisiae	[ui:yhr002w] [pn:similarity to bovine miochondrial carrier protein/grave"s disease carrier protein:putative mitochondrial carrier yhr002w] [gtcfc:12.3] [keggfc:14.2] [sgdfc:1.3.7.7.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4092	4103578_f1_1	6630	20733	810	270	YPR011C	653	3.7(10)-64	Saccharomyces cerevisiae	[ui:ypr011c] [pn:similarity to adp/atp carrier proteins and graves disease carrier protein] [gtcfc:12.3] [keggfc:14.2] [sgdfc:1.3.7.7.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3292	24395161_f2_2	6631	20734	579	193	YPR011C	163	1.0(10)-11	Saccharomyces cerevisiae	[ui:ypr011c] [pn:similarity to adp/atp carrier proteins and graves disease carrier protein] [gtcfc:14.2] [sgdfc:1.3.7.7.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1318	32462785_f2_3	6632	20735	267	89	YBR235W	208	1.3(10)-15	Saccharomyces cerevisiae	[ui:ybr235w] [pn:similarity to bumetanide-sensitive na-k-cl cotransport protein:hypothetical 124.0 kd protein in pcs60-abd1 intergenic region] [gn:ybr160l] [gtcfc:12.4:12.5:12.6] [keggfc:14.2] [sgdfc:1.8.2:7.2.2:7.2.3:17.0.0] [db:gtc-db:gtc-]

CONTIG2248	34094015_f2_1	6633	20736	1458	486	YBR235W	268	3.6(10)-20	Saccharomyces cerevisiae	[ui:ybr235w] [pn:similarity to bumetanide-sensitive na-k-cl cotransport protein:hypothetical 124.0 kd protein in pcs60-abd1 intergenic region] [gn:ybr1601] [gtcfc:12.4:12.5:12.6] [keggfc:14.2] [sgdfc:1.8.2:7.2.2:7.2.3:17.0.0] [db:gtc-
CONTIG3606	14644442_c1_5	6634	20737	1434	478	YBR235W	1191	3.7(10)-121	Saccharomyces cerevisiae	[ui:ybr235w] [pn:similarity to bumetanide-sensitive na-k-cl cotransport protein:hypothetical 124.0 kd protein in pcs60-abd1 intergenic region] [gn:ybr1601] [gtcfc:12.4:12.5:12.6] [keggfc:14.2] [sgdfc:1.8.2:7.2.2:7.2.3:17.0.0] [db:gtc-
CONTIG5398	20351377_f1_4	6635	20738	1530	510	YBR296C	988	9.3(10)-141	Saccharomyces cerevisiae	[ui:ybr296c] [pn:strong similarity to phosphate-repressible phosphate permease:putative phosphate-repressible phosphate permease ybr29c] [gn:ybr2113] [gtcfc:12.4:12.6:13.10] [keggfc:14.2] [sgdfc:1.4.3:1.8.2:7.2.3:17.0.0] [db:gtc-sacch
CONTIG1600	26376660_f1_2	6636	20739	792	264	YCR037C	368	7.5(10)-33	Saccharomyces cerevisiae	[ui:ycr037c] [pn:member of the phosphate permease family:inorganic phosphate transporter pho87] [gn:pho87:ycr37c:ycr524] [gtcfc:12.4:13.10] [keggfc:14.2] [sgdfc:1.4.3:1.8.2:7.2.3:17.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2512	783532_c1_2	6637	20740	504	168	YCR037C	519	3.8(10)-49	Saccharomyces cerevisiae	[ui:ycr037c] [pn:member of the phosphate permease family:inorganic phosphate transporter pho87] [gn:pho87:ycr37c:ycr524] [gtcfc:12.4:13.10] [keggfc:14.2] [sgdfc:1.4.3:1.8.2:7.2.3:17.0.0] [db:gtc-saccharomyces cerevisiae]
b3x14152.x	210967_c3_3	6638	20741	969	323	YCR037C	256	7.7(10)-21	Saccharomyces cerevisiae	[ui:ycr037c] [pn:member of the phosphate permease family:inorganic phosphate transporter pho87] [gn:pho87:ycr37c:ycr524] [gtcfc:12.4:13.10] [keggfc:14.2] [sgdfc:1.4.3:1.8.2:7.2.3:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2431	20486557_c2_6	6639	20742	246	82	YJL198W	144	6.7(10)-9	Saccharomyces cerevisiae	[ui:yjl198w] [pn:strong similarity to pho87p:hypothetical 97.7 kd membrane protein in prp21-ubp12 intergenic region] [gn:j0336] [gtcfc:12.4:12.6:13.10] [keggfc:14.2] [sgdfc:1.4.3:1.8.2:7.2.3:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2844	14178762_c2_5	6640	20743	960	320	YJL198W	105	0.01299	Saccharomyces cerevisiae	[ui:yjl198w] [pn:strong similarity to pho87p:hypothetical 97.7 kd membrane protein in prp21-ubp12 intergenic region] [gn:j0336] [gtcfc:12.4:12.6:13.10] [keggfc:14.2] [sgdfc:1.4.3:1.8.2:7.2.3:17.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG1635	24804812_f1_1	6641	20744	729		YJL117W	162	1.2(10)-10	Saccharomyces cerevisiae	[ui:yjl117w] [pn:inorganic phospate transporter:inorganic phosphate transporter pho86] [gn:pho86:j0744] [gtcfc:12.4:13.10] [keggfc:14.2] [sgdfc:1.4.3:1.8.2:7.2.3] [db:gtc-saccharomyces cerevisiae]
CONTIG481	10579187_c3_3	6642	20745	219		YJL117W	73	0.00017	Saccharomyces cerevisiae	[ui:yjl117w] [pn:inorganic phospase transporter:inorganic phosphate transporter pho86] [gn:pho86:j0744] [gtcfc:12.4:13.10] [sgdfc:1.4.3:1.8.2:7.2.3] [db:gtc-saccharomyces cerevisiae]
CONTIG5446	14881535_f1_2	6643	20746	2487		YLR092W	1744	9.3(10)-180	Saccharomyces cerevisiae	[ui:ylr092w] [pn:strong similarity to sul1p] [gn:se12] [gtcfc:12.4:12.6] [keggfc:14.2] [sgdfc:1.2.3:1.8.2:7.2.3:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3415	788317_f1_1	6644	20747	765	255	YNR013C	118	0.00032	Saccharomyces cerevisiae	[ui:ynr013c] [pn:similarity to membrane protein pho87p and hypothetical protein yjl198w:hypothetical protein in urk1-smm1 intergenic region] [gn:n2052] [gtcfc:12.4:12.6:13.10] [keggfc:14.2] [sgdfc:1.4.3:1.8.2:7.2.3:17.0.0] [db

CONTIG3530	11876286_c2_6	6645	20748	264	88	YNR013C	165	3.8(10)-11	Saccharomyces cerevisiae	[ui:ynr013c] [pn:similarity to membrane protein pho87p and hypothetical protein yjl198w:hypothetical 99.5 kd protein in urk1-smm1 intergenic region] [gn:n2052] [gtcfc:12.4:12.6:13.10] [keggfc:14.2] [sgdfc:1.4.3:1.8.2:7.2.3:17.0.0] [db
CONTIG2761	4039134_c1_2	6646	20749	1266	422	YNR013C	1153	3.8(10)-117	Saccharomyces cerevisiae	[ui:ynr013c] [pn:similarity to membrane protein pho87p and hypothetical protein yjl198w:hypothetical 99.5 kd protein in urk1-smm1 intergenic region] [gn:n2052] [gtcfc:12.4:12.6:13.10] [keggfc:14.2] [sgdfc:1.4.3:1.8.2:7.2.3:17.0.0] [db
CONTIG3466	4475255_c3_4	6647	20750	420	140	YPR138C	343	2.7(10)-31	Saccharomyces cerevisiae	[ui:ypr138c] [pn:strong similarity to ammonium transport proteins:ammonium transporter mep3] [gn:mep3] [gtcfc:12.5] [keggfc:14.2] [sgdfc:1.2.3:7.2.2:17.0.0] [db:gtc-saccharomyces cerevisiae]
b9x10b25.x	3140754_c2_2	6648	20751	528	176	YPR138C	578	3.3(10)-56	Saccharomyces cerevisiae	[ui:ypr138c] [pn:strong similarity to ammonium transport proteins:ammonium transporter mep3] [gn:mep3:p9659] [gtcfc:12.5] [keggfc:14.2] [sgdfc:1.2.3:7.2.2:17.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG238	4375052_c3_1	6649	20752	678	226	YAL026C	792	5.9(10)-78	Saccharomyces cerevisiae	[ui:yal026c] [pn:p-type amino-phospholipids-atpase:probable calcium-transporting atpase 3:endoplasmic reticulum ca2+-atpase] [gn:pmc1:drs2:fun38] [gtcfc:12.2:12.5:12.6:12.16] [ec:3.6.1.38] [keggfc:14.1] [sgdfc:7.2.2:7.8.0] [db:gtc-sac]
CONTIG2297	26367325_c1_3	6650	20753	975	325	YAL026C	1093	9.0(10)-111	Saccharomyces cerevisiae	[ui:yal026c] [pn:p-type amino-phospholipids-atpase:probable calcium-transporting atpase 3:endoplasmic reticulum ca2+-atpase] [gn:pmc1:drs2:fun38] [gtcfc:12.2:12.5:12.6:12.16] [ec:3.6.1.38] [keggfc:14.1] [sgdfc:7.2.2:7.8.0] [db:gtc-sac]
CONTIG3268	5906250_c2_7	6651	20754	1353	451	YAL026C	761	1.3(10)-74	Saccharomyces cerevisiae	[ui:yal026c] [pn:p-type amino-phospholipids-atpase:probable calcium-transporting atpase 3:endoplasmic reticulum ca2+-atpase] [gn:pmc1:drs2:fun38] [gtcfc:12.2:12.5:12.6:12.16] [ec:3.6.1.38] [keggfc:14.1] [sgdfc:7.2.2:7.8.0] [db:gtc-sac]
CONTIG5035	483516_c3_15	6652	20755	390	130	YAL026C	319	2.6(10)-27	Saccharomyces cerevisiae	[ui:yal026c] [pn:p-type amino-phospholipids-atpase:probable calcium-transporting atpase 3:endoplasmic reticulum ca2+-atpase] [gn:pmc1:drs2:fun38] [gtcfc:12.2:12.5:12.6:12.16] [ec:3.6.1.38] [keggfc:14.1] [sgdfc:7.2.2:7.8.0] [db:gtc-sac]

CONTIG5397	24413193_c1_18	6653	20756	684	228	YDR456W	611	1.1(10)-59	Saccharomyces cerevisiae	[ui:ydr456w] [pn:similarity to mammalian na+-h+ antiporters] [gtcfc:12.5:12.6] [keggfc:14.2] [sgdfc:1.8.2:7.2.2:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1608	23879781_c3_9	6654	20757	948	316	YLR138W	433	1.1(10)-45	Saccharomyces cerevisiae	[ui:ylr138w] [pn:putative na+/h+ antiporter] [gn:nha1] [gtcfc:12.5:12.6] [keggfc:14.2] [sgdfc:1.8.2:7.2.2] [db:gtc-saccharomyces cerevisiae]
CONTIG5606	7115936_f3_23	6655	20758	1239	413	YLR138W	1185	1.6(10)-120	Saccharomyces cerevisiae	[ui:ylr138w] [pn:putative na+/h+ antiporter] [gn:nha1] [gtcfc:12.5:12.6] [keggfc:14.2] [sgdfc:1.8.2:7.2.2] [db:gtc-saccharomyces cerevisiae]
CONTIG5606	35180166_f2_15	6656.	20759	1434	478	YLR138W	465	5.4(10)-58	Saccharomyces cerevisiae	[ui:ylr138w] [pn:putative na+/h+ antiporter] [gn:nha1] [gtcfc:12.5:12.6] [keggfc:14.2] [sgdfc:1.8.2:7.2.2] [db:gtc-saccharomyces cerevisiae]
CONTIG4942	29330192_c3_24	6657	20760	1653	551	YDR091C	2313	4.7(10)-240	Saccharomyces cerevisiae	[ui:ydr091c] [pn:strong similarity to human rnase l inhibitor and m.jannaschii abc transporter protein] [gtcfc:12.6:10.2] [keggfc:14.2] [sgdfc:7.9.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1100	19562952_c1_1	6658	20761	627	209	YDR406W	414	2.2(10)-37	Saccharomyces cerevisiae	[ui:ydr406w] [pn:atp-binding cassette transporter family member] [gn:pdr15] [gtcfc:12.6] [keggfc:14.2] [sgdfc:7.9.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5296	26797286_c2_12	6659	20762	1833	611	YDR406W	1504	2.5(10)-154	Saccharomyces cerevisiae	[ui:ydr406w] [pn:atp-binding cassette transporter family member] [gn:pdr15] [gtcfc:12.6] [keggfc:14.2] [sgdfc:7.9.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5296	865925_c3_14	6660	20763	804	268	YDR406W	486	4.9(10)-45	Saccharomyces cerevisiae	[ui:ydr406w] [pn:atp-binding cassette transporter family member] [gn:pdr15] [gtcfc:12.6] [keggfc:14.2] [sgdfc:7.9.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5761	5101436_f3_12	6661	20764	1842	614	YER036C	2436	4.2(10)-253	Saccharomyces cerevisiae	[ui:yer036c] [pn:similarity to members of the abc transporter family:probable atp-dependent transporter yer036c] [gtcfc:12.6] [keggfc:14.2] [sgdfc:7.9.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3011	25425802_c2_8	6662	20765	843	281	YFL028C	657	1.3(10)-64	Saccharomyces cerevisiae	[ui:yfl028c] [pn:atp-binding cassette transporter family member:probable atp-dependent transporter yfl028c] [gn:caf16] [gtcfc:12.6] [keggfc:14.2] [sgdfc:7.9.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4658	15907831_c3_7	6663	20766	825	275	YFL028C	560	2.7(10)-54	Saccharomyces cerevisiae	[ui:yfl028c] [pn:atp-binding cassette transporter family member:probable atp-dependent transporter yfl028c] [gn:caf16] [gtcfc:12.6] [keggfc:14.2] [sgdfc:7.9.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4530	14570388_f3_4	6664	20767	276	92	YLL048C	263	3.1(10)-21	Saccharomyces cerevisiae	[ui:yll048c] [pn:similarity to rat organic anion transporter] [gtcfc:12.4:12.6] [keggfc:14.2] [sgdfc:7.9.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2029	20320275_c1_1	6665	20768	336	112	YLR188W	277	2.5(10)-23	Saccharomyces cerevisiae	[ui:ylr188w] [pn:atp-binding cassette transporter family member:atp-dependent permease mdl1] [gn:mdl1] [gtcfc:12.6:11.1] [keggfc:14.2] [sgdfc:7.9.0] [db:gtc-saccharomyces cerevisiae]
b3x19039.x	20019533_f2_1	6666	20769	501	167	YLR188W	412	5.2(10)-38	Saccharomyces cerevisiae	[ui:ylr188w] [pn:atp-binding cassette transporter family member:atp-dependent permease mdl1] [gn:mdl1] [gtcfc:12.6:11.1] [keggfc:14.2] [sgdfc:7.9.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4368	34023325_c3_7	6667	20770	900	300	YOL075C	443	1.0(10)-40	Saccharomyces cerevisiae	[ui:yol075c] [pn:similarity to a.gambiae atp-binding-cassette protein] [gtcfc:12.6] [keggfc:14.2] [sgdfc:7.9.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4643	23859467_f2_2	6668	20771	861	287	YOL075C	434	9.3(10)-40	Saccharomyces cerevisiae	[ui:yol075c] [pn:similarity to a.gambiae atp-binding-cassette protein] [gtcfc:12.6] [keggfc:14.2] [sgdfc:7.9.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4643	21912952_f3_4	6669	20772	1557	519	YOL075C	918	3.1(10)-92	Saccharomyces cerevisiae	[ui:yol075c] [pn:similarity to a.gambiae atp-binding-cassette protein] [gtcfc:12.6] [keggfc:14.2] [sgdfc:7.9.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4029	819077_c2_8	6670	20773	2232	744	YPL270W	1053	1.6(10)-106	Saccharomyces cerevisiae	[ui:ypl270w] [pn:atp-binding cassette:abc transporter family member:atp-dependent permease mdl2] [gn:mdl2:ssh1] [gtcfc:12.6:11.1] [keggfc:14.2] [sgdfc:7.9.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5597	2142151_c3_21	6671	20774	1278	426	YBR290W	450	1.2(10)-42	Saccharomyces cerevisiae	[ui:ybr290w] [pn:metal homeostatis protein:metal homeostatis protein bsd2] [gn:bsd2:ybr2037] [gtcfc:12.6] [keggfc:14.2] [sgdfc:1.8.1:7.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5220	25394527_c1_8	6672	20775	423	141	YDR270W	316	3.3(10)-27	Saccharomyces cerevisiae	[ui:ydr270w] [pn:probable copper-transporting atpase] [gn:ccc2] [gtcfc:12.6] [keggfc:14.2] [sgdfc:1.8.1:7.2.1:7.8.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5220	11134712_c1_7	6673	20776	2880	960	YDR270W	558	7.0(10)-91	Saccharomyces cerevisiae	[ui:ydr270w] [pn:probable copper-transporting atpase] [gn:ccc2] [gtcfc:12.6] [keggfc:14.2] [sgdfc:1.8.1:7.2.1:7.8.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5221	4723903_c1_16	6674	20777	1911	637	YDR270W	173	5.4(10)-16	Saccharomyces cerevisiae	[ui:ydr270w] [pn:probable copper-transporting atpase] [gn:ccc2] [gtcfc:12.6] [keggfc:14.2] [db:gtc-saccharomyces cerevisiae]
CONTIG1580	34236641_f3_3	6675	20778	369	123	YLR130C	90	0.0016	Saccharomyces cerevisiae	[ui:ylr130c] [pn:low affinity zinc transporter] [gn:zrt2] [gtcfc:12.6] [keggfc:14.2] [sgdfc:1.8.1:7.2.1]

CONTIG5819	5895067_f2_5	6676	20779	387	129	YLR130C	442	8.6(10)-42	Saccharomyces cerevisiae	[ui:ylr130c] [pn:low affinity zinc transporter] [gn:zrt2] [gtcfc:12.6] [keggfc:14.2] [sgdfc:1.8.1.7.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG2369	4490632_c1_4	6677	20780	1035	345	YAL067C	406	7.0(10)-38	Saccharomyces cerevisiae	[ui:yal067c] [pn:suppressor of sulfoxyde ethionine resistance:hypothetical 68.8 kd protein in gdh3 5"region] [gn:seo1] [gtcfc:12.6:13.3] [keggfc:14.2] [sgdfc:7.7.0:7.10.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4389	3016876_c1_4	6678	20781	246	82	YAL067C	168	1.0(10)-11	Saccharomyces cerevisiae	[ui:yal067c] [pn:suppressor of sulfoxyde ethionine resistance:hypothetical 68.8 kd protein in gdh3 5"region] [gn:seo1] [gtcfc:12.6:13.3] [keggfc:14.2] [sgdfc:7.7.0:7.10.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4389	555342_c3_6	6679	20782	1293	431	YAL067C	792	7.0(10)-79	Saccharomyces cerevisiae	[ui:yal067c] [pn:suppressor of sulfoxyde ethionine resistance:hypothetical 68.8 kd protein in gdh3 5"region] [gn:seo1] [gtcfc:12.6:13.3] [keggfc:14.2] [sgdfc:7.7.0:7.10.0:17.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5195	22558275_c1_8	6680	20783	861	287	YAL067C	777	2.7(10)-77	Saccharomyces cerevisiae	[ui:yal067c] [pn:suppressor of sulfoxyde ethionine resistance:hypothetical 68.8 kd protein in gdh3 5"region] [gn:seo1] [gtcfc:12.6:13.3] [keggfc:14.2] [sgdfc:7.7.0:7.10.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5195	9798555_c3_9	6681	20784	1092	364	YAL067C	682	3.2(10)-67	Saccharomyces cerevisiae	[ui:yal067c] [pn:suppressor of sulfoxyde ethionine resistance:hypothetical 68.8 kd protein in gdh3 5"region] [gn:seo1] [gtcfc:12.6:13.3] [keggfc:14.2] [sgdfc:7.7.0:7.10.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5471	26462875_f3_8	6682	20785	663	221	YAL067C	187	9.3(10)-14	Saccharomyces cerevisiae	[ui:yal067c] [pn:suppressor of sulfoxyde ethionine resistance:hypothetical 68.8 kd protein in gdh3 5"region] [gn:seo1] [gtcfc:12.6:13.3] [keggfc:14.2] [sgdfc:7.7.0:7.10.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5813	9875126_c2_47	6683	20786	396	132	YMR123W	179	6.4(10)-14	Saccharomyces cerevisiae	[ui:ymr123w] [pn:resistance against pichia farinosa killer toxin:smk toxin when expressed by a multi copy plasmid] [gn:pkr1] [gtcfc:12.6:13.3] [keggfc:14.2] [sgdfc:7.10.0:17.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4533	16220688_c2_5	6684	20787	2466	822	YDR093W	2400	2.7(10)-249	Saccharomyces cerevisiae	[ui:ydr093w] [pn:similarity to p.falciparum calcium-transporting atpase 2:probable calcium-transporting atpase 4] [gn:drs2:yd8557] [gtcfc:12.6] [ec:3.6.1.38] [keggfc:14.1] [sgdfc:7.8.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4834	26445187_f3_4	6685	20788	2445	815	YDR093W	1527	9.1(10)-157	Saccharomyces cerevisiae	[ui:ydr093w] [pn:similarity to p.falciparum calcium-transporting atpase 2:probable calcium-transporting atpase 4] [gn:drs2:yd8557] [gtcfc:12.6] [ec:3.6.1.38] [keggfc:14.1] [sgdfc:7.8.0] [db:gtc-saccharomyces cerevisiae]
CONTIG326	33695388_c3_3	6686	20789	555	185	YER166W	606	8.0(10)-58	Saccharomyces cerevisiae	[ui:yer166w] [pn:similarity to p.falciparum atpase 2:probable calcium-transporting atpase 5] [gn:sygp-orf7] [gtcfc:12.6] [ec:3.6.1.38] [keggfc:14.1] [sgdfc:7.8.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4501	4031306_c1_9	6687	20790	390	130	YER166W	240	8.1(10)-19	Saccharomyces cerevisiae	[ui:yer166w] [pn:similarity to p.falciparum atpase p.falciparum atpase 2:probable calcium-transporting atpase 5] [gn:sygp-orf7] [gtcfc:12.6] [ec:3.6.1.38] [keggfc:14.1] [sgdfc:7.8.0] [db:gtc-saccharomyces cerevisiae]
CONTIG608	4814625_c3_1	6688	20791	501	167	YER166W	515	4.2(10)-48	Saccharomyces cerevisiae	[ui:yer166w] [pn:similarity to p.falciparum atpase p.falciparum atpase 2:probable calcium-transporting atpase 5] [gn:sygp-orf7] [gtcfc:12.6] [ec:3.6.1.38] [keggfc:14.1] [sgdfc:7.8.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3066	12790912_c3_10	6689	20792	2457	819	YMR162C	1665	2.2(10)-171	Saccharomyces cerevisiae	[ui:ymr162c] [pn:similarity to atpases] [gtcfc:12.6] [keggfc:14.2] [sgdfc:7.8.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5758	26812517_c2_21	6690	20793	990	330	YMR162C	386	2.5(10)-34	Saccharomyces cerevisiae	[ui:ymr162c] [pn:similarity to atpases] [gtcfc:12.6] [keggfc:14.2] [sgdfc:7.8.0] [db:gtc-saccharomyces cerevisiae]
b1x15548.x	23631392_c2_3	6691	20794	579	193	YMR162C	463	1.6(10)-42	Saccharomyces cerevisiae	[ui:ymr162c] [pn:similarity to atpases] [gtcfc:12.6] [keggfc:14.2] [sgdfc:7.8.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1020	5085349_c1_3	6692	20795	993	331	YMR162C	623	1.3(10)-59	Saccharomyces cerevisiae	[ui:ymr162c] [pn:similarity to atpases] [gtcfc:12.6] [keggfc:14.2] [sgdfc:7.7.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1766	7313802_f1_1	6693	20796	801	267	YGR260W	229	2.2(10)-18	Saccharomyces cerevisiae	[ui:ygr260w] [pn:similarity to allantoate transport protein:hypothetical 60.1 kd protein in rad2-apl6 intergenic region] [gtcfc:12.6] [keggfc:14.2] [sgdfc:7.7.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4034	175056_c1_4	6694	20797	1446	482	YGR260W	622	7.2(10)-61	Saccharomyces cerevisiae	[ui:ygr260w] [pn:similarity to allantoate transport protein:hypothetical 60.1 kd protein in rad2-apl6 intergenic region] [gtcfc:12.6] [keggfc:14.2] [sgdfc:7.7.0:17.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3312	7057_f1_1	6695	20798	1533	511	YIL166C	1028	6.9(10)-104	Saccharomyces cerevisiae	[ui:yil166c] [pn:similarity to allantoate permease dal5p:hypothetical 61.9 kd protein in suc2 5"region] [gtcfc:12.6] [keggfc:14.2] [sgdfc:7.7.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5018	25446900_c3_19	6696	20799	1242	414	YIL166C	859	5.5(10)-86	Saccharomyces cerevisiae	[ui:yil166c] [pn:similarity to allantoate permease dal5p:hypothetical 61.9 kd protein in suc2 5"region] [gtcfc:12.6] [keggfc:14.2] [sgdfc:7.7.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5018	12929035_c3_18	6697	20800	324	108	YIL166C	109	2.0(10)-5	Saccharomyces cerevisiae	[ui:yil166c] [pn:similarity to allantoate permease dal5p:hypothetical 61.9 kd protein in suc2 5"region] [gtcfc:12.6] [keggfc:14.2] [sgdfc:7.7.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5818	6035255_f1_2	6698	20801	1794	598	YIL166C	1074	9.1(10)-109	Saccharomyces cerevisiae	[ui:yil166c] [pn:similarity to allantoate permease dal5p:hypothetical 61.9 kd protein in suc2 5"region] [gtcfc:12.6] [keggfc:14.2] [sgdfc:7.7.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3436	34158510_f2_3	6699	20802	1254	418	YLR004C	467	1.8(10)-44	Saccharomyces cerevisiae	[ui:ylr004c] [pn:similarity to allantoate transport protein] [gtcfc:12.6] [keggfc:14.2] [sgdfc:7.7.0:17.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5192	1304627_c3_17	6700	20803	1563	521	YLR004C	1244	8.9(10)-127	Saccharomyces cerevisiae	[ui:ylr004c] [pn:similarity to allantoate transport protein] [gtcfc:12.6] [keggfc:14.2] [sgdfc:7.7.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4360	9954506_c1_3	6701	20804	681	227	YBL089W	230	1.0(10)-29	Saccharomyces cerevisiae	[ui:ybl089w] [pn:weak similarity to a.thaliana aminoacid permease aap3:hypothetical 57.1 kd protein in map2-tel1 intergenic region] [gn:ybl0703] [gtcfc:12.6] [keggfc:14.2] [sgdfc:7.11.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5736	1053127_f1_7	6702	20805	513	171	YBL011W	349	5.2(10)-31	Saccharomyces cerevisiae	[ui:ybl011w] [pn:suppresses a choline-transport mutant:hypothetical 85.7 kd protein in rrn6-hir1 intergenic region] [gn:sct1:ybl0315:ybl0309] [gtcfc:12.6:12.13] [keggfc:14.2] [sgdfc:7.11.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5736	24268805_f2_13	6703	20806	1794	598	YBL011W	1097	3.3(10)-111	Saccharomyces cerevisiae	[ui:ybl011w] [pn:suppresses a choline-transport mutant:hypothetical 85.7 kd protein in rrn6-hir1 intergenic region] [gn:sct1:ybl0315:ybl0309] [gtcfc:12.6:12.13] [keggfc:14.2] [sgdfc:7.11.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5819	35555166_c3_52	6704	20807	672	224	YBL011W	472	2.0(10)-44	Saccharomyces cerevisiae	[ui:ybl011w] [pn:suppresses a choline-transport mutant:hypothetical 85.7 kd protein in rrn6-hir1 intergenic region] [gn:sct1:ybl0315:ybl0309] [gtcfc:12.6:12.13] [sgdfc:7.11.0] [keggfc:14.2] [db:gtc-saccharomyces cerevisiae]
CONTIG4250	3912830_c2_5	6705	20808	507	169	YDL206W	187	1.3(10)-13	Saccharomyces cerevisiae	[ui:ydl206w] [pn:weak similarity to transporter proteins] [gtcfc:12.6] [keggfc:14.2] [sgdfc:7.11.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4250	31796927_c3_6	6706	20809	1527	509	YDL206W	158	3.3(10)-8	Saccharomyces cerevisiae	[ui:ydl206w] [pn:weak similarity to transporter proteins] [gtcfc:12.6] [keggfc:14.2] [sgdfc:7.11.0] [db:gtc-saccharomyces cerevisiae]
CONTIG583	43867055_c3_2	6707	20810	624	208	YEL064C	456	2.7(10)-43	Saccharomyces cerevisiae	[ui:yel064c] [pn:similarity to ybl089w:hypothetical 53.3 kd protein in hxt8-can1 intergenic region] [gtcfc:12.6] [keggfc:14.2] [sgdfc:7.11.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG12	24414062_c3_4	6708	20811	399	133	YER119C	250	6.2(10)-21	Saccharomyces cerevisiae	[ui:yer119c] [pn:weak similarity to e.herbicola tyrosine permease:hypothetical 48.8 kd protein in ssu81-scs2 intergenic region] [gtcfc:12.6] [keggfc:14.2] [sgdfc:7.11.0:17.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3058	24414062_f1_1	6709	20812	798	266	YER119C	413	$1.0(10)-38$	Saccharomyces cerevisiae	[ui:yer119c] [pn:weak similarity to e.herbicola tyrosine permease:hypothetical 48.8 kd protein in ssu81-scs2 intergenic region] [gtcfc:12.6] [keggfc:14.2] [sgdfc:7.11.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1878	9869051_c2_2	6710	20813	1200	400	YIL088C	684	$1.3(10)-77$	Saccharomyces cerevisiae	[ui:yil088c] [pn:similarity to a.thaliana aminoacid permease aap4:hypothetical 53.7 kd protein in sga1-sds3 intergenic region] [gtcfc:12.1:11.1] [keggfc:14.2] [sgdfc:7.11.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3768	816902_c3_4	6711	20814	720	240	YIL006W	432	$9.9(10)-41$	Saccharomyces cerevisiae	[ui:yil006w] [pn:similarity to fix1p:putative mitochondrial carrier yil006w] [gtcfc:12.6] [keggfc:14.2] [sgdfc:1.7.4:7.11.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3513	4970052_c3_10	6712	20815	1452	484	YJR001W	350	$6.2(10)-56$	Saccharomyces cerevisiae	[ui:yjr001w] [pn:weak similarity to a.thaliana aminoacid permease aap4:hypothetical 65.3 kd protein in pre3-sag1 intergenic region] [gn:j1409:yjr83] [keggfc:14.2] [sgdfc:7.11.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5231	5112760_f3_5	6713	20816	1536	512	YJR001W	865	$1.3(10)-86$	Saccharomyces cerevisiae	[ui:yjr001w] [pn:weak similarity to a.thaliana aminoacid permease aap4:hypothetical 65.3 kd protein in pre3-sag1 intergenic region] [gn:j1409:yjr83] [sgdfc:7.11.0:17.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG1449	24422183_f3_2	6714	20817	471	157	YJR124C	259	6.0(10)-22	Saccharomyces cerevisiae	[ui:yjr124c] [pn:weak similarity to staphylococcus multidrug resistance protein:hypothetical 49.7 kd protein in rps5-zms1 intergenic region] [gn:j2046] [gtcfc:12.6] [keggfc:14.2] [sgdfc:7.11.0-17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1449	29687515_f1_1	6715	20818	294	98	YJR124C	212	9.8(10)-17	Saccharomyces cerevisiae	[ui:yjr124c] [pn:weak similarity to staphylococcus multidrug resistance protein:hypothetical 49.7 kd protein in rps5-zms1 intergenic region] [gn:j2046] [gtcfc:12.6] [keggfc:14.2] [sgdfc:7.11.0-17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3638	433325_c2_4	6716	20819	576	192	YJR124C	401	1.8(10)-37	Saccharomyces cerevisiae	[ui:yjr124c] [pn:weak similarity to staphylococcus multidrug resistance protein:hypothetical 49.7 kd protein in rps5-zms1 intergenic region] [gn:j2046] [gtcfc:12.6] [keggfc:14.2] [sgdfc:7.11.0-17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5664	18887_f1_3	6717	20820	1443	481	YJR124C	573	1.1(10)-55	Saccharomyces cerevisiae	[ui:yjr124c] [pn:weak similarity to staphylococcus multidrug resistance protein:hypothetical 49.7 kd protein in rps5-zms1 intergenic region] [gn:j2046] [gtcfc:12.6] [keggfc:14.2] [sgdfc:7.11.0-17.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5288	4319661_f3_10	6718	20821	1332	444	YKL221W	793	5.5(10)-79	Saccharomyces cerevisiae	[ui:ykl221w] [pn:weak similarity to human x-linked pest-containing transporter:hypothetical 52.3 kd protein in fre2 5"region] [gtcfc:12.6] [keggfc:14.2] [sgdfc:7.11.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG167	11776042_f1_1	6719	20822	864	288	YKL146W	245	3.2(10)-27	Saccharomyces cerevisiae	[ui:ykl146w] [pn:strong similarity to s.pombe hypothetical protein c3h1.09c:hypothetical 75.5 kd protein in sdh1-cim5/yta3 intergenic region] [gn:ykl600] [keggfc:14.2] [sgdfc:7.11.0:17.0.0] [db:gtc-saccharomyces cerevisia]
CONTIG3818	32535156_c1_1	6720	20823	432	144	YKL146W	242	1.5(10)-19	Saccharomyces cerevisiae	[ui:ykl146w] [pn:strong similarity to s.pombe hypothetical protein c3h1.09c:hypothetical 75.5 kd protein in sdh1-cim5/yta3 intergenic region] [gn:ykl600] [keggfc:14.2] [sgdfc:7.11.0:17.0.0] [db:gtc-saccharomyces cerevisia]
CONTIG5819	4375257_c3_53	6721	20824	1248	416	YKR067W	711	2.7(10)-70	Saccharomyces cerevisiae	[ui:ykr067w] [pn:strong similarity to scl1p:hypothetical 83.6 kd protein in ccp1-sis2 intergenic region] [gtcfc:12.6] [keggfc:14.2] [sgdfc:7.11.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4080	19539067_c3_6	6722	20825	1344	448	YNL125C	561	2.1(10)-54	Saccharomyces cerevisiae	[ui:ynl125c] [pn:similarity to ykl221w and human x-linked pest-containing transporter:hypothetical 73.8 kd protein in spc98-tom70 intergenic region] [gn:nl882:nl223:esbp6] [gtcfc:12.6] [keggfc:14.2] [sgdfc:7.11.0:17.0.0] [db:gtc-sacch
CONTIG4189	1455090_f3_2	6723	20826	498	166	YNL125C	173	8.9(10)-16	Saccharomyces cerevisiae	[ui:ynl125c] [pn:similarity to ykl221w and human pest-containing transporter:hypothetical 73.8 kd protein in spc98-tom70 intergenic region] [gn:nl882:nl223:esbp6] [gtcfc:12.6] [keggfc:14.2] [sgdfc:7.11.0:17.0.0] [db:gtc-sacch
CONTIG1652	20443932_f1_2	6724	20827	690	230	YNL003C	694	1.7(10)-68	Saccharomyces cerevisiae	[ui:ynl003c] [pn:similarity to mitochondrial rat tricarboxylate transport protein precursor:putative mitochondrial carrier protein pet8] [gn:pet8:n2012] [gtcfc:12.6:1.2:12.16] [keggfc:14.2] [sgdfc:7.11.0] [db:gtc-saccharomyces cerevis
CONTIG1160	26582562_f2_2	6725	20828	423	141	YOL119C	216	4.7(10)-17	Saccharomyces cerevisiae	[ui:yol119c] [pn:similarity to monocarboxylate transport proteins] [gtcfc:12.6] [keggfc:14.2] [sgdfc:7.11.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG19	7051302_c3_1	6726	20829	315	105	YOL119C	124	4.2(10)-7	Saccharomyces cerevisiae	[ui:yol119c] [pn:similarity to monocarboxylate transporter proteins] [gtcfc:12.6] [keggfc:14.2] [sgdfc:7.11.0:17.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4765	7051302_c1_7	6727	20830	984	328	YOL119C	510	5.4(10)-49	Saccharomyces cerevisiae	[ui:yol119c] [pn:similarity to monocarboxylate transporter proteins] [gtcfc:12.6] [keggfc:14.2] [sgdfc:7.11.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG675	5312800_c1_2	6728	20831	1035	345	YOL119C	322	8.5(10)-29	Saccharomyces cerevisiae	[ui:yol119c] [pn:similarity to monocarboxylate transporter proteins] [gtcfc:12.6] [keggfc:14.2] [sgdfc:7.11.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3557	20500024_c1_4	6729	20832	1146	382	YOL119C	716	8.0(10)-71	Saccharomyces cerevisiae	[ui:yol119c] [pn:similarity to monocarboxylate transporter proteins] [gtcfc:12.6] [keggfc:14.2] [sgdfc:7.11.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4874	4117278_c3_6	6730	20833	1848	616	YOR291W	1395	8.9(10)-143	Saccharomyces cerevisiae	[ui:yor291w] [pn:similarity to cation translocating atpases] [gtcfc:12.6] [keggfc:14.2] [sgdfc:7.11.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5817	33650312_f2_18	6731	20834	1443	481	YOR291W	476	9.6(10)-59	Saccharomyces cerevisiae	[ui:yor291w] [pn:similarity to cation translocating atpases] [gtcfc:12.6] [keggfc:14.2] [sgdfc:7.11.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5817	24398450_f3_38	6732	20835	240	80	YOR291W	224	3.7(10)-17	Saccharomyces cerevisiae	[ui:yor291w] [pn:similarity to cation translocating atpases] [gtcfc:12.6] [keggfc:14.2] [sgdfc:7.11.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4492	22087875_c2_8	6733	20836	1437	479	YHL017W	104	0.019	Saccharomyces cerevisiae	[ui:yhl017w] [pn:strong similarity to ptm1p:hypothetical 61.2 kd protein in apm2-dur3 intergenic region precursor] [gtcfc:12.6:14.3] [keggfc:14.2] [sgdfc:17.0.0:13.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4655	24431555_c3_2	6734	20837	1860	620	YHL017W	692	$2.7(10)-68$	Saccharomyces cerevisiae	[ui:yhl017w] [pn:strong similarity to ptm1p:hypothetical 61.2 kd protein in apm2-dur3 intergenic region precursor] [gtcfc:12.6:14.3] [keggfc:14.2] [sgdfc:17.0.0:13.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG688	24431555_c2_2	6735	20838	447	149	YHL017W	123	$6.0(10)-7$	Saccharomyces cerevisiae	[ui:yhl017w] [pn:strong similarity to ptm1p:hypothetical 61.2 kd protein in apm2-dur3 intergenic region precursor] [gtcfc:12.6:14.3] [keggfc:14.2] [sgdfc:17.0.0:13.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5638	23838432_c1_15	6736	20839	1767	589	YCL037C	96	0.05899	Saccharomyces cerevisiae	[ui:ycl037c] [pn:suppressor of rho3:hypothetical 51.8 kd protein in glk1-ste50 intergenic region] [gn:sro9:ycl37c] [gtcfc:12.6] [keggfc:14.2] [sgdfc:1.8.1] [db:gtc-saccharomyces cerevisiae]
CONTIG2117	14100916_f1_1	6737	20840	1107	369	YDR515W	114	0.00056	Saccharomyces cerevisiae	[ui:ydr515w] [pn:copper homeostasis protein] [gn:slf1] [gtcfc:12.6] [keggfc:14.2] [sgdfc:1.8.1] [db:gtc-saccharomyces cerevisiae]

CONTIG4560	24095311_f2_1	6738	20841	336	YFL041W	217	5.9(10)-17	Saccharomyces cerevisiae	[ui:yfl041w] [pn:strong similarity to cell surface ferroxidase precursor fet3p:hypothetical 70.9 kd protein in sec53-act1 intergenic region precursor] [gtcfc:12.6] [keggfc:14.2] [sgdfc:1.8.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5327	25994007_f3_5	6739	20842	1617	YGL160W	310	7.5(10)-32	Saccharomyces cerevisiae	[ui:ygl160w] [pn:similarity to hypothetical protein ylr047c and fre2p:hypothetical 65.8 kd protein in sut1-rck1 intergenic region] [gn:g1837] [gtcfc:12.6] [keggfc:14.2] [sgdfc:1.8.1] [db:gtc-saccharomyces cerevisiae]
CONTIG2454	6906942_c1_3	6740	20843	1137	YJR049C	379	3.1(10)-34	Saccharomyces cerevisiae	[ui:yjr049c] [pn:associated with ferric reductase activity:utr1 protein:unknown transcript 1 protein] [gn:utr1:j16551] [keggfc:14.2] [sgdfc:1.8.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5618	24470936_c2_21	6741	20844	1026	YJR049C	671	4.7(10)-66	Saccharomyces cerevisiae	[ui:yjr049c] [pn:associated with ferric reductase activity:utr1 protein:unknown transcript 1 protein] [gn:utr1:j16551] [gtcfc:12.6] [keggfc:14.2] [sgdfc:1.8.1] [db:gtc-saccharomyces cerevisiae]

CONTIG1675	32507707_f3_2	6742	20845	915	305	YJR126C	450	7.4(10)-42	Saccharomyces cerevisiae	[ui:yjr126c] [pn:similarity to human prostate-specific membrane antigen and transferrin receptor protein:hypothetical 92.0 kd protein in rps5-zms1 intergenic region] [gn:j2050] [gtcfc:12.6] [keggfc:14.2] [sgdfc:1.8.1] [db:gtc-saccharo
CONTIG2183	10658266_f1_2	6743	20846	1584	528	YJR126C	247	3.8(10)-31	Saccharomyces cerevisiae	[ui:yjr126c] [pn:similarity to human prostate-specific membrane antigen and transferrin receptor protein:hypothetical 92.0 kd protein in rps5-zms1 intergenic region] [gn:j2050] [gtcfc:12.6] [keggfc:14.2] [sgdfc:1.8.1] [db:gtc-saccharo
b2x15488.y	881262_c3_2	6744	20847	276	92	YJR126C	130	1.8(10)-7	Saccharomyces cerevisiae	[ui:yjr126c] [pn:similarity to human prostate-specific membrane antigen and transferrin receptor protein:hypothetical 92.0 kd protein in rps5-zms1 intergenic region] [gn:j2050] [gtcfc:12.6] [keggfc:14.2] [sgdfc:1.8.1] [db:gtc-saccharo
CONTIG3296	978125_c1_5	6745	20848	1023	341	YLL051C	136	5.2(10)-6	Saccharomyces cerevisiae	[ui:yll051c] [pn:strong similarity to ferric reductase fre2p] [gtcfc:14.2] [sgdfc:1.8.1] [db:gtc-saccharomyces cerevisiae]

CONTIG2351	34553768_c2_6	6746	20849	2178	726	YNR060W	801	7.7(10)-80	Saccharomyces cerevisiae	[ui:ynr060w] [pn:strong similarity to fre2p and hypothetical protein yor381w, and similarity to fre1p:hypothetical 82.0 kd protein in bio3-hxt17 intergenic region precursor] [gn:n3518] [gtcfc:12.6] [keggfc:14.2] [sgdfc:1.8.1] [db:gtc-
CONTIG3089	5906687_c1_3	6747	20850	837	279	YNR060W	348	5.9(10)-31	Saccharomyces cerevisiae	[ui:ynr060w] [pn:strong similarity to fre2p and hypothetical protein yor381w, and similarity to fre1p:hypothetical 82.0 kd protein in bio3-hxt17 intergenic region precursor] [gn:n3518] [gtcfc:12.6] [keggfc:14.2] [sgdfc:1.8.1] [db:gtc-
CONTIG4409	16609568_f1_1	6748	20851	1800	600	YNR060W	628	3.2(10)-73	Saccharomyces cerevisiae	[ui:ynr060w] [pn:strong similarity to fre2p and hypothetical protein yor381w, and similarity to fre1p:hypothetical 82.0 kd protein in bio3-hxt17 intergenic region precursor] [gn:n3518] [gtcfc:12.6] [keggfc:14.2] [sgdfc:1.8.1] [db:gtc-
CONTIG4657	24414812_f1_1	6749	20852	1560	520	YNR060W	701	3.1(10)-69	Saccharomyces cerevisiae	[ui:ynr060w] [pn:strong similarity to fre2p and hypothetical protein yor381w, and similarity to fre1p:hypothetical 82.0 kd protein in bio3-hxt17 intergenic region precursor] [gn:n3518] [gtcfc:14.2] [keggfc:14.2] [sgdfc:1.8.1]

CONTIG4589	23484552_f1_1	6750	20853	1296	432	YNR060W	283	1.2(10)-22	Saccharomyces cerevisiae	[ui:ynr060w] [pn:strong similarity to fre2p and hypothetical protein yor381w, and similarity to fre1p:hypothetical 82.0 kd protein in bio3-hxt17 intergenic region precursor] [gn:n3518] [gtcfc:12.6] [keggfc:14.2] [sgdfc:1.8.1] [db:gtc-
CONTIG4620	2343803_f1_1	6751	20854	1650	550	YNR060W	705	1.2(10)-69	Saccharomyces cerevisiae	[ui:ynr060w] [pn:strong similarity to fre2p and hypothetical protein yor381w, and similarity to fre1p:hypothetical 82.0 kd protein in bio3-hxt17 intergenic region precursor] [gn:n3518] [gtcfc:12.6] [keggfc:14.2] [sgdfc:1.8.1] [db:gtc-
CONTIG2018	2401017_f2_1	6752	20855	903	301	YOR381W	415	2.7(10)-38	Saccharomyces cerevisiae	[ui:yor381w] [pn:strong similarity to ferric reductase fre2p] [gtcfc:12.6] [keggfc:14.2] [sgdfc:1.8.1] [db:gtc-saccharomyces cerevisiae]
CONTIG1464	6742183_f2_2	6753	20856	822	274	YOR381W	257	3.7(10)-21	Saccharomyces cerevisiae	[ui:yor381w] [pn:strong similarity to ferric reductase fre2p] [gtcfc:12.6] [keggfc:14.2] [sgdfc:1.8.1] [db:gtc-saccharomyces cerevisiae]
CONTIG2530	1995906_c2_5	6754	20857	2043	681	YOR381W	715	1.0(10)-70	Saccharomyces cerevisiae	[ui:yor381w] [pn:strong similarity to ferric reductase fre2p] [gtcfc:12.6] [keggfc:14.2] [sgdfc:1.8.1] [db:gtc-saccharomyces cerevisiae]

CONTIG4317	1953885_f3_2	6755	20858	2097	699	YOR381W	746	5.2(10)-74	Saccharomyces cerevisiae	[ui:yor381w] [pn:strong similarity to ferric reductase fre2p] [gtcfc:12.6] [keggfc:14.2] [sgdfc:1.8.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5391	12597202_c3_21	6756	20859	1119	373	YOR384W	232	9.6(10)-19	Saccharomyces cerevisiae	[ui:yor384w] [pn:strong similarity to ferric reductase fre2p] [gtcfc:12.6] [keggfc:14.2] [sgdfc:1.8.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5247	30703938_c2_19	6757	20860	1221	407	YPR129W	200	1.8(10)-31	Saccharomyces cerevisiae	[ui:ypr129w] [pn:suppressor of clathrin deficiency:scd6 protein] [gn:scd6:p96659] [gtcfc:12.6] [keggfc:14.2] [sgdfc:8.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2449	13863760_f3_2	6758	20861	558	186	YLR109W	261	1.3(10)-22	Saccharomyces cerevisiae	[ui:ylr109w] [pn:similarity to c.boidinii peroxisomal membrane protein 20k a:putative peroxisomal membrane protein] [gn:l2916:l93354] [gtcfc:12.6] [keggfc:14.2] [sgdfc:9.8.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4653	13070413_f3_6	6759	20862	633	211	YLR109W	187	9.0(10)-15	Saccharomyces cerevisiae	[ui:ylr109w] [pn:similarity to c.boidinii peroxisomal membrane protein 20k a:putative peroxisomal membrane protein] [gn:l2916:l93354] [gtcfc:12.6] [keggfc:14.2] [sgdfc:9.8.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5494	14556527_f1_1	6760	20863	738	246	YLR251W	184	2.5(10)-26	Saccharomyces cerevisiae	[ui:ylr251w] [pn:similarity to peroxisomal rat membrane protein pmp22] [gtcfc:12.6] [keggfc:14.2] [sgdfc:9.8.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5494	23990636_f1_2	6761	20864	675	225	YLR251W	319	9.4(10)-29	Saccharomyces cerevisiae	[ui:lr251w] [pn:similarity to peroxisomal rat membrane protein pmp22] [gtcfc:12.6] [keggfc:14.2] [sgdfc:9.8.0] [db:gtc-saccharomyces cerevisiae]
CONTIG540	23626625_c3_3	6762	20865	483	161	YOL147C	150	7.5(10)-11	Saccharomyces cerevisiae	[ui:yol147c] [pn:peroxisomal membrane protein] [gn:pmp27] [gtcfc:12.6] [keggfc:14.2] [sgdfc:9.8.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3007	4485902_f1_2	6763	20866	549	183	YDL127W	391	2.2(10)-36	Saccharomyces cerevisiae	[ui:ydl127w] [pn:cyclin, g1/s-specific cyclin pcl2:cyclin hcs26 homolog] [gn:pcl2:cln4] [gtcfc:12.8] [keggfc:13.1] [sgdfc:3.8.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4591	4475176_c3_8	6764	20867	1146	382	YDL127W	348	7.9(10)-32	Saccharomyces cerevisiae	[ui:ydl127w] [pn:cyclin, g1/s-specific:g1/s-specific cyclin pcl2:cyclin hcs26 homolog] [gn:pcl2:cln4] [gtcfc:12.8] [keggfc:13.1] [sgdfc:3.8.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1013	24698791_f2_1	6765	20868	708	236	Q02959	438	7.0(10)-41	Saccharomyces cerevisiae	[gn:hos3:ypl116w:iph11w] [sr;baker's yeast] [sp:q02959] [db:swissprot]
b2x12717.y	10558180_f3_1	6766	20869	528	176	Q02959	451	2.5(10)-42	Saccharomyces cerevisiae	[gn:hos3:ypl116w:iph11w] [sr;baker's yeast] [de:hos3 protein] [sp:q02959] [db:swissprot]
CONTIG5811	1273292_f3_16	6767	20870	1326	442	S74213	1059	3.6(10)-107	Methylophilus methylotrophus	[pn:formamidase, a] [gn:fmda] [ec:3.5.1.49] [db:pir]
b3x16051.y	23562594_c2_3	6768	20871	216	72	S72165	106	8.9(10)-6	Rhizobium leguminosarum	[pn:probable alcohol dehydrogenase] [db:pir]

CONTIG3137	4728300_f3_3	6769	20872	225	75	E69538	92	0.00129	Archaeoglobus fulgidus	[pn:conserved hypothetical transmembrane protein af2309] [db:pir]
CONTIG4762	22438207_c1_12	6770	20873	420	140	S78075	238	3.6(10)-20	Saccharomyces cerevisiae	[pn:hypothetical protein yjr135w-a] [db:pir] [mp:10r]
CONTIG5765	24489665_f2_6	6771	20874	570	190	S78074	309	1.1(10)-27	Saccharomyces cerevisiae	[pn:hypothetical protein ykl053c-a] [db:pir] [mp:11l]
CONTIG4792	16251002_f1_1	6772	20875	2436	812	S71461	180	3.6(10)-11	Coprinus cinereus	[pn:rad9 protein] [db:pir]
CONTIG4237	954687_c1_5	6773	20876	357	119	JC5710	98	6.2(10)-5	Mus musculus	[pn:tat binding protein-1 interacting protein] [sr:, house mouse] [db:pir]
CONTIG5502	14881512_f1_1	6774	20877	777	259	S71489	321	9.8(10)-29	Rattus norvegicus	[pn:sulfoalanine decarboxylase,] [sr:, norway rat] [ec:4.1.1.29] [db:pir]
CONTIG4934	29376628_f1_1	6775	20878	2859	953	AF036485	95	0.07499	no gb taxonomy match	[pn:unknown] [db:genpept-bct] [de:plasmid pnz4000 replication protein (repb2) gene, complete cds; andunknown gene.] [nt:orfc2]
CONTIG5610	21679692_f2_4	6776	20879	1047	349	U53868	95	0.16	Clostridium acetobutylicum	[pn:mtlr] [gn:mtlr] [sr:clostridium acetobutylicum strain=dsm 792] [db:genpept-bct] [de:clostridium acetobutylicum mannitol-specific phosphotransferasesystem (pts) system, mtla, mtlr, mtlf, and mtld genes, completecds.] [nt:putative p
CONTIG125	627291_f3_1	6777	20880	594	198	AL021287	181	3.2(10)-13	Mycobacterium tuberculosis	[pn:monoxygenase] [gn:mtv012.64c] [db:genpept-bct] [de:mycobacterium tuberculosis sequence v012.] [nt:mtv012.64c, len: 524. probable monoxygenase,]

CONTIG2722	29898518_f1_1	6778	20881	360	120	AL021287	92	0.00129	Mycobacterium tuberculosis	[pn:monoxygenase] [gn:mtv012.64c] [db:genpept-bct] [de:mycobacterium tuberculosis sequence v012.] [nt:mtv012.64c, len: 524, probable monoxygenase,]
CONTIG5776	5179031_c2_28	6779	20882	762	254	AL021287	308	4.4(10)-27	Mycobacterium tuberculosis	[pn:monoxygenase] [gn:mtv012.64c] [db:genpept-bct] [de:mycobacterium tuberculosis sequence v012.] [nt:mtv012.64c, len: 524, probable monoxygenase,]
CONTIG573	35437539_c1_2	6780	20883	1029	343	AL021287	400	2.3(10)-37	Mycobacterium tuberculosis	[pn:monoxygenase] [gn:mtv012.64c] [db:genpept-bct] [de:mycobacterium tuberculosis sequence v012.] [nt:mtv012.64c, len: 524, probable monoxygenase,]
CONTIG5133	11753752_f3_4	6781	20884	984	328	AL021841	224	1.1(10)-18	Mycobacterium tuberculosis	[pn:hypothetical protein mtv016.42] [gn:mtv016.42] [db:genpept-bct] [de:mycobacterium tuberculosis sequence v016.] [nt:mtv016.42, len: 243. unknown but some similarity to]
CONTIG4574	34250002_f1_1	6782	20885	2475	825	AL021942	419	4.5(10)-36	Mycobacterium tuberculosis	[pn:hypothetical protein] [gn:mtv039.22] [db:genpept-bct] [de:mycobacterium tuberculosis sequence v039.] [nt:mtv039.22, len: 877. unknown. contains ps00699]
CONTIG5446	24650037_c1_7	6783	20886	240	80	AF036171	95	0.00062	Dictyostelium discoideum	[pn:homeobox-containing protein] [gn:hbx-2] [db:genpept-inv] [de:dictyostelium discoideum homeobox-containing protein (hbx-2) mrna,partial cds.]

CONTIG2839	3941375_c3_8	6784	20887	1053	351	AF051898	102	0.01499	Dictyostelium discoideum	[pn:coronin binding protein] [gn:db10] [db:genpept-inv] [de:dictyostelium discoideum coronin binding protein (db10) mrna,complete cds.]
b2x13496.x	24117127_c3_2	6785	20888	681	227	Z83109	90	0.51	Caenorhabditis elegans	[pn:f44g3.8] [db:genpept-inv] [de:caenorhabditis elegans cosmid f44g3, complete sequence.]
CONTIG1133	6131312_f3_1	6786	20889	642	214	AF043699	192	7.7(10)-14	Caenorhabditis elegans	[gn:k02f2.3] [sr:caenorhabditis elegans strain=bristol n2] [db:genpept-inv] [de:caenorhabditis elegans cosmid k02f2.] [nt:similar to a human orf (gb:d13642) and human]
b1x13240.x	24807651_f3_1	6787	20890	732	244	AF043699	271	2.8(10)-22	Caenorhabditis elegans	[gn:k02f2.3] [sr:caenorhabditis elegans strain=bristol n2] [db:genpept-inv] [de:caenorhabditis elegans cosmid k02f2.] [nt:similar to a human orf (gb:d13642) and human]
b1x13240.y	11765686_c1_1	6788	20891	594	198	AF043699	342	7.7(10)-30	Caenorhabditis elegans	[gn:k02f2.3] [sr:caenorhabditis elegans strain=bristol n2] [db:genpept-inv] [de:caenorhabditis elegans cosmid k02f2.] [nt:similar to a human orf (gb:d13642) and human]
CONTIG4777	34252143_c3_11	6789	20892	210	70	AL021481	100	0.00021	Caenorhabditis elegans	[pn:y43f4b.5] [db:genpept-inv] [de:caenorhabditis elegans cosmid y43f4b, complete sequence.]
CONTIG5500	35603436_f1_3	6790	20893	909	303	Z82287	141	3.1(10)-7	Caenorhabditis elegans	[pn:zk550.b] [db:genpept-inv] [de:caenorhabditis elegans cosmid zk550, complete sequence.] [nt:protein predicted using genefinder; preliminary]

CONTIG4756	4022311_c1_10	6791	20894	285	95	Z98269	171	4.5(10)-13	Drosophila melanogaster	[gn:eg:87b1.6] [sr:fruit fly] [db:genpept-inv] [de:drosophila melanogaster cosmid 87b1.]
CONTIG4769	14726437_c2_8	6792	20895	2088	696	AL022018	103	0.07099	Drosophila melanogaster	[gn:eg:8d8.4] [sr:fruit fly] [db:genpept-inv] [de:drosophila melanogaster cosmid 8d8.] [nt:1-evidence=predicted by content:]
CONTIG3480	4453186_f3_2	6793	20896	2217	739	U86010	92	0.87	Drosophila melanogaster	[pn:zinc-finger nuclear protein hindsight] [gn:hindsight] [sr:fruit fly] [db:genpept-inv] [de:drosophila melanogaster zinc-finger nuclear protein hindsight, complete cds.] [nt:required for germ band retraction during drosophila]
CONTIG4924	24099031_c3_12	6794	20897	930	310	AB006362	1019	6.2(10)-103	Candida albicans	[gn:casln1] [sr:candida albicans dna] [db:genpept-pln] [de:candida albicans casln1 gene, complete cds.] [nt:similar to slnlp of s. cerevisiae]
CONTIG5238	34650257_f3_3	6795	20898	1851	617	AB006362	2584	9.0(10)-269	Candida albicans	[gn:casln1] [sr:candida albicans dna] [db:genpept-pln] [de:candida albicans casln1 gene, complete cds.] [nt:similar to slnlp of s. cerevisiae]
CONTIG5238	9953800_f3_4	6796	20899	186	62	AB006362	249	7.5(10)-20	Candida albicans	[gn:casln1] [sr:candida albicans dna] [db:genpept-pln] [de:candida albicans casln1 gene, complete cds.] [nt:similar to slnlp of s. cerevisiae]
CONTIG4924	31925174_c1_10	6797	20900	1020	340	AB006362	1109	1.8(10)-112	Candida albicans	[gn:casln1] [sr:candida albicans dna] [db:genpept-pln] [de:candida albicans casln1 gene, complete cds.] [nt:similar to slnlp of s. cerevisiae]

CONTIG2524	25673907_f2_1	6798	20901	729	243	AB006363	1079	2.7(10)-109	Candida albicans	[gn:canik1] [sr:candida albicans dna] [db:genpept-pln] [de:candida albicans canik1 gene, complete cds.] [nt:homologue of histidine kinase]
CONTIG704	402082_f2_1	6799	20902	282	94	AB006363	250	4.2(10)-20	Candida albicans	[gn:canik1] [sr:candida albicans dna] [db:genpept-pln] [de:candida albicans canik1 gene, complete cds.] [nt:homologue of histidine kinase]
CONTIG704	3131388_f3_2	6800	20903	1197	399	AB006363	1548	5.5(10)-159	Candida albicans	[gn:canik1] [sr:candida albicans dna] [db:genpept-pln] [de:candida albicans canik1 gene, complete cds.] [nt:homologue of histidine kinase]
b9x13n67.x	29315663_c3_3	6801	20904	696	232	AB006363	922	1.2(10)-92	Candida albicans	[gn:canik1] [sr:candida albicans dna] [db:genpept-pln] [de:candida albicans canik1 gene, complete cds.] [nt:homologue of histidine kinase]
CONTIG553	25587591_f2_2	6802	20905	195	65	AB010636	139	4.9(10)-9	Candida parapsilosis	[gn:sadh] [sr:candida parapsilosis dna] [db:genpept-pln] [de:candida parapsilosis gene for sadh, complete cds.]
CONTIG5661	22437512_c3_15	6803	20906	1146	382	AB010636	1187	9.8(10)-121	Candida parapsilosis	[pn:sadh] [gn:sadh] [sr:candida parapsilosis dna] [db:genpept-pln] [de:candida parapsilosis gene for sadh, complete cds.]
CONTIG3416	157892_f2_3	6804	20907	1095	365	AF013273	1664	1.8(10)-170	Candida albicans	[pn:histidine kinase 1] [db:genpept-pln] [de:candida albicans histidine kinase 1 gene, complete cds.] [nt:two-component phopho-relay protein homolog; cahk1]

CONTIG4713	5079500_f2_1	6805	20908	3003	1001	AF013273	4730	0	Candida albicans	[pn:histidine kinase 1] [db:genpept-pln] [de:candida albicans histidine kinase 1 gene, complete cds.] [nt:two-component phopho-relay protein homolog; cahk1]
CONTIG4845	9821038_c1_4	6806	20909	3009	1003	AF013273	5056	0	Candida albicans	[pn:histidine kinase 1] [db:genpept-pln] [de:candida albicans histidine kinase 1 gene, complete cds.] [nt:two-component phopho-relay protein homolog; cahk1]
CONTIG1906	24422265_c2_4	6807	20910	672	224	AF038152	408	1.1(10)-52	Mycosphaerella graminicola	[pn:4-hydroxyphenylpyruvate dioxygenase] [gn:hppd] [fn:converts 4-hydroxyphenylpyruvate to] [db:genpept-pln] [ec:1.13.11.27] [de:mycosphaerella graminicola 4-hydroxyphenylpyruvate dioxygenase(hppd) gene, complete cds.] [nt:tyrosine ca
CONTIG5194	835177_f2_2	6808	20911	834	278	AF038154	1171	4.9(10)-119	Candida albicans	[pn:14-3-3 protein] [gn:bmh] [db:genpept-pln] [de:candida albicans 14-3-3 protein (bmh) gene, complete cds.]
CONTIG5598	34157200_f3_15	6809	20912	471	157	AF042334	151	2.7(10)-10	Arabidopsis thaliana	[pn:jab1] [gn:jab1] [sr:thale cress] [db:genpept-pln] [de:arabidopsis thaliana jab1 (jab1) mrna, complete cds.] [nt:similar to jun activation domain binding protein]
CONTIG5598	26272312_f2_9	6810	20913	918	306	AF042334	410	2.1(10)-38	Arabidopsis thaliana	[pn:jab1] [gn:jab1] [sr:thale cress] [db:genpept-pln] [de:arabidopsis thaliana jab1 (jab1) mrna, complete cds.] [nt:similar to jun activation domain binding protein]

CONTIG128	25407686_c3_1	6811	20914	522	174	AF043330	150	4.5(10)-10	Candida albicans	[pn:secreted aspartyl proteinase] [gn:sap8] [db:genpept-pln] [de:candida albicans secreted aspartyl proteinase (sap8) gene, completecds.] [nt:sap8p]
CONTIG776	4798431_c2_1	6812	20915	666	222	AF043330	915	6.5(10)-92	Candida albicans	[pn:secreted aspartyl proteinase] [gn:sap8] [db:genpept-pln] [de:candida albicans secreted aspartyl proteinase (sap8) gene, completecds.] [nt:sap8p]
CONTIG4521	9843750_c3_5	6813	20916	1713	571	AF043331	2215	1.1(10)-229	Candida albicans	[pn:secreted aspartyl proteinase] [gn:sap9] [db:genpept-pln] [de:candida albicans secreted aspartyl proteinase (sap9) gene, completecds.] [nt:sap9p]
b3x13783.y	35803410_f3_1	6814	20917	366	122	AF043331	101	0.00013	Candida albicans	[pn:secreted aspartyl proteinase] [gn:sap9] [db:genpept-pln] [de:candida albicans secreted aspartyl proteinase (sap9) gene, completecds.] [nt:sap9p]
CONTIG4761	4507692_c3_8	6815	20918	942	314	AF045774	1603	8.0(10)-165	Candida albicans	[pn:sir2] [gn:sir2] [db:genpept-pln] [de:candida albicans sir2 (sir2) gene, complete cds.] [nt:similar to saccharomyces cerevisiae sir2]
b2x15833.x	2390833_f2_1	6816	20919	504	168	AF045774	524	1.8(10)-50	Candida albicans	[pn:sir2] [gn:sir2] [db:genpept-pln] [de:candida albicans sir2 (sir2) gene, complete cds.] [nt:similar to saccharomyces cerevisiae sir2]
CONTIG1957	10945312_f2_1	6817	20920	585	195	AF049069	622	7.2(10)-61	Pinus radiata	[pn:pre87] [sr:monterey pine] [db:genpept-pln] [de:pinus radiata pre87 mrna, complete cds.]

CONTIG4287	33360900_c1_8	6818	20921	1497	499	AJ223459	360	4.5(10)-31	Emericella nidulans	[pn:prna protein] [gn:prna] [fn:transcriptional activator] [db:genpept-pln] [de:aspergillus nidulans prna gene.]
CONTIG1313	175765_c2_3	6819	20922	771	257	AJ223508	435	5.7(10)-40	Arabidopsis thaliana	[pn:zwille protein] [gn:zwille] [sr:thale cress] [db:genpept-pln] [de:arabidopsis thaliana mrna for zwille protein.]
b2x14678.y	25651050_f2_1	6820	20923	855	285	AC002334	96	0.11	Arabidopsis thaliana	[pn:similar to disease resistance protein] [gn:f25i18.21] [sr:thale cress] [db:genpept-pln] [de:arabidopsis thaliana chromosome ii bac f25i18 genomic sequence,complete sequence.]
CONTIG4766	1602I900_c3_7	6821	20924	849	283	AC002340	242	4.4(10)-20	Arabidopsis thaliana	[gn:t11j7.11] [sr:thale cress] [db:genpept-pln] [de:arabidopsis thaliana chromosome ii bac t11j7 genomic sequence,complete sequence.] [nt:hypothetical protein]
CONTIG2283	3617000_c3_4	6822	20925	1002	334	AC002561	571	7.7(10)-54	Arabidopsis thaliana	[pn:putative atp-dependent rna helicase] [gn:t24p15.18] [sr:thale cress] [db:genpept-pln] [de:arabidopsis thaliana chromosome ii bac t24p15 genomic sequence,complete sequence.]
CONTIG4297	22710042_c3_7	6823	20926	1017	339	AC003033	103	0.029	Arabidopsis thaliana	[pn:putative disease resistance protein (cf-2.2)] [gn:t21l14.4] [sr:thale cress] [db:genpept-pln] [de:arabidopsis thaliana chromosome ii bac t21l14 genomic sequence,complete sequence.]

CONTIG4144	822026_f3_3	6824	20927	873	291	AC003673	201	$4.4(10)-23$	Arabidopsis thaliana	[gn:f19f24.4] [sr:thale cress] [db:genpept-pln] [de:arabidopsis thaliana chromosome ii bac f19f24 genomic sequence,complete sequence.] [nt:unknown protein]
CONTIG2776	522953_c2_7	6825	20928	1632	544	AL021768	94	0.0057	Arabidopsis thaliana	[pn:resistance protein rpp5 - like] [db:genpept-pln] [de:arabidopsis thaliana dna chromosome 4, bac clone f24j7 (essaiiproject).] [nt:similarity to downy mildew resistance protein rpp5.]
CONTIG4818	392055_c2_8	6826	20929	972	324	AL021890	99	$4.4(10)-7$	Arabidopsis thaliana	[pn:putative protein] [gn:t865.20] [sr:thale cress] [db:genpept-pln] [de:arabidopsis thaliana dna chromosome 4, bac clone t865 (essaiiproject).] [nt:similarity to nadh dehydrogenase chain 4.]
CONTIG3745	26572343_c3_9	6827	20930	222	74	Y17007	221	$3.7(10)-17$	Candida albicans	[pn:piruvate decarboxylase] [gn:pdc2] [db:genpept-pln] [de:candida albicans pdc2 gene.]
CONTIG3745	36365936_c3_8	6828	20931	1980	660	Y17007	3094	0	Candida albicans	[pn:piruvate decarboxylase] [gn:pdc2] [db:genpept-pln] [de:candida albicans pdc2 gene.]
CONTIG3703	7063438_c1_6	6829	20932	477	159	AJ222805	637	$1.8(10)-62$	Candida albicans	[pn:srp54 protein] [gn:srp54] [fn:54 kd subunit of the signal recognition] [db:genpept-pln] [de:candida albicans mrna for srp54 protein homologue.]
CONTIG4262	25445438_f1_2	6830	20933	936	312	U84588	97	0.00016	Candida albicans	[db:genpept-pln] [de:candida albicans dihydrofolate reductase (dfr1) gene, complete cds.] [nt:orf1]

CONTIG4297	3914061_c3_6	6831	20934	837	279	U84588	91	0.00063	Candida albicans [db:genpept-pln] [de:candida albicans dihydrofolate reductase (dfr1) gene, complete cds.] [nt:orf1]
CONTIG4915	23609406_c2_9	6832	20935	1185	395	U84588	122	4.5(10)-7	Candida albicans [db:genpept-pln] [de:candida albicans dihydrofolate reductase (dfr1) gene, complete cds.] [nt:orf1]
CONTIG5656	9820801_f2_8	6833	20936	1734	578	U84588	403	1.2(10)-37	Candida albicans [db:genpept-pln] [de:candida albicans dihydrofolate reductase (dfr1) gene, complete cds.] [nt:orf1]
CONTIG5656	3163432_c1_15	6834	20937	585	195	U84588	993	3.5(10)-100	Candida albicans [db:genpept-pln] [de:candida albicans dihydrofolate reductase (dfr1) gene, complete cds.]
CONTIG5021	15891378_c3_12	6835	20938	1068	356	U96385	97	0.014	Penicillium chrysogenum [pn:gata transcription factor] [gn:nreb] [db:genpept-pln] [de:penicillium chrysogenum gata transcription factor (nreb) gene,complete cds.] [nt:nreb; nitrogen regulatory gata factor]
CONTIG5116	16605035_c1_7	6836	20939	2448	816	Z97209	100	0.035	Schizosaccharomyces pombe [pn:hypothetical protein] [gn:spac19g12.17c] [sr:fission yeast] [db:genpept-pln] [de:s.pombe chromosome i cosmid c19g12.] [nt:spac19g12.17c, partial; unknown, len:223aa, similar]

CONTIG3661	4381317_f2_1	6837	20940	354	118	AL009227	104	5.7(10)-6	Schizosaccharomyces pombe [pn:hypothetical protein] [gn:spac27d7.04] [sr:fission yeast] [db:genpept-pln] [de:s.pombe chromosome i cosmid c27d7.] [nt:spac27d7.04, unknown, len:96aa, similar eg. to]
CONTIG2520	24020463_c3_3	6838	20941	873	291	AL021817	105	0.00169	Schizosaccharomyces pombe [pn:hypothetical protein] [gn:spac8e11.05c] [sr:fission yeast] [db:genpept-pln] [de:s.pombe chromosome i cosmid c8e11.] [nt:spac8e11.05c, unknown, len:338aa]
CONTIG4146	19923386_f1_1	6839	20942	735	245	AL022117	642	5.5(10)-63	Schizosaccharomyces pombe [pn:putative o-methyltransferase] [gn:spbc119.03] [sr:fission yeast] [db:genpept-pln] [de:s.pombe chromosome ii cosmid c119.] [nt:spbc119.03, putative o-methyltransferase,]
CONTIG5242	26375057_f1_1	6840	20943	729	243	AL022305	464	4.0(10)-44	Schizosaccharomyces pombe [pn:hypothetical protein] [gn:spbc14c8.06] [sr:fission yeast] [db:genpept-pln] [de:s.pombe chromosome ii cosmid c14c8.] [nt:spbc14c8.06, unknown, len:377aa, similar eg. to h.]
CONTIG2785	14242216_c2_4	6841	20944	1191	397	AL022305	330	1.0(10)-39	Schizosaccharomyces pombe [pn:hypothetical protein] [gn:spbc14c8.14c] [sr:fission yeast] [db:genpept-pln] [de:s.pombe chromosome ii cosmid c14c8.] [nt:spbc14c8.14c, unknown (appears frame-shifted as]

CONTIG	ID								Organism	Description
CONTIG4913	214583_c2_9	6842	20945	663	221	AL021748	247	6.2(10)-21	Schizosaccharomyces pombe	[pn:adenosine deaminase] [gn:spbc16a3.06] [sr:fission yeast] [db:genpept-pln] [de:s.pombe chromosome ii cosmid c16a3.] [nt:spbc16a3.06, probable adenosine deaminase; contains]
CONTIG454	23625277_c3_4	6843	20946	759	253	AL021748	139	1.5(10)-6	Schizosaccharomyces pombe	[pn:hypothetical protein] [gn:spbc16a3.11] [sr:fission yeast] [db:genpept-pln] [de:s.pombe chromosome ii cosmid c16a3.] [nt:spbc16a3.11, unknown, len:872aa, similar eg. to ()]
CONTIG1614	23867677_c1_2	6844	20947	1224	408	AL022104	240	1.2(10)-22	Schizosaccharomyces pombe	[pn:hypothetical protein] [gn:spbc16h5.12c] [sr:fission yeast] [db:genpept-pln] [de:s.pombe chromosome ii cosmid c16h5.] [nt:spbc16h5.12c, unknown; (possible alternative n])
CONTIG1278	10756307_c2_4	6845	20948	462	154	AL022304	189	1.7(10)-14	Schizosaccharomyces pombe	[pn:hypothetical protein] [gn:spbc18h10.06c] [sr:fission yeast] [db:genpept-pln] [de:s.pombe chromosome ii cosmid c18h10.] [nt:spbc18h10.06c, unknown, len:357aa, similar eg. to]
CONTIG5247	4938912_f1_3	6846	20949	801	267	AL021839	483	3.8(10)-46	Schizosaccharomyces pombe	[pn:hypothetical protein] [gn:spbc19g7.16] [sr:fission yeast] [db:genpept-pln] [de:s.pombe chromosome ii cosmid c19g7.] [nt:spbc19g7.16, unknown, len:429aa, similar eg. to s.]

CONTIG5120	22063431_f1_1	6847	20950	1344	448	AL021746	242	3.7(10)-27	Schizosaccharomyces pombe [pn:hypothetical anaphase promoting factor] [gn:spbc1e8.06] [sr:fission yeast] [db:genpept-pln] [de:s.pombe chromosome ii cosmid c1e8.] [nt:spbc1e8.06, possible anaphase promoting factor]
CONTIG772	24304652_f2_1	6848	20951	714	238	AL021747	276	1.0(10)-30	Schizosaccharomyces pombe [pn:hypothetical mitotic feedback control protein] [gn:spbc20f10.06] [sr:fission yeast] [db:genpept-pln] [de:s.pombe chromosome ii cosmid c20f10.] [nt:spbc20f10.06, putative mitotic feedback control]
CONTIG4577	9777127_f1_1	6849	20952	1425	475	AL021747	102	0.00719	Schizosaccharomyces pombe [pn:hypothetical protein] [gn:spbc20f10.10] [db:genpept-pln] [sr:fission yeast] [de:s.pombe chromosome ii cosmid c20f10.] [nt:spbc20f10.10, unknown, len:243aa, similar eg. to]
b2x14795.y	5883505_c1_3	6850	20953	429	143	AL021816	137	7.4(10)-9	Schizosaccharomyces pombe [pn:hypothetical protein] [gn:spbc24e9.11c] [sr:fission yeast] [db:genpept-pln] [de:s.pombe chromosome ii cosmid c24e9.] [nt:spbc24e9.11c, probable transporter, len:322aa,]
CONTIG5236	34037817_f1_4	6851	20954	744	248	AL021816	331	5.0(10)-30	Schizosaccharomyces pombe [pn:hypothetical protein] [gn:spbc24e9.14c] [sr:fission yeast] [db:genpept-pln] [de:s.pombe chromosome ii cosmid c24e9.] [nt:spbc24e9.14c, unknown, len:238aa, similar eg. to]

CONTIG5818	24509812_c2_42	6852	20955	1851	617	AL022299	835	2.0(10)-83	Schizosaccharomyces pombe [pn:hypothetical protein] [gn:spbc29a3.06] [sr:fission yeast] [db:genpept-pln] [de:s.pombe chromosome ii cosmid c29a3.] [nt:spbc29a3.06, similar eg. to]
CONTIG3167	23984817_f2_3	6853	20956	1245	415	AL022299	118	7.9(10)-8	Schizosaccharomyces pombe [pn:hypothetical protein] [gn:spbc29a3.08] [sr:fission yeast] [db:genpept-pln] [de:s.pombe chromosome ii cosmid c29a3.] [nt:spbc29a3.08, unknown; len:199aa; some sililarity at]
b1x13326.y	10241630_f2_1	6854	20957	285	95	AL022103	210	3.2(10)-17	Schizosaccharomyces pombe [pn:putative protein transport protein] [gn:spbc2g2.03c] [sr:fission yeast] [db:genpept-pln] [de:s.pombe chromosome ii cosmid c2g2.] [nt:spbc2g2.03c, putative protein transport protein.]
CONTIG5458	23437627_c1_10	6855	20958	924	308	AL022103	278	2.1(10)-24	Schizosaccharomyces pombe [pn:hypothetical protein] [gn:spbc2g2.15c] [sr:fission yeast] [db:genpept-pln] [de:s.pombe chromosome ii cosmid c2g2.] [nt:spbc2g2.15c, unknown, len:218aa, similar eg. to m.]
CONTIG2557	15087583_f2_2	6856	20959	276	92	AL022071	92	0.00209	Schizosaccharomyces pombe [pn:hypothetical protein] [gn:spbc354.05c] [sr:fission yeast] [db:genpept-pln] [de:s.pombe chromosome ii cosmid c354.] [nt:spbc354.05c, unknown, len:793aa, similar eg. to the]

CONTIG									
CONTIG1612	36222075_f2_1	6857	20960	1023	341	AL022244	843	2.7(10)-84	Schizosaccharomyces pombe	[pn:hypothetical protein] [gn:spbc3b8.07c] [sr:fission yeast] [db:genpept-pln] [de:s.pombe chromosome ii cosmid c3b8.] [nt:spbc3b8.07c, unknown (putative transmembrane).]
CONTIG5039	33260311_f1_1	6858	20961	201	67	AL022070	125	3.3(10)-8	Schizosaccharomyces pombe	[pn:hypothetical protein] [gn:spbc3b9.12] [sr:fission yeast] [db:genpept-pln] [de:s.pombe chromosome ii cosmid c3b9.] [nt:spbc3b9.12, unknown, len:132aa, similar eg. to s.]
CONTIG3249	4894061_c3_5	6859	20962	540	180	AL021730	90	0.14999	Schizosaccharomyces pombe	[pn:hypothetical protein] [gn:spbc4c3.06] [sr:fission yeast] [db:genpept-pln] [de:s.pombe chromosome ii cosmid c4c3.] [nt:spbc4c3.06, unknown, len:818aa, similar eg. to.]
CONTIG2788	968791_f3_3	6860	20963	876	292	AL021730	183	4.9(10)-19	Schizosaccharomyces pombe	[pn:hypothetical protein] [gn:spbc4c3.07] [sr:fission yeast] [db:genpept-pln] [de:s.pombe chromosome ii cosmid c4c3.] [nt:spbc4c3.07, unknown, len:302aa, similar eg. to a.]
CONTIG4780	22299050_c1_7	6861	20964	246	82	U75447	94	0.0016	Yarrowia lipolytica	[pn:p-type calcium atpase] [gn:sca1] [db:genpept-pln] [de:yarrowia lipolytica p-type calcium atpase (sca1) gene, completecds.] [nt:secretory calcium atpase]

CONTIG5097	19573500_f1_2	6862	20965	504	168	AB008430	114	1.3(10)-5	Homo sapiens	[pn:cdep] [fn:rho guanine nucleotide exchange factor] [sr:homo sapiens embryo cartilage chondrocyte cdna to mrna] [db:genpept-pri2] [de:homo sapiens mrna for cdep, complete cds.] [nt:band 4.1 superfamily]
CONTIG3365	6651700_c3_3	6863	20966	810	270	AB011145	135	1.8(10)-6	Homo sapiens	[pn:kiaa0573 protein] [gn:kiaa0573] [sr:homo sapiens male brain cdna to mrna, clone_lib:pbluescriptii s] [db:genpept-pri2] [de:homo sapiens mrna for kiaa0573 protein, partial cds.]
CONTIG5647	30292180_f1_3	6864	20967	1857	619	AB011157	350	1.2(10)-31	Homo sapiens	[pn:kiaa0585 protein] [gn:kiaa0585] [sr:homo sapiens male brain cdna to mrna, clone_lib:pbluescriptii s] [db:genpept-pri2] [de:homo sapiens mrna for kiaa0585 protein, partial cds.]
CONTIG1181	21979002_c1_1	6865	20968	525	175	AF042384	419	2.3(10)-39	Homo sapiens	[pn:bc-2 protein] [sr:human] [db:genpept-pri2] [de:homo sapiens bc-2 protein mrna, complete cds.] [nt:p32; putative breast adenocarcinoma marker]
CONTIG5594	23829663_c3_19	6866	20969	939	313	AF042384	157	3.2(10)-10	Homo sapiens	[pn:bc-2 protein] [sr:human] [db:genpept-pri2] [de:homo sapiens bc-2 protein mrna, complete cds.] [nt:p32; putative breast adenocarcinoma marker]

b9x10y60.x	29454517_c1_3	6867	20970	621	207	AF047599	128	4.0(10)-6	Homo sapiens	[pn:origin recognition complex subunit 5] [gn:orc5l] [sr:human] [db:genpept-pri2] [de:homo sapiens origin recognition complex subunit 5 (orc5l) mrna,complete cds.] [nt:orc5p]
CONTIG2379	2850811_f2_3	6868	20971	591	197	AF048977	162	7.2(10)-11	Homo sapiens	[pn:ser/arg-related nuclear matrix protein] [gn:srm160] [fn:splicing factor] [sr:human] [db:genpept-pri2] [de:homo sapiens ser/arg-related nuclear matrix protein (srm160) mrna,complete cds.] [nt:160 kda]
CONTIG5765	13832755_f2_7	6869	20972	1761	587	U60337	486	1.2(10)-45	Homo sapiens	[pn:beta-mannosidase] [sr:human] [db:genpept-pri2] [de:homo sapiens beta-mannosidase mrna, complete cds.] [nt:acid hydrolase; glycosyl hydrolase; lysosomal]
CONTIG5202	1412961_c2_7	6870	20973	726	242	U61837	112	2.7(10)-6	Homo sapiens	[pn:putative cyclin g1 interacting protein] [sr:human] [db:genpept-pri2] [de:homo sapiens putative cyclin g1 interacting protein mrna, completecds.] [nt:putative]
CONTIG4457	21993765_c1_6	6871	20974	666	222	Y15173	93	0.039	no gb taxonomy match	[gn:e2] [or:human papillomavirus type 75] [db:genpept-vrl] [de:human papillomavirus type 75 e6, e7, e1, e2, e4, l2, and l1 genes.]
CONTIG1609	24500031_c2_5	6872	20975	1056	352	Y08997	766	3.2(10)-75	Xenopus laevis	[pn:146kda nuclear protein] [sr:african clawed frog] [db:genpept-vrl] [de:xenopus laevis mrna for 146 kda nuclear protein.]

CONTIG5304	16800013_f3_5	6873	20976	360	120	CONTIG7411D	289	2.1(10)-26	Streptococcus pneumoniae	[pn:nuclear pore complex glycoprotein p62] [sr:oncorhynchus mykiss cdna to mrna, clone:povc-ap-75] [de:oncorhynchus mykiss mrna for nuclear pore complex glycoprotein p62,complete cds.]
CONTIG5340	23868830_c3_9	6874	20977	963	321	CONTIG400C	114	8.5(10)-6	Enterococcus faecium	[ui:spovc] [pn:hypothetical protein:probable peptidyl-trna hydrolase:stage v sporulation protein c] [gn:pth] [gtcfc:10.6] [ec:3.1.1.29] [keggfc:14.1] [bsorffc:6.2.1] [db:gtc-bacillus subtilis]
CONTIG5184	25516263_f1_2	6875	20978	603	201	CONTIG422C	122	1.5(10)-7	Enterococcus faecium	[gn:a540l] [or:paramecium bursaria chlorella virus 1] [db:genpept-vrl] [de:paramecium bursaria chlorella virus 1 genome, complete sequence.]
CONTIG5648	4958425_c1_13	6876	20979	360	120	CONTIG422C	91	0.00032	Enterococcus faecium	[gn:a540l] [or:paramecium bursaria chlorella virus 1] [db:genpept-vrl] [de:paramecium bursaria chlorella virus 1 genome, complete sequence.]
CONTIG5414	14664636_f1_1	6877	20980	2652	884	CONTIG427C	95	0.049	Enterococcus faecium	[pn:b. burgdorferi predicted coding region bb0039] [gn:bb0039] [sr:lyme disease spirochete] [db:genbank] [de:borrelia burgdorferi (section 3 of 70) of the complete genome.] [nt:hypothetical protein; identified by genemark.]

CONTIG5168	799133_c1_10	6878	20981	1188	396	CONTIG49 1C	93	0.034	Enterococcus faecium	[ui:trea] [pn:trehalose-6-phosphate hydrolase] [gn:trec] [gtcfc:1.4.7.2] [ec:3.2.1.93] [keggfc:7.1] [bsorffc:2.1.1] [db:gtc-bacillus subtilis]
CONTIG1818	12554653_f2_3	6879	20982	213	71	CONTIG51 4C	105	6.5(10)-7	Enterococcus faecium	or:saccharomyces cerevisiae pn:unknown gn:internal orf g1669 le:6964 re:7365 di:direct sr:baker's yeast
CONTIG2704	1416683_c2_6	6880	20983	1047	349	CONTIG18 7C	111	0.00081	Acinetobacter baumannii	[ui:ybr208c] [pn:urea amidolyase] [gn:dur1:2] [gtcfc:2.6:4.1:5.3] [keggfc:14.2] [sgdfc:1.1.4:1.2.1:1.3.1] [db:gtc-saccharomyces cerevisiae]
CONTIG3210	5314142_f3_3	6881	20984	507	169	CONTIG18 8C	102	2.0(10)-5	Acinetobacter baumannii	[ui:mj0304] [pn:ferripyochelin binding protein:fbp:hypothetical protein] [gtcfc:12.5] [keggfc:14.1] [tigrfc:13.5] [db:gtc-methanococcus jannaschii]
CONTIG2059	6542500_c2_4	6882	20985	519	173	CONTIG20 3C	95	9.8(10)-6	Acinetobacter baumannii	[ui:b0454] [pn:hypothetical protein:hypothetical 14.4 kd protein in tesb-hha intergenic region] [gn:ybaz] [gtcfc:14.1] [keggfc:14.2] [rileyfc:5.7.0] [db:gtc-escherichia coli]
CONTIG5811	22783_c1_24	6883	20986	1098	366	CONTIG21 0C	93	0.01099	Acinetobacter baumannii	esterase (ec 3.1.1.-) - pseudomonas putida this enzyme catalyzes the hydrolysis of ester bonds and are found widely in animals, plants and microorganisms. this enzyme is useful for transesterification, synthesis of esters, and resolution of racemic mixt

CONTIG2940	29303436_f1_2	6884	20987	204	68	CONTIG220C	91	0.00022	Acinetobacter baumannii	[ui:b21156] [pn:lysine-specific permease] [gn:lysp:cadr] [gtc:12.1] [keggfc:14.2] [rileyfc:4.1.1] [db:gtc-escherichia coli]
CONTIG33	10314008_c3_2	6885	20988	687	229	CONTIG223C	92	0.01799	Acinetobacter baumannii	[ui:mg244] [pn:rep helicase, single-stranded dna-dependent atpase:rep:probable dna helicase] [gtfc:9.6:10.8] [ec:3.6.1.-] [keggfc:9.7] [tigrfc:10.2] [db:gtc-mycoplasma genitalium]
CONTIG2262	33990932_c2_4	6886	20989	309	103	CONTIG138C	138	4.5(10)-10	Pseudomonas aeruginosa	RANGE ON: [GTC P.aeruginosa, rel 2.0, contig]
CONTIG1833	10175182_c2_3	6887	20990	282	94	CONTIG284C	121	2.2(10)-8	Pseudomonas aeruginosa	RANGE ON: [GTC P.aeruginosa, rel 2.0, contig]
CONTIG4031	20839217_cl_3	6888	20991	249	83	CONTIG332C	124	8.6(10)-8	Pseudomonas aeruginosa	RANGE ON: [GTC P.aeruginosa, rel 2.0, contig]
b9x10g13.y	4897052_f1_1	6889	20992	255	85	CONTIG351C	140	1.3(10)-10	Pseudomonas aeruginosa	RANGE ON: [GTC P.aeruginosa, rel 2.0, contig]
CONTIG1078	25593802_f3_2	6890	20993	348	116	CONTIG358C	93	2.7(10)-5	Pseudomonas aeruginosa	RANGE ON: [GTC P.aeruginosa, rel 2.0, contig]
CONTIG3119	6725307_cl_4	6891	20994	222	74	CONTIG358C	115	8.0(10)-8	Pseudomonas aeruginosa	RANGE ON: [GTC P.aeruginosa, rel 2.0, contig]
CONTIG3803	24473433_f3_4	6892	20995	345	115	CONTIG358C	144	4.7(10)-11	Pseudomonas aeruginosa	RANGE ON: [GTC P.aeruginosa, rel 2.0, contig]
CONTIG5220	11975300_f2_2	6893	20996	216	72	CONTIG358C	95	1.6(10)-5	Pseudomonas aeruginosa	RANGE ON: [GTC P.aeruginosa, rel 2.0, contig]
CONTIG4957	19704411_f2_4	6894	20997	384	128	CONTIG362C	97	6.5(10)-5	Pseudomonas aeruginosa	RANGE ON: [GTC P.aeruginosa, rel 2.0, contig]
CONTIG4068	22314540_fl_1	6895	20998	447	149	CONTIG489	98	0.00084	Enterobacter cloacae	RANGE ON: [E.cloacae, GTC contig, rel 2.0]
CONTIG4525	4415882_f3_3	6896	20999	570	190	Contig088H	97	0.00029	Clostridium acetobutylicum	or:borrelia burgdorferi gn:orfa le:713 re:1801 di:direct sr:lyme disease spirochete

CONTIG5121	4500063_f2_2	6897	21000	1497	499	Contig107 H	91	0.027	Clostridium acetobutylicum	[ui:b4043] [pn:lexa:lexa repressor] [gn:lexa:exra:spr:tsl:umua] [gtcfc:10.2] [ec:3.4.21.88] [keggfc:14.1] [rileyfc:2.0.0] [db:gtc-escherichia coli]
CONTIG775	14554762_f3_2	6898	21001	357	119	Contig133 H	92	0.00013	Clostridium acetobutylicum	[ui:yxio] [pn:hypothetical protein:hypothetical 47.3 kd protein in wapa-lict intergenic region] [gn:s3ar] [gtcfc:14.1] [keggfc:14.2] [bsorffc:8.1.1] [db:gtc-bacillus subtilis]
CONTIG824	9773431_f2_1	6899	21002	555	185	Contig144 H	97	0.0035	Clostridium acetobutylicum	[ui:mth172] [pn:conserved protein] [gtcfc:14.1:14.2] [keggfc:14.2] [genomfc:14.2] [db:gtc-methanobacterium thermoautotrophicum]
CONTIG5529	16697933_f2_5	6900	21003	183	61	Contig155 H	92	1.5(10)-5	Clostridium acetobutylicum	Hypothetical protein
CONTIG5355	14585016_c1_7	6901	21004	528	176	Contig155 H	119	2.1(10)-8	Clostridium acetobutylicum	Hypothetical protein
b9x11k74.x	24651557_f3_1	6902	21005	495	165	Contig164 H	98	0.00259	Clostridium acetobutylicum	[ui:adda] [pn:atp-dependent deoxyribonuclease:subunit a:atp-dependent nuclease subunit a] [gn:rece5] [gtcfc:10.10] [keggfc:14.2] [bsorffc:4.1.2] [db:gtc-bacillus subtilis]
CONTIG2868	21562643_f1_1	6903	21006	1227	409	Contig215 H	100	0.0054	Clostridium acetobutylicum	Hypothetical protein

CONTIG1221	447882_f2_1	6904	21007	1236	412	Contig215 H	115	0.00016	Clostridium acetobutylicum	[ui:ybbd] [pn:hypothetical protein:hypothetical 70.6 kd protein in feua 5"region precursor:orf1] [gn:yzba] [gtcfc:1.6:5.13:6.5:7.2:14.1] [ec:3.2.1.21] [keggfc:1.6:5.13:6.5:7.1] [bsorffc:8.1.1] [db:gtc-bacillus subtilis]
CONTIG5230	15814030_f2_9	6905	21008	291	97	Contig227 H	92	3.7(10)-5	Clostridium acetobutylicum	or:mycobacterium tuberculosis pn:unknown protein le:242 re:769 di:complement sr:mycobacterium tuberculosis (strain erdman) dna nt:orf f175; putative
CONTIG4630	24414063_f3_4	6906	21009	2046	682	Contig244 H	92	0.12	Clostridium acetobutylicum	or:bacteroides ovatus pn:arabinosidase gn:asdi ec:3.2.1.55 le:110 re:2092 di:direct
CONTIG10	22300262_f3_2	6907	21010	213	71					
CONTIG100	5347840_c1_2	6908	21011	186	62					
CONTIG1001	23601510_f2_1	6909	21012	300	100					
CONTIG1002	26457258_f1_1	6910	21013	546	182					
CONTIG1002	26203425_c2_3	6911	21014	186	62					
CONTIG1004	5942800_f3_1	6912	21015	225	75					
CONTIG1008	21538911_c3_3	6913	21016	234	78					
CONTIG101	3180311_f1_1	6914	21017	651	217					
CONTIG101	16132215_f3_7	6915	21018	462	154					
CONTIG1010	10578905_c2_5	6916	21019	444	148					
CONTIG1016	24255251_f3_2	6917	21020	243	81					
CONTIG1017	31814567_c2_2	6918	21021	519	173					
CONTIG1018	34100952_f3_1	6919	21022	183	61					
CONTIG1018	4095275_c3_3	6920	21023	684	228					
CONTIG1019	24226451_c2_2	6921	21024	198	66					
CONTIG102	5859375_c1_5	6922	21025	201	67					
CONTIG102	11718750_c3_7	6923	21026	204	68					

CONTIG1022	13867925_c3_2	6924	21027	189	63
CONTIG1023	24250305_f1_2	6925	21028	249	83
CONTIG1028	11187875_f2_1	6926	21029	240	80
CONTIG103	5079800_c2_2	6927	21030	609	203
CONTIG103	34257883_f3_2	6928	21031	195	65
CONTIG1033	6062550_f2_1	6929	21032	303	101
CONTIG1035	4784761_f2_1	6930	21033	729	243
CONTIG1037	9806716_c3_2	6931	21034	699	233
CONTIG1038	32567_f2_1	6932	21035	390	130
CONTIG104	5208427_f3_1	6933	21036	522	174
CONTIG1040	16894806_c3_3	6934	21037	771	257
CONTIG1043	15734582_f3_2	6935	21038	327	109
CONTIG1045	29782059_f3_3	6936	21039	183	61
CONTIG1046	24257217_f1_1	6937	21040	186	62
CONTIG1048	473160_c1_2	6938	21041	183	61
CONTIG1048	36446876_f1_1	6939	21042	195	65
CONTIG105	20485902_f1_2	6940	21043	435	145
CONTIG1051	2925912_f3_3	6941	21044	219	73
CONTIG1051	5207636_f1_1	6942	21045	186	62
CONTIG1052	3937786_c1_3	6943	21046	186	62
CONTIG1052	6692949_c1_3	6944	21047	303	101
CONTIG1053	4712_c2_4	6945	21048	306	102
CONTIG1053	26382803_c1_4	6946	21049	189	63
CONTIG1055	35807778_f1_1	6947	21050	816	272
CONTIG1057	0_c3_4	6948	21051	279	93
CONTIG1058	14304017_c3_5	6949	21052	288	96
CONTIG1058	31504056_f2_2	6950	21053	189	63
CONTIG1059	24468902_c3_4	6951	21054	375	125
CONTIG1059	22439035_f2_1	6952	21055	597	199
CONTIG106	7157791_f3_1	6953	21056	615	205
CONTIG1061	36132760_c1_1	6954	21057	183	61
CONTIG1062	2000_f2_1	6955	21058	231	77
CONTIG1063	24032201_c2_2	6956	21059	285	95
CONTIG1065					

CONTIG1066	796886_f1_1	6957	21060	303	101
CONTIG1066	24017516_c1_3	6958	21061	255	85
CONTIG1068	4089137_f2_1	6959	21062	297	99
CONTIG1069	31557_f3_2	6960	21063	264	88
CONTIG1070	23439058_f2_3	6961	21064	243	81
CONTIG1071	29322706_f3_1	6962	21065	516	172
CONTIG1073	48588_f3_2	6963	21066	213	71
CONTIG1074	16022156_c1_3	6964	21067	1017	339
CONTIG1079	4687760_f2_3	6965	21068	318	106
CONTIG1080	4085885_f2_1	6966	21069	594	198
CONTIG1084	6103508_f3_1	6967	21070	879	293
CONTIG1089	865699_c1_4	6968	21071	312	104
CONTIG1089	2150767_c3_5	6969	21072	942	314
CONTIG109	1968876_f1_1	6970	21073	210	70
CONTIG109	4882186_f1_2	6971	21074	231	77
CONTIG109	16585287_c2_3	6972	21075	321	107
CONTIG1091	26832260_c2_5	6973	21076	183	61
CONTIG1092	19938901_f3_3	6974	21077	897	299
CONTIG1092	22479188_c2_4	6975	21078	222	74
CONTIG1093	26620877_f2_2	6976	21079	198	66
CONTIG1093	22460937_f2_3	6977	21080	243	81
CONTIG1094	23446900_f1_1	6978	21081	375	125
CONTIG1095	5_f2_4	6979	21082	345	115
CONTIG1095	3994127_c1_6	6980	21083	210	70
CONTIG1096	26225437_f2_1	6981	21084	231	77
CONTIG1097	10720300_f3_1	6982	21085	282	94
CONTIG1098	5908140_f1_1	6983	21086	297	99
CONTIG1098	11884802_c1_4	6984	21087	186	62
CONTIG1099	21742762_f1_1	6985	21088	315	105
CONTIG1099	9782531_c3_2	6986	21089	321	107
CONTIG1102	25672206_f1_1	6987	21090	372	124
CONTIG1102	30250831_f3_2	6988	21091	189	63
CONTIG1107	3132125_f1_2	6989	21092	186	62

CONTIGI1108	30648285_c3_5	6990	21093	219	73
CONTIGI1110	36588553_f1_1	6991	21094	213	71
CONTIGI1111	6697178_c2_1	6992	21095	306	102
CONTIGI1114	21584752_f2_2	6993	21096	717	239
CONTIGI1115	3907762_c2_2	6994	21097	918	306
CONTIGI1116	22073307_f3_3	6995	21098	228	76
CONTIGI1118	9897711_c2_4	6996	21099	198	66
CONTIGI112	870450_f2_3	6997	21100	231	77
CONTIGI1121	2832662_f3_3	6998	21101	186	62
CONTIGI1123	21735305_f3_1	6999	21102	231	77
CONTIGI1123	6343899_c1_1	7000	21103	192	64
CONTIGI1124	253755_c3_2	7001	21104	237	79
CONTIGI1124	25438750_c3_3	7002	21105	267	89
CONTIGI1125	4390953_c1_1	7003	21106	189	63
CONTIGI1125	1173752_f3_2	7004	21107	372	124
CONTIGI1128	24808588_c1_5	7005	21108	279	93
CONTIGI1128	35602092_c3_8	7006	21109	360	120
CONTIGI1131	22304715_c1_1	7007	21110	285	95
CONTIGI1138	4454502_c1_3	7008	21111	768	256
CONTIGI1140	23448776_c2_1	7009	21112	468	156
CONTIGI1141	29298215_c2_3	7010	21113	252	84
CONTIGI1141	15129181_c3_4	7011	21114	684	228
CONTIGI1142	4895438_f2_1	7012	21115	282	94
CONTIGI1143	6067902_f3_2	7013	21116	630	210
CONTIGI1144	9922752_c2_2	7014	21117	186	62
CONTIGI1145	6643802_f1_1	7015	21118	366	122
CONTIGI1145	24414000_f2_2	7016	21119	213	71
CONTIGI1147	26589717_c3_6	7017	21120	201	67
CONTIGI1151	34100307_f2_2	7018	21121	372	124
CONTIGI1155	29339701_f1_2	7019	21122	465	155
CONTIGI1157	35742325_f3_2	7020	21123	639	213
CONTIGI116	13788432_c1_2	7021	21124	195	65
CONTIGI1160	6820182_c1_5	7022	21125	294	98

CONTIG1161	14085250_f1_2	7023	21126	303	101
CONTIG1162	16222192_f3_3	7024	21127	186	62
CONTIG1163	15636326_c3_3	7025	21128	249	83
CONTIG1168	4878400_f3_2	7026	21129	516	172
CONTIG117	12534767_f2_1	7027	21130	219	73
CONTIG1171	34195262_c1_2	7028	21131	189	63
CONTIG1172	5082000_f3_1	7029	21132	636	212
CONTIG1175	1062917_f1_1	7030	21133	780	260
CONTIG1178	4774132_c1_4	7031	21134	354	118
CONTIG1178	12192275_c3_5	7032	21135	189	63
CONTIG1178	19787554_c3_6	7033	21136	468	156
CONTIG118	14453443_c3_7	7034	21137	621	207
CONTIG1183	6850628_c3_2	7035	21138	489	163
CONTIG1184	6894050_f1_1	7036	21139	213	71
CONTIG1186	5087910_f1_1	7037	21140	477	159
CONTIG1186	2532550_f2_2	7038	21141	336	112
CONTIG1186	22087882_c1_4	7039	21142	291	97
CONTIG1193	20345278_f1_3	7040	21143	234	78
CONTIG1193	14720378_c1_7	7041	21144	189	63
CONTIG1194	660200_c2_3	7042	21145	327	109
CONTIG1195	4948787_f2_2	7043	21146	222	74
CONTIG1195	4962966_f2_3	7044	21147	216	72
CONTIG1197	22344127_c3_3	7045	21148	213	71
CONTIG12	25425767_f3_1	7046	21149	207	69
CONTIG12	35193800_c1_2	7047	21150	186	62
CONTIG1201	21723386_f2_2	7048	21151	192	64
CONTIG1201	29475766_c3_3	7049	21152	234	78
CONTIG1204	1985905_f3_1	7050	21153	204	68
CONTIG1205	25681317_c3_3	7051	21154	258	86
CONTIG1208	25554562_f2_1	7052	21155	489	163
CONTIG121	26428438_c1_2	7053	21156	432	144
CONTIG1210	35834412_f1_1	7054	21157	759	253
CONTIG1215	23600192_c1_3	7055	21158	723	241

CONTIG1218	10360938_c2_6	7056	21159	438	146
CONTIG1222	24320282_c2_5	7057	21160	213	71
CONTIG1223	20112762_f2_1	7058	21161	198	66
CONTIG1223	31266525_c1_2	7059	21162	186	62
CONTIG1224	22845635_c1_2	7060	21163	426	142
CONTIG1227	24256910_c2_3	7061	21164	258	86
CONTIG1228	5164062_f2_1	7062	21165	873	291
CONTIG1228	604125_f3_2	7063	21166	246	82
CONTIG123	13851587_c2_4	7064	21167	333	111
CONTIG1232	24797760_f3_1	7065	21168	183	61
CONTIG1233	22267035_f1_1	7066	21169	1005	335
CONTIG1233	3960782_f2_2	7067	21170	441	147
CONTIG1234	12925900_f2_1	7068	21171	357	119
CONTIG1235	25448513_f3_2	7069	21172	189	63
CONTIG1235	9957312_f3_4	7070	21173	198	66
CONTIG1236	34023312_f1_1	7071	21174	198	66
CONTIG1237	36611640_c3_3	7072	21175	906	302
CONTIG1238	19792250_f1_1	7073	21176	216	72
CONTIG1238	1370337_f3_2	7074	21177	183	61
CONTIG1238	20345086_c1_3	7075	21178	213	71
CONTIG1238	22767057_c1_4	7076	21179	291	97
CONTIG1239	12350312_f2_1	7077	21180	816	272
CONTIG124	9806262_c2_3	7078	21181	288	96
CONTIG1241	6820432_f1_1	7079	21182	234	78
CONTIG1241	12298438_c2_2	7080	21183	738	246
CONTIG1244	1228160_f1_1	7081	21184	228	76
CONTIG1244	976418_f3_3	7082	21185	192	64
CONTIG1245	194075_f3_2	7083	21186	348	116
CONTIG1248	14563912_f3_2	7084	21187	240	80
CONTIG1253	26350002_f3_2	7085	21188	186	62
CONTIG1254	16594050_f1_1	7086	21189	303	101
CONTIG1255	29568785_f2_1	7087	21190	255	85
CONTIG1258	32157802_c3_4	7088	21191	186	62

CONTIG1259	26798428_c3_3	7089	21192	537	179
CONTIG1260	250450_f3_3	7090	21193	183	61
CONTIG1261	2384652_c3_3	7091	21194	798	266
CONTIG1262	2939700_c3_7	7092	21195	228	76
CONTIG1263	24390942_f1_1	7093	21196	231	77
CONTIG1263	29567000_f1_3	7094	21197	210	70
CONTIG1265	14474056_c1_3	7095	21198	201	67
CONTIG1267	127_f2_2	7096	21199	342	114
CONTIG1267	5269592_f2_3	7097	21200	249	83
CONTIG127	26836712_f3_1	7098	21201	246	82
CONTIG1270	24414056_f3_5	7099	21202	210	70
CONTIG1270	17085963_c1_7	7100	21203	192	64
CONTIG1272	15839392_f2_2	7101	21204	381	127
CONTIG1272	24250262_f3_3	7102	21205	291	97
CONTIG1279	13707552_c2_2	7103	21206	264	88
CONTIG1279	35194007_c3_3	7104	21207	327	109
CONTIG1283	29412817_f2_1	7105	21208	777	259
CONTIG1285	24338136_c1_5	7106	21209	375	125
CONTIG1285	189387_c3_6	7107	21210	771	257
CONTIG1288	9846001_c2_1	7108	21211	240	80
CONTIG1291	11847262_f3_2	7109	21212	921	307
CONTIG1292	23863402_c3_4	7110	21213	879	293
CONTIG1293	6126417_f2_1	7111	21214	477	159
CONTIG1294	20438406_c1_2	7112	21215	1071	357
CONTIG1295	35805128_f1_1	7113	21216	285	95
CONTIG1295	22050051_c1_3	7114	21217	183	61
CONTIG1296	22303925_f2_1	7115	21218	240	80
CONTIG1297	33879153_f2_2	7116	21219	336	112
CONTIG1298	34159627_c3_3	7117	21220	276	92
CONTIG13	21759636_f1_2	7118	21221	204	68
CONTIG1302	9949027_f2_2	7119	21222	192	64
CONTIG1302	29944625_c1_5	7120	21223	279	93
CONTIG1304	32453302_f1_1	7121	21224	183	61

CONTIG1304	24883568_c2_10	7122	21225	258	86
CONTIG1306	29495275_c3_2	7123	21226	690	230
CONTIG1308	33617010_f1_3	7124	21227	267	89
CONTIG1308	34180462_c1_6	7125	21228	225	75
CONTIG1310	23550277_c1_3	7126	21229	822	274
CONTIG1312	24115812_f2_1	7127	21230	366	122
CONTIG1313	26365677_c3_4	7128	21231	225	75
CONTIG1313	2265875_c3_5	7129	21232	435	145
CONTIG1314	5079788_c1_1	7130	21233	933	311
CONTIG1318	34195328_f1_2	7131	21234	591	197
CONTIG1319	14648425_f3_3	7132	21235	249	83
CONTIG1319	23472192_c2_5	7133	21236	216	72
CONTIG1322	24845251_c3_5	7134	21237	192	64
CONTIG1328	1969080_f1_1	7135	21238	201	67
CONTIG1328	24398427_c3_3	7136	21239	291	97
CONTIG1330	3245181_f1_1	7137	21240	210	70
CONTIG1330	30593762_f3_2	7138	21241	198	66
CONTIG1331	21878333_c1_1	7139	21242	186	62
CONTIG1331	4861090_c1_3	7140	21243	186	62
CONTIG1331	26569625_c2_4	7141	21244	243	81
CONTIG1331	245625_c3_5	7142	21245	198	66
CONTIG1334	5120452_c3_3	7143	21246	516	172
CONTIG1337	4378313_f2_4	7144	21247	216	72
CONTIG1337	4096875_c1_6	7145	21248	417	139
CONTIG1338	24806502_c2_2	7146	21249	717	239
CONTIG1339	29692163_c2_1	7147	21250	186	62
CONTIG1340	10166527_f2_2	7148	21251	768	256
CONTIG1340	25679656_f3_3	7149	21252	264	88
CONTIG1342	4875302_f1_1	7150	21253	219	73
CONTIG1345	6022135_f3_1	7151	21254	186	62
CONTIG1345	24220377_c2_2	7152	21255	357	119
CONTIG1347	16281455_f3_2	7153	21256	351	117
CONTIG1348	23460285_f3_2	7154	21257	519	173

CONTIG1348	7225900_c2_4	7155	21258	183	61
CONTIG1348	19723186_c2_5	7156	21259	201	67
CONTIG1348	29430160_c3_7	7157	21260	213	71
CONTIG1349	22924017_f3_3	7158	21261	186	62
CONTIG1349	23835925_c1_4	7159	21262	321	107
CONTIG1350	33317762_f1_1	7160	21263	429	143
CONTIG1352	797750_f1_1	7161	21264	264	88
CONTIG1353	787511_f1_1	7162	21265	192	64
CONTIG1353	23709688_f2_2	7163	21266	192	64
CONTIG1353	21500776_c3_4	7164	21267	303	101
CONTIG1355	5172553_f1_2	7165	21268	222	74
CONTIG1355	14971013_f2_3	7166	21269	294	98
CONTIG1355	25580287_c2_6	7167	21270	192	64
CONTIG1356	2353208_f2_1	7168	21271	249	83
CONTIG1357	14540917_f3_2	7169	21272	279	93
CONTIG1359	2947263_c1_3	7170	21273	1023	341
CONTIG1360	6367186_f3_2	7171	21274	288	96
CONTIG1360	3322177_c1_4	7172	21275	204	68
CONTIG1362	29925662_c3_3	7173	21276	225	75
CONTIG1364	10203150_c1_1	7174	21277	333	111
CONTIG1364	33703431_c2_2	7175	21278	258	86
CONTIG1366	10172500_c2_4	7176	21279	201	67
CONTIG1368	5954427_c1_2	7177	21280	297	99
CONTIG1369	34193752_c1_3	7178	21281	228	76
CONTIG1372	5332763_f1_1	7179	21282	189	63
CONTIG1376	6063135_c3_3	7180	21283	324	108
CONTIG1378	47200_f2_2	7181	21284	186	62
CONTIG1379	992950_f3_2	7182	21285	213	71
CONTIG1379	4875807_f3_3	7183	21286	849	283
CONTIG138	35410788_c2_4	7184	21287	186	62
CONTIG1380	4689452_c1_2	7185	21288	324	108
CONTIG1380	4803500_c2_3	7186	21289	282	94
CONTIG1381	14219443_f3_4	7187	21290	195	65

CONTIG1382	656327_f3_3	7188	21291	432	144
CONTIG1383	2006928_f3_1	7189	21292	240	80
CONTIG1383	4892250_f3_2	7190	21293	927	309
CONTIG1383	3131301_c3_4	7191	21294	291	97
CONTIG1384	26573312_c3_4	7192	21295	1059	353
CONTIG1385	3234657_f2_2	7193	21296	186	62
CONTIG1385	24430192_c1_4	7194	21297	216	72
CONTIG1389	26807790_c1_1	7195	21298	741	247
CONTIG1389	23868930_c2_2	7196	21299	183	61
CONTIG139	10207317_f3_2	7197	21300	204	68
CONTIG1391	116250_c1_1	7198	21301	198	66
CONTIG1391	20523263_c2_4	7199	21302	198	66
CONTIG1394	78188_f2_1	7200	21303	288	96
CONTIG1395	24272287_f1_1	7201	21304	279	93
CONTIG1397	7033383_c2_1	7202	21305	1140	380
CONTIG14	24342200_f2_2	7203	21306	222	74
CONTIG1400	32612677_f1_1	7204	21307	225	75
CONTIG1401	1111076_c2_2	7205	21308	228	76
CONTIG1402	34422253_c3_5	7206	21309	1008	336
CONTIG1403	22067317_f1_1	7207	21310	225	75
CONTIG1403	16408375_c3_6	7208	21311	201	67
CONTIG1404	23617127_c2_4	7209	21312	183	61
CONTIG1404	35331637_c2_5	7210	21313	201	67
CONTIG1404	19562802_c3_6	7211	21314	657	219
CONTIG1405	26777343_f2_1	7212	21315	507	169
CONTIG1406	10814177_f1_1	7213	21316	243	81
CONTIG1406	2739002_c1_3	7214	21317	294	98
CONTIG1407	10677165_f1_2	7215	21318	459	153
CONTIG1408	10439750_f2_4	7216	21319	324	108
CONTIG141	11500_f1_1	7217	21320	261	87
CONTIG141	9946002_f1_2	7218	21321	216	72
CONTIG1410	267953_f1_1	7219	21322	882	294
CONTIG1415	3947127_c2_3	7220	21323	1275	425

CONTIG1418	19813138_f3_2	7221	21324	354	118
CONTIG1418	2996163s_c1_3	7222	21325	282	94
CONTIG1418	5274132_c2_4	7223	21326	231	77
CONTIG1419	4395287_f1_1	7224	21327	210	70
CONTIG1419	13781556_f3_2	7225	21328	228	76
CONTIG1421	9814066_c2_1	7226	21329	1032	344
CONTIG1423	34484753_c2_1	7227	21330	336	112
CONTIG1425	26376627_c3_3	7228	21331	204	68
CONTIG1428	267131_f1_1	7229	21332	225	75
CONTIG1428	35366563_c2_2	7230	21333	183	61
CONTIG1429	4882785_f2_1	7231	21334	732	244
CONTIG1434	24272161_f3_2	7232	21335	201	67
CONTIG1437	32316902_f2_3	7233	21336	393	131
CONTIG1437	31337752_f1_2	7234	21337	345	115
CONTIG1439	4413392_f3_6	7235	21338	189	63
CONTIG144	4781505_c2_2	7236	21339	216	72
CONTIG1441	35960061_f1_1	7237	21340	192	64
CONTIG1441	3906252_f3_2	7238	21341	189	63
CONTIG1442	26803752_c1_5	7239	21342	384	128
CONTIG1444	4085925_c1_2	7240	21343	201	67
CONTIG1446	2401038_f2_1	7241	21344	780	260
CONTIG1447	30173462_c2_4	7242	21345	192	64
CONTIG145	5867837_f3_2	7243	21346	228	76
CONTIG1452	29335950_c3_3	7244	21347	213	71
CONTIG1453	34584805_f1_1	7245	21348	699	233
CONTIG1454	2814013_f2_2	7246	21349	621	207
CONTIG1454	22867812_c2_5	7247	21350	219	73
CONTIG1461	5312535_f2_1	7248	21351	207	69
CONTIG1462	2038912_f2_1	7249	21352	645	215
CONTIG1463	21679052_c1_3	7250	21353	855	285
CONTIG1465	1454566_f2_3	7251	21354	216	72
CONTIG1466	1228427_c1_2	7252	21355	399	133
CONTIG1471	14573755_c3_5	7253	21356	252	84

CONTIG1473	26376390_f3_2	7254	21357	318	106
CONTIG1473	26600758_c3_3	7255	21358	522	174
CONTIG1475	10989463_c2_2	7256	21359	228	76
CONTIG148	36135962_f2_2	7257	21360	216	72
CONTIG1480	21895761_f1_1	7258	21361	351	117
CONTIG1480	26351411_f2_2	7259	21362	693	231
CONTIG1484	35321875_c2_4	7260	21363	198	66
CONTIG1485	4820181_f2_3	7261	21364	210	70
CONTIG1487	32140885_f3_5	7262	21365	252	84
CONTIG1488	4898638_c1_3	7263	21366	192	64
CONTIG1489	5084380_f2_2	7264	21367	195	65
CONTIG1489	23676402_c1_5	7265	21368	303	101
CONTIG1489	32039063_c2_6	7266	21369	186	62
CONTIG1491	2166663_f1_1	7267	21370	489	163
CONTIG1491	24414063_c2_3	7268	21371	255	85
CONTIG1491	31507163_c3_4	7269	21372	351	117
CONTIG1491	24803188_c3_5	7270	21373	189	63
CONTIG1493	5890930_f2_3	7271	21374	267	89
CONTIG1494	11907805_c2_3	7272	21375	267	89
CONTIG1496	953312_f3_1	7273	21376	795	265
CONTIG1497	14742312_f1_2	7274	21377	183	61
CONTIG1497	24619026_c2_7	7275	21378	216	72
CONTIG1497	36142125_c2_8	7276	21379	579	193
CONTIG1498	955305_c3_2	7277	21380	201	67
CONTIG1498	11875675_c3_3	7278	21381	189	63
CONTIG150	23860252_c1_1	7279	21382	225	75
CONTIG1500	25566967_f1_2	7280	21383	246	82
CONTIG1501	10722327_f2_3	7281	21384	183	61
CONTIG1501	24016962_c2_5	7282	21385	219	73
CONTIG1503	23594026_c3_3	7283	21386	189	63
CONTIG1505	21725637_c2_4	7284	21387	204	68
CONTIG1507	36337811_c3_4	7285	21388	420	140
CONTIG1508	23631262_c3_2	7286	21389	618	206

CONTIG1510	13678425_f2_1	7287	21390	234	78
CONTIG1511	24846080_f2_1	7288	21391	582	194
CONTIG1513	24062512_c3_1	7289	21392	300	100
CONTIG1518	2664593_f1_1	7290	21393	276	92
CONTIG1519	10975260_f1_2	7291	21394	201	67
CONTIG1519	26816927_f3_4	7292	21395	270	90
CONTIG1520	9812626_f3_1	7293	21396	186	62
CONTIG1520	24492782_c2_2	7294	21397	195	65
CONTIG1521	23440875_f1_1	7295	21398	195	65
CONTIG1521	32289591_f2_3	7296	21399	429	143
CONTIG1521	26257886_c1_5	7297	21400	1329	443
CONTIG1523	495787_f1_1	7298	21401	408	136
CONTIG1525	22065900_f3_2	7299	21402	198	66
CONTIG1526	36339537_f3_3	7300	21403	288	96
CONTIG1527	812550_c1_1	7301	21404	249	83
CONTIG1528	32136265_f2_2	7302	21405	192	64
CONTIG1528	4406576_c1_4	7303	21406	192	64
CONTIG1529	33399142_f1_1	7304	21407	204	68
CONTIG153	555432_c3_5	7305	21408	489	163
CONTIG1534	7037782_f2_2	7306	21409	273	91
CONTIG1535	13958137_f3_3	7307	21410	204	68
CONTIG1535	980252_f3_4	7308	21411	369	123
CONTIG1535	2937950_c3_5	7309	21412	198	66
CONTIG1536	36636588_c3_4	7310	21413	240	80
CONTIG1537	4977250_f3_4	7311	21414	192	64
CONTIG1538	4720077_f2_2	7312	21415	297	99
CONTIG1538	16250393_c3_4	7313	21416	237	79
CONTIG1539	32595637_f1_1	7314	21417	423	141
CONTIG154	11135837_c1_1	7315	21418	192	64
CONTIG154	6256312_c1_2	7316	21419	207	69
CONTIG1540	12923432_f2_1	7317	21420	516	172
CONTIG1540	1213308_f3_3	7318	21421	198	66
CONTIG1541	11973151_c2_2	7319	21422	531	177

CONTIG1542	12923401_c2_6	7320	21423	294	98
CONTIG1544	4101510_c2_3	7321	21424	255	85
CONTIG1545	16454830_f2_3	7322	21425	189	63
CONTIG1545	392050_f3_4	7323	21426	522	174
CONTIG1546	23862763_c1_4	7324	21427	201	67
CONTIG1546	31838286_c2_5	7325	21428	210	70
CONTIG1547	34585765_f1_1	7326	21429	189	63
CONTIG1547	32082526_c1_3	7327	21430	195	65
CONTIG1548	21568786_f2_2	7328	21431	237	79
CONTIG1549	240762_f3_1	7329	21432	345	115
CONTIG1549	23863125_c1_3	7330	21433	231	77
CONTIG1551	19567176_f2_2	7331	21434	276	92
CONTIG1552	24862882_f1_1	7332	21435	270	90
CONTIG1555	23829687_f1_1	7333	21436	537	179
CONTIG1555	31379050_c1_4	7334	21437	204	68
CONTIG1558	24395002_c3_6	7335	21438	267	89
CONTIG1560	5111015_c3_2	7336	21439	189	63
CONTIG1561	36444640_f1_1	7337	21440	348	116
CONTIG1561	21600887_c3_6	7338	21441	249	83
CONTIG1563	970140_c2_3	7339	21442	231	77
CONTIG1566	4865665_c3_5	7340	21443	186	62
CONTIG1567	11976662_f1_1	7341	21444	363	121
CONTIG1567	20314010_f2_2	7342	21445	225	75
CONTIG1567	1365751_c2_4	7343	21446	552	184
CONTIG1569	1961318l_c1_1	7344	21447	198	66
CONTIG157	4111650_f3_2	7345	21448	285	95
CONTIG157	4064751_c3_3	7346	21449·	231	77
CONTIG1570	25503431_f2_2	7347	21450	417	139
CONTIG1571	4860961_c3_3	7348	21451	789	263
CONTIG1572	31366305_c1_4	7349	21452	189	63
CONTIG1573	14868752_f2_2	7350	21453	402	134
CONTIG1576	2_c1_7	7351	21454	186	62
CONTIG1578	14665887_c2_3	7352	21455	186	62

CONTIG1579	CONTIG1579	12703175_f1_1	7353	21456	309	103
CONTIG1579	CONTIG1579	4334632_c3_5	7354	21457	612	204
CONTIG158	CONTIG158	6142267_f3_1	7355	21458	186	62
CONTIG1580	CONTIG1580	29339701_c3_7	7356	21459	480	160
CONTIG1581	CONTIG1581	24395162_c2_4	7357	21460	273	91
CONTIG1581	CONTIG1581	5939160_c3_5	7358	21461	333	111
CONTIG1582	CONTIG1582	24315676_f1_1	7359	21462	273	91
CONTIG1582	CONTIG1582	823390_f1_1	7360	21463	432	144
CONTIG1583	CONTIG1583	6650075_f1_2	7361	21464	183	61
CONTIG1584	CONTIG1584	34198427_c3_5	7362	21465	429	143
CONTIG1586	CONTIG1586	6678467_f3_2	7363	21466	288	96
CONTIG1587	CONTIG1587	22272186_c1_3	7364	21467	234	78
CONTIG1589	CONTIG1589	4703161_c3_3	7365	21468	366	122
CONTIG1590	CONTIG1590	5289715_c1_5	7366	21469	195	65
CONTIG1594	CONTIG1594	160302_f1_2	7367	21470	297	99
CONTIG1598	CONTIG1598	35183305_c1_2	7368	21471	195	65
CONTIG16	CONTIG16	23595342_f3_1	7369	21472	192	64
CONTIG160	CONTIG160	25500882_c3_3	7370	21473	507	169
CONTIG1600	CONTIG1600	16182293_f1_1	7371	21474	387	129
CONTIG1603	CONTIG1603	25520411_c3_6	7372	21475	219	73
CONTIG1603	CONTIG1603	9925003_c3_7	7373	21476	210	70
CONTIG1604	CONTIG1604	29469150_f1_1	7374	21477	1191	397
CONTIG1611	CONTIG1611	9804630_c2_2	7375	21478	192	64
CONTIG1613	CONTIG1613	7136715_f3_3	7376	21479	444	148
CONTIG1613	CONTIG1613	6267005_c2_4	7377	21480	207	69
CONTIG1616	CONTIG1616	9813802_c3_5	7378	21481	216	72
CONTIG1616	CONTIG1616	14256887_f2_2	7379	21482	198	66
CONTIG1617	CONTIG1617	24398390_c3_4	7380	21483	261	87
CONTIG1620	CONTIG1620	31926005_c3_6	7381	21484	765	255
CONTIG1623	CONTIG1623	32597262_f2_1	7382	21485	888	296
CONTIG1628	CONTIG1628	10751262_f1_1	7383	21486	285	95
CONTIG1628	CONTIG1628	13707193_f2_2	7384	21487	198	66
CONTIG1628	CONTIG1628	32319655_f3_3	7385	21488	285	95

CONTIG1628	33212812_c3_5	7386	21489	567	189
CONTIG1629	23928387_f3_2	7387	21490	210	70
CONTIG163	10242953_f1_1	7388	21491	465	155
CONTIG163	21660805_f3_4	7389	21492	192	64
CONTIG1630	1171936_f1_1	7390	21493	228	76
CONTIG1630	33785450_c3_6	7391	21494	300	100
CONTIG1631	22362640_f2_3	7392	21495	264	88
CONTIG1634	12584555_f2_1	7393	21496	195	65
CONTIG1635	24414167_f1_2	7394	21497	189	63
CONTIG1636	22849053_f3_1	7395	21498	288	96
CONTIG1637	1211592_f2_1	7396	21499	198	66
CONTIG1639	20744093_f1_1	7397	21500	186	62
CONTIG1639	22071003_c2_2	7398	21501	228	76
CONTIG1640	31822538_c1_3	7399	21502	219	73
CONTIG1641	24413463_c3_5	7400	21503	291	97
CONTIG1642	33791532_c1_5	7401	21504	909	303
CONTIG1642	24491437_c2_6	7402	21505	216	72
CONTIG1643	23987800_c3_4	7403	21506	183	61
CONTIG1644	781500_c1_1	7404	21507	645	215
CONTIG165	58332_f3_1	7405	21508	960	320
CONTIG1651	2539142_c2_2	7406	21509	519	173
CONTIG1651	23593812_c2_3	7407	21510	291	97
CONTIG1653	4330262_c2_2	7408	21511	222	74
CONTIG1653	24023407_c3_3	7409	21512	213	71
CONTIG1654	35350817_f3_1	7410	21513	558	186
CONTIG1655	14566550_c1_2	7411	21514	297	99
CONTIG1655	40905_c3_4	7412	21515	264	88
CONTIG1655	24392252_c3_5	7413	21516	351	117
CONTIG1656	21677000_c3_4	7414	21517	216	72
CONTIG1658	581567_f3_4	7415	21518	225	75
CONTIG1664	2068756_c3_2	7416	21519	183	61
CONTIG1665	6720640_f2_1	7417	21520	303	101
CONTIG1666	50650_f1_2	7418	21521	324	108

CONTIG1667	553962_c3_6	7419	21522	186	62
CONTIG1674	392762_c3_2	7420	21523	267	89
CONTIG1679	2755302_c2_1	7421	21524	261	87
CONTIG1679	5860637_c3_2	7422	21525	234	78
CONTIG168	19381l_c1_3	7423	21526	201	67
CONTIG168	9923561_c2_4	7424	21527	348	116
CONTIG1680	6831436_f1_1	7425	21528	222	74
CONTIG1680	3917562_f1_2	7426	21529	195	65
CONTIG1680	29488177_c2_4	7427	21530	183	61
CONTIG1682	31801892_f2_3	7428	21531	207	69
CONTIG1687	2063800_f3_3	7429	21532	198	66
CONTIG1687	26773387_c3_6	7430	21533	198	66
CONTIG1689	1216512_c1_2	7431	21534	243	81
CONTIG1696	23942152_c1_3	7432	21535	297	99
CONTIG1697	35351586_c2_3	7433	21536	267	89
CONTIG170	22464562_c3_5	7434	21537	201	67
CONTIG170	11835142_c3_6	7435	21538	216	72
CONTIG1700	4742141_c2_2	7436	21539	189	63
CONTIG1701	47264450_f1_2	7437	21540	660	220
CONTIG1701	12523392_c1_4	7438	21541	498	166
CONTIG1702	24786002_f3_3	7439	21542	1053	351
CONTIG1702	35205382_c3_6	7440	21543	357	119
CONTIG1703	1409450_c3_4	7441	21544	198	66
CONTIG1703	13671875_c3_5	7442	21545	354	118
CONTIG1704	10290807_f3_3	7443	21546	183	61
CONTIG1704	15912_c3_5	7444	21547	279	93
CONTIG1707	20345052_f2_1	7445	21548	195	65
CONTIG1708	22287635_f3_8	7446	21549	249	83
CONTIG1710	13859437_f3_1	7447	21550	195	65
CONTIG1711	35440677_f3_1	7448	21551	189	63
CONTIG1711	24100302_f3_3	7449	21552	801	267
CONTIG1712	4975682_f2_1	7450	21553	705	235
CONTIG1714	22767057_c2_2	7451	21554	675	225

CONTIG1714	20345086_c3_4	7452	21555	80
CONTIG1715	6835937_f1_1	7453	21556	70
CONTIG1715	5879562_f2_5	7454	21557	71
CONTIG1721	970180_f2_2	7455	21558	80
CONTIG1722	5117250_f3_1	7456	21559	63
CONTIG1722	2958782_c2_2	7457	21560	62
CONTIG1723	33204686_f3_3	7458	21561	72
CONTIG1723	2567209_c1_4	7459	21562	62
CONTIG1724	23910878_c2_3	7460	21563	68
CONTIG1725	4015950_c2_2	7461	21564	137
CONTIG1726	30556707_f3_1	7462	21565	219
CONTIG1726	23850655_c3_2	7463	21566	215
CONTIG1728	13148479_c3_4	7464	21567	77
CONTIG1730	175137_c2_2	7465	21568	84
CONTIG1731	189003_c1_5	7466	21569	68
CONTIG1731	21523467_c1_6	7467	21570	64
CONTIG1733	21757052_f2_1	7468	21571	62
CONTIG1737	1992337_c1_4	7469	21572	68
CONTIG1739	5265760_f3_3	7470	21573	92
CONTIG1739	5287887_c2_4	7471	21574	64
CONTIG1743	4063136_c2_4	7472	21575	192
CONTIG1743	30172510_f2_4	7473	21576	708
CONTIG1744	25995715_f2_5	7474	21577	183
CONTIG1744	4197013_c1_8	7475	21578	234
CONTIG1745	24423142_c2_4	7476	21579	116
CONTIG1748	11971901_c3_3	7477	21580	552
CONTIG1748	34194677_c3_4	7478	21581	94
CONTIG1749	22378931_c1_2	7479	21582	135
CONTIG1751	1206558_f3_1	7480	21583	97
CONTIG1751	1_c1_3	7481	21584	132
CONTIG1752	29300138_f2_1	7482	21585	115
CONTIG1753	33876437_f1_1	7483	21586	62
CONTIG1753	23720302_c3_4	7484	21587	228
				149

CONTIG1759	210202_c2_2	7485	21588	201	67
CONTIG176	19539000_f1_1	7486	21589	189	63
CONTIG1761	4723313_f1_1	7487	21590	240	80
CONTIG1763	5939068_c1_2	7488	21591	198	66
CONTIG1765	24015750_c3_3	7489	21592	186	62
CONTIG1766	2819525_f2_3	7490	21593	240	80
CONTIG1767	26377213_f2_1	7491	21594	264	88
CONTIG1767	3336502_f2_2	7492	21595	372	124
CONTIG1768	4687531_c1_3	7493	21596	543	181
CONTIG1769	13165627_c2_2	7494	21597	648	216
CONTIG1769	860751_c2_3	7495	21598	264	88
CONTIG1774	26426437_f3_2	7496	21599	1194	398
CONTIG1775	25579766_f3_1	7497	21600	219	73
CONTIG1776	14504552_c2_6	7498	21601	315	105
CONTIG1777	21907276_c3_4	7499	21602	186	62
CONTIG1780	6681587_f3_3	7500	21603	288	96
CONTIG1780	30271881_c1_4	7501	21604	264	88
CONTIG1782	21881451_f1_1	7502	21605	507	169
CONTIG1782	14657513_f1_2	7503	21606	237	79
CONTIG1782	23595283_f3_5	7504	21607	261	87
CONTIG1785	31760052_f1_2	7505	21608	207	69
CONTIG1786	3946900_f1_1	7506	21609	321	107
CONTIG1786	2942212_f2_2	7507	21610	633	211
CONTIG1787	4892186_f3_3	7508	21611	252	84
CONTIG1789	35166002_f2_1	7509	21612	186	62
CONTIG1790	20820781_f3_2	7510	21613	873	291
CONTIG1790	85177_c3_5	7511	21614	195	65
CONTIG1791	4689378_c2_4	7512	21615	672	224
CONTIG1792	4687632_c3_4	7513	21616	276	92
CONTIG1794	22069052_f1_1	7514	21617	210	70
CONTIG1794	5891333_f1_2	7515	21618	186	62
CONTIG1794	1210760_c2_3	7516	21619	207	69
CONTIG1795	25431325_f2_3	7517	21620	207	69

CONTIG1796	4531437_f1_2	7518	21621	255	85
CONTIG1798	22709505_f2_2	7519	21622	261	87
CONTIG1799	13944051_c1_5	7520	21623	213	71
CONTIG1799	4886380_c3_6	7521	21624	409	
CONTIG180	13100692_c2_5	7522	21625	306	102
CONTIG1800	40037787_c2_1	7523	21626	759	253
CONTIG1802	511457_f2_1	7524	21627	1143	381
CONTIG1805	9897807_f2_4	7525	21628	216	72
CONTIG1805	7114027_c1_5	7526	21629	852	284
CONTIG1808	10632317_f3_1	7527	21630	477	159
CONTIG1808	14943905_c3_3	7528	21631	480	160
CONTIG181	34179688_c2_3	7529	21632	474	158
CONTIG1810	4353260_f3_5	7530	21633	201	67
CONTIG1810	19766250_c2_7	7531	21634	195	65
CONTIG1810	21650312_c3_9	7532	21635	408	136
CONTIG1812	271952_f3_2	7533	21636	348	116
CONTIG1813	24022762_f3_2	7534	21637	189	63
CONTIG1813	1953175_c1_3	7535	21638	198	66
CONTIG1814	24257786_c2_4	7536	21639	240	80
CONTIG1814	32692188_c3_6	7537	21640	183	61
CONTIG1816	4063915_c2_4	7538	21641	192	64
CONTIG1817	4741377_c1_3	7539	21642	282	94
CONTIG182	2011457_f2_1	7540	21643	612	204
CONTIG1821	23547502_c2_4	7541	21644	735	245
CONTIG1822	7078427_c2_3	7542	21645	315	105
CONTIG1823	35188317_f1_1	7543	21646	540	180
CONTIG1823	22031706_c1_2	7544	21647	207	69
CONTIG1823	390925_f1_3	7545	21648	255	85
CONTIG1825	15867067_f2_3	7546	21649	999	333
CONTIG1826	43943762_c1_2	7547	21650	798	266
CONTIG1828	25423501_f1_1	7548	21651	426	142
CONTIG1829	2166025_f2_1	7549	21652	921	307
CONTIG1829	29976417_c2_3	7550	21653	210	70

CONTIG1829	29532501_c3_4	7551	21654	276	92
CONTIG183	19718875_c3_1	7552	21655	186	62
CONTIG1830	19931265_f1_2	7553	21656	72	
CONTIG1832	24220277_f2_2	7554	21657	417	139
CONTIG1835	21875325_f3_1	7555	21658	219	73
CONTIG1837	23711638_f3_2	7556	21659	792	264
CONTIG1838	3906253_c2_3	7557	21660	216	72
CONTIG1838	1462875_c3_4	7558	21661	219	73
CONTIG1839	24093812_f2_3	7559	21662	351	117
CONTIG1839	21955362_c2_5	7560	21663	204	68
CONTIG1841	29375312_f2_1	7561	21664	189	63
CONTIG1844	35175385_f2_1	7562	21665	288	96
CONTIG1844	11878885_c3_4	7563	21666	519	173
CONTIG1845	31641965_f2_1	7564	21667	258	86
CONTIG1845	24412812_f3_3	7565	21668	261	87
CONTIG1846	2375812_f2_1	7566	21669	1071	357
CONTIG1847	4969506_c2_6	7567	21670	1257	419
CONTIG185	24697030_c3_3	7568	21671	195	65
CONTIG1852	173192_f2_1	7569	21672	432	144
CONTIG1852	3908162_c3_3	7570	21673	204	68
CONTIG1856	26439062_f1_1	7571	21674	243	81
CONTIG1856	11110037_f1_2	7572	21675	246	82
CONTIG1858	21484713_c1_3	7573	21676	315	105
CONTIG1860	26461567_c3_1	7574	21677	222	74
CONTIG1862	24650941_c2_3	7575	21678	534	178
CONTIG1863	9960316_f1_1	7576	21679	216	72
CONTIG1864	23532187_f1_1	7577	21680	876	292
CONTIG1866	24667828_f1_1	7578	21681	252	84
CONTIG1866	6051555_f2_3	7579	21682	207	69
CONTIG1866	13726557_c2_5	7580	21683	183	61
CONTIG1867	23635881_f2_1	7581	21684	867	289
CONTIG1868	14490927_f3_2	7582	21685	204	68
CONTIG1868	4727192_c1_3	7583	21686	312	104

CONTIG1868	4890680_c3_5	7584	21687	360	120
CONTIG1869	4803550_c3_3	7585	21688	219	73
CONTIG1875	4710051_c3_4	7586	21689	312	104
CONTIG1878	24801886_f1_1	7587	21690	261	87
CONTIG1878	10730000_c3_3	7588	21691	183	61
CONTIG1879	20422577_f1_2	7589	21692	504	168
CONTIG1879	23865887_c2_5	7590	21693	189	63
CONTIG1880	36042130_c2_4	7591	21694	258	86
CONTIG1882	29500375_c2_6	7592	21695	204	68
CONTIG1882	32085452_c2_7	7593	21696	195	65
CONTIG1884	1970075_c3_3	7594	21697	231	77
CONTIG1887	24007161_f2_4	7595	21698	189	63
CONTIG1887	29500375_c2_6	7596	21699	618	206
CONTIG1889	24040887_c2_4	7597	21700	729	243
CONTIG1889	1219663_c3_5	7598	21701	207	69
CONTIG189	21959468_c2_2	7599	21702	585	195
CONTIG1892	4703510_f3_1	7600	21703	1017	339
CONTIG1893	21727187_f2_1	7601	21704	198	66
CONTIG1893	23712642_f2_2	7602	21705	267	89
CONTIG1894	11812676_f2_1	7603	21706	807	269
CONTIG1894	24900300_c3_6	7604	21707	261	87
CONTIG1899	25562688_f1_1	7605	21708	189	63
CONTIG1899	26464177_c3_4	7606	21709	303	101
CONTIG190	35949186_c1_1	7607	21710	216	72
CONTIG1900	189003_c2_4	7608	21711	198	66
CONTIG1901	23628938_c3_3	7609	21712	381	127
CONTIG1904	207658_f2_2	7610	21713	276	92
CONTIG1905	26761442_f3_3	7611	21714	234	78
CONTIG1906	11220463_f2_2	7612	21715	240	80
CONTIG1908	24022062_f1_1	7613	21716	195	65
CONTIG1908	21500007_c1_2	7614	21717	234	78
CONTIG1908	5172126_c2_3	7615	21718	222	74
CONTIG1908	5321051_c3_6	7616	21719	183	61

CONTIG1909	4820441_f3_1	7617	21720	207	69
CONTIG1910	11885387_c3_5	7618	21721	249	83
CONTIG1911	10635253_f1_1	7619	21722	1113	371
CONTIG1912	81882_c2_1	7620	21723	246	82
CONTIG1914	9806312_f2_4	7621	21724	186	62
CONTIG1915	792057_c1_1	7622	21725	189	63
CONTIG1919	4970962_f1_1	7623	21726	267	89
CONTIG1919	3501892_c2_7	7624	21727	219	73
CONTIG1920	15714052_f2_1	7625	21728	201	67
CONTIG1921	36367183_c3_3	7626	21729	363	121
CONTIG1925	4865950_f1_1	7627	21730	507	169
CONTIG1925	4344128_f2_4	7628	21731	210	70
CONTIG1925	12128135_f3_5	7629	21732	597	199
CONTIG1929	26758388_f1_2	7630	21733	252	84
CONTIG193	22453138_f1_1	7631	21734	354	118
CONTIG1931	20428132_c1_4	7632	21735	867	289
CONTIG1932	10034687_f1_1	7633	21736	204	68
CONTIG1932	24337752_f3_3	7634	21737	237	79
CONTIG1935	16523403_f1_2	7635	21738	243	81
CONTIG1937	10555530_c2_2	7636	21739	1095	365
CONTIG1938	12634575_f3_3	7637	21740	192	64
CONTIG1938	100637_c3_6	7638	21741	513	171
CONTIG1939	4961505_c3_1	7639	21742	321	107
CONTIG1942	36589213_c1_2	7640	21743	255	85
CONTIG1942	24241557_c3_3	7641	21744	207	69
CONTIG1943	12555555_c3_4	7642	21745	240	80
CONTIG1945	12010417_f1_1	7643	21746	441	147
CONTIG1945	13868757_f2_2	7644	21747	192	64
CONTIG1946	4298403_f1_1	7645	21748	237	79
CONTIG1946	9797753_f2_3	7646	21749	249	83
CONTIG1949	24614137_f3_1	7647	21750	201	67
CONTIG1953	6038128_c2_6	7648	21751	723	241
CONTIG1954	1464430_f2_3	7649	21752	531	177

CONTIG1954	35346942_c1_7	7650	21753	207	69
CONTIG1955	22445326_f1_1	7651	21754	405	135
CONTIG1955	2929511_f2_5	7652	21755	312	104
CONTIG1959	4141005_c1_3	7653	21756	210	70
CONTIG196	23651410_f1_1	7654	21757	558	186
CONTIG196	25601066_c2_4	7655	21758	306	102
CONTIG1960	4694055_c2_7	7656	21759	441	147
CONTIG1963	82502_f1_1	7657	21760	1479	493
CONTIG1964	35196913_c1_2	7658	21761	285	95
CONTIG1966	23925400_f2_2	7659	21762	912	304
CONTIG1966	11719216_f3_3	7660	21763	390	130
CONTIG1968	19562586_c1_3	7661	21764	417	139
CONTIG1970	23600887_c1_2	7662	21765	225	75
CONTIG1970	32627_c2_4	7663	21766	192	64
CONTIG1971	34567840_c2_6	7664	21767	1089	363
CONTIG1972	16220432_c1_4	7665	21768	585	195
CONTIG1973	22275425_f3_1	7666	21769	219	73
CONTIG1973	19628812_c2_3	7667	21770	183	61
CONTIG1974	34614062_c3_7	7668	21771	294	98
CONTIG1975	2980150_f2_2	7669	21772	204	68
CONTIG1982	26438_c2_4	7670	21773	189	63
CONTIG1983	30517700_c1_2	7671	21774	195	65
CONTIG1983	35423410_c1_3	7672	21775	300	100
CONTIG1985	21692875_f1_1	7673	21776	222	74
CONTIG1986	10632757_f1_1	7674	21777	972	324
CONTIG1986	26772175_c3_3	7675	21778	228	76
CONTIG1987	12115943_c1_5	7676	21779	408	136
CONTIG1990	5353467_f3_3	7677	21780	498	166
CONTIG1991	14494061_f2_2	7678	21781	627	209
CONTIG1992	21696938_f1_2	7679	21782	186	62
CONTIG1994	4328311_c1_4	7680	21783	231	77
CONTIG1994	12582927_c2_5	7681	21784	564	188
CONTIG1995	973535_c2_2	7682	21785	246	82

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CONTIG1996	3336502_f3_2	7683	21786	372	124
CONTIG1997	860056_f2_2	7684	21787	273	91
CONTIG1997	9772055_f3_6	7685	21788	195	65
CONTIG1998	4729717_f3_3	7686	21789	204	68
CONTIG1998	12284500_c2_6	7687	21790	339	113
CONTIG1999	1312_f3_2	7688	21791	279	93
CONTIG1999	14652127_c3_4	7689	21792	303	101
CONTIG2	5859667_c1_1	7690	21793	294	98
CONTIG2001	20334635_f3_1	7691	21794	249	83
CONTIG2004	34068800_f3_4	7692	21795	567	189
CONTIG2005	29381260_f2_2	7693	21796	321	107
CONTIG2005	34554717_c2_4	7694	21797	276	92
CONTIG2006	24400905_f1_1	7695	21798	216	72
CONTIG2006	19921890_f1_2	7696	21799	210	70
CONTIG2006	12500010_f1_3	7697	21800	186	62
CONTIG2006	21953140_f2_4	7698	21801	255	85
CONTIG2007	21961012_f2_2	7699	21802	1161	387
CONTIG2007	35554062_f2_3	7700	21803	183	61
CONTIG2009	2923508_c3_4	7701	21804	306	102
CONTIG2012	14928292_c1_3	7702	21805	243	81
CONTIG2015	33991062_c1_2	7703	21806	270	90
CONTIG2017	4472813_c2_4	7704	21807	831	277
CONTIG202	2449218_f3_2	7705	21808	510	170
CONTIG2022	893806_c1_2	7706	21809	402	134
CONTIG2024	20968927_c2_3	7707	21810	285	95
CONTIG2026	882093_c1_2	7708	21811	228	76
CONTIG203	36222686_c2_2	7709	21812	201	67
CONTIG2032	5860930_f2_1	7710	21813	198	66
CONTIG2034	29578378_f2_4	7711	21814	183	61
CONTIG2034	25431566_f3_7	7712	21815	276	92
CONTIG2034	1954687_c1_8	7713	21816	891	297
CONTIG2035	5328452_c3_4	7714	21817	477	159
CONTIG2038	19975151_c3_2	7715	21818	603	201

CONTIG2040	94127_f1_1	7716	21819	573	191
CONTIG2040	21522817_c2_3	7717	21820	252	84
CONTIG2043	23673260_c1_2	7718	21821	186	62
CONTIG2043	205191_c2_3	7719	21822	333	111
CONTIG2047	14254500_c3_5	7720	21823	243	81
CONTIG2049	24259687_f3_3	7721	21824	228	76
CONTIG2050	22444752_c2_7	7722	21825	213	71
CONTIG2051	25440636_c2_6	7723	21826	690	230
CONTIG2052	16847338_f2_2	7724	21827	213	71
CONTIG2052	9766903_f3_3	7725	21828	237	79
CONTIG2054	20398525_c2_2	7726	21829	201	67
CONTIG2055	1988135_c3_4	7727	21830	306	102
CONTIG2055	34276090_c3_5	7728	21831	198	66
CONTIG2057	433207_c3_4	7729	21832	789	263
CONTIG2059	9886457_f3_3	7730	21833	276	92
CONTIG2061	3937562_f3_1	7731	21834	180	60
CONTIG2061	35431878_c3_2	7732	21835	207	69
CONTIG2062	32713126_f3_1	7733	21836	1155	385
CONTIG2065	34255028_c1_3	7734	21837	330	110
CONTIG2069	1976661_f2_2	7735	21838	357	119
CONTIG2071	26445132_c3_3	7736	21839	228	76
CONTIG2072	2926500_f1_1	7737	21840	207	69
CONTIG2072	24022927_c1_5	7738	21841	183	61
CONTIG2073	4004436_c1_2	7739	21842	297	99
CONTIG2074	14454451_f3_4	7740	21843	276	92
CONTIG2074	34065686_c1_5	7741	21844	390	130
CONTIG2075	21678763_c1_5	7742	21845	1488	496
CONTIG2076	2553192_c2_3	7743	21846	282	94
CONTIG2076	26173187_c3_4	7744	21847	198	66
CONTIG2081	24886067_c1_6	7745	21848	210	70
CONTIG2081	26445317_c3_9	7746	21849	261	87
CONTIG2084	21955011_f1_1	7747	21850	186	62
CONTIG2084	22895703_f2_2	7748	21851	303	101

CONTIG2085	4022802_f1_1	7749	21852	189	63
CONTIG2085	4459806_f2_3	7750	21853	195	65
CONTIG2085	915633_f2_4	7751	21854	228	76
CONTIG2087	12001630_f3_2	7752	21855	564	188
CONTIG2087	19765711_f3_3	7753	21856	438	146
CONTIG2087	33362800_c3_5	7754	21857	258	86
CONTIG2088	24062512_f2_3	7755	21858	414	138
CONTIG2092	23954010_c2_3	7756	21859	330	110
CONTIG2093	15725817_f1_1	7757	21860	1251	417
CONTIG2095	26610628_c2_3	7758	21861	189	63
CONTIG2097	5288942_f2_1	7759	21862	1158	386
CONTIG2098	20348377_c3_2	7760	21863	738	246
CONTIG21	5995343_c2_1	7761	21864	192	64
CONTIG2100	23593951_c1_1	7762	21865	357	119
CONTIG2101	507005_c2_2	7763	21866	312	104
CONTIG2102	14493963_f1_3	7764	21867	213	71
CONTIG2104	26041327_f1_1	7765	21868	210	70
CONTIG2104	29313527_f1_2	7766	21869	195	65
CONTIG2104	29891305_c1_4	7767	21870	237	79
CONTIG2106	20580453_c2_4	7768	21871	189	63
CONTIG2106	23473380_c3_5	7769	21872	222	74
CONTIG2108	9767515_c1_5	7770	21873	192	64
CONTIG211	23914800_f1_1	7771	21874	303	101
CONTIG211	23628525_f1_2	7772	21875	252	84
CONTIG2115	16432942_c1_3	7773	21876	198	66
CONTIG2115	789715_c1_4	7774	21877	210	70
CONTIG2116	31429762_f3_2	7775	21878	201	67
CONTIG2116	117013_c1_4	7776	21879	276	92
CONTIG2116	22053411_c3_6	7777	21880	186	62
CONTIG2118	1459663_c2_4	7778	21881	195	65
CONTIG2118	6048377_c3_5	7779	21882	252	84
CONTIG2118	25428936_c3_6	7780	21883	1176	392
CONTIG2119	34564531_c1_1	7781	21884	372	124

CONTIG212	14117192_f2_1	7782	21885	486	162
CONTIG2120	33391880_f1_1	7783	21886	213	71
CONTIG2122	26457937_f1_1	7784	21887	249	83
CONTIG2122	9766253_f3_4	7785	21888	222	74
CONTIG2122	20423326_c1_6	7786	21889	198	66
CONTIG2126	23437812_f3_1	7787	21890	528	176
CONTIG2132	24804687_f2_2	7788	21891	246	82
CONTIG2132	2578436_f3_3	7789	21892	375	125
CONTIG2132	4961561_c3_10	7790	21893	183	61
CONTIG2134	885053_c2_4	7791	21894	531	177
CONTIG2135	1953382_f2_3	7792	21895	462	154
CONTIG2135	31299082_f3_6	7793	21896	285	95
CONTIG2137	21492916_f3_2	7794	21897	504	168
CONTIG2138	24486088_f2_1	7795	21898	468	156
CONTIG2138	24019388_f3_2	7796	21899	663	221
CONTIG2139	10188175_f2_1	7797	21900	267	89
CONTIG2139	11722175_f2_2	7798	21901	219	73
CONTIG2139	33785676_f3_3	7799	21902	648	216
CONTIG2141	24297757_c2_3	7800	21903	795	265
CONTIG2142	24416500_f2_2	7801	21904	210	70
CONTIG2142	16416062_f3_4	7802	21905	225	75
CONTIG2142	33330017_c3_5	7803	21906	411	137
CONTIG2143	3942186_f2_2	7804	21907	396	132
CONTIG2143	33210012_f3_3	7805	21908	195	65
CONTIG2144	23480752_c3_3	7806	21909	1029	343
CONTIG2148	1975701_f1_1	7807	21910	237	79
CONTIG2149	785702_f2_1	7808	21911	219	73
CONTIG2149	1953125_c1_2	7809	21912	252	84
CONTIG2150	4109762_f3_3	7810	21913	213	71
CONTIG2150	19724035_c2_4	7811	21914	282	94
CONTIG2151	24306532_c3_4	7812	21915	1257	419
CONTIG2155	29375275_c2_6	7813	21916	183	61
CONTIG2155	31328_c3_8	7814	21917	426	142

CONTIG2158	19725061_f2_2	7815	21918	183	61
CONTIG2158	19177_f3_3	7816	21919	972	324
CONTIG2159	878162_c2_4	7817	21920	186	62
CONTIG2159	25422178_f1_2	7818	21921	192	64
CONTIG216	24306527_c2_6	7819	21922	825	275
CONTIG216	5956575_c1_1	7820	21923	198	66
CONTIG2161	10724007_c2_3	7821	21924	237	79
CONTIG2162	6776533_f3_1	7822	21925	192	64
CONTIG2164	5086052_f2_1	7823	21926	213	71
CONTIG2165	33603430_c3_2	7824	21927	1023	341
CONTIG2166	4094015_f2_3	7825	21928	216	72
CONTIG2167	14878407_f1_1	7826	21929	510	170
CONTIG2167	26345750_c2_4	7827	21930	588	196
CONTIG2169	23517083_f1_1	7828	21931	471	157
CONTIG2169	23829400_c1_3	7829	21932	348	116
CONTIG217	26613161_f2_1	7830	21933	519	173
CONTIG2170	24399010_f1_2	7831	21934	1125	375
CONTIG2170	24485875_c2_7	7832	21935	369	123
CONTIG2172	48760_f3_3	7833	21936	240	80
CONTIG2173	24470778_f2_1	7834	21937	288	96
CONTIG2178	23522192_c1_3	7835	21938	348	116
CONTIG2178	16582785_c3_5	7836	21939	309	103
CONTIG2179	12300807_f1_2	7837	21940	330	110
CONTIG2179	36128377_f1_3	7838	21941	222	74
CONTIG218	1968937_f3_2	7839	21942	231	77
CONTIG2180	25601503_f3_3	7840	21943	333	111
CONTIG2180	19712_c3_7	7841	21944	201	67
CONTIG2183	3020803_f1_1	7842	21945	360	120
CONTIG2184	26839843_c1_1	7843	21946	192	64
CONTIG2184	5250302_c3_2	7844	21947	201	67
CONTIG2185	36109627_c2_2	7845	21948	1362	454
CONTIG2186	14636337_f2_2	7846	21949	207	69
CONTIG2187	24484687_f1_2	7847	21950	189	63

CONTIG2188	21496056_c3_2	7848	21951	216	72
CONTIG2194	25675936_f3_3	7849	21952	483	161
CONTIG2195	1953175_f2_1	7850	21953	198	66
CONTIG2195	24022762_c1_4	7851	21954	198	66
CONTIG2196	2039582_c1_2	7852	21955	258	86
CONTIG2199	11879628_f1_2	7853	21956	207	69
CONTIG2199	29875627_f3_6	7854	21957	225	75
CONTIG2199	4765887_c1_7	7855	21958	300	100
CONTIG2200	33707062_c1_3	7856	21959	879	293
CONTIG2201	17596083_c3_2	7857	21960	240	80
CONTIG2202	24019382_f1_1	7858	21961	1119	373
CONTIG2204	35429578_c2_9	7859	21962	408	136
CONTIG2208	15633583_f3_4	7860	21963	216	72
CONTIG2211	786550_c3_2	7861	21964	396	132
CONTIG2211	6829787_f1_1	7862	21965	243	81
CONTIG2211	890941_c1_6	7863	21966	192	64
CONTIG2214	15630250_c1_4	7864	21967	192	64
CONTIG2215	1052151_c3_7	7865	21968	261	87
CONTIG2216	12287803_f3_2	7866	21969	198	66
CONTIG222	7812_c1_1	7867	21970	186	62
CONTIG222	24297127_c2_2	7868	21971	216	72
CONTIG2220	4803911_c1_2	7869	21972	183	61
CONTIG2222	22454663_f1_1	7870	21973	210	70
CONTIG2222	9957807_f2_3	7871	21974	408	136
CONTIG2223	1223838_f3_2	7872	21975	201	67
CONTIG2225	14159376_c3_4	7873	21976	183	61
CONTIG2226	26697131_f1_1	7874	21977	1251	417
CONTIG2228	26297137_f2_1	7875	21978	228	76
CONTIG223	26836712_f1_1	7876	21979	246	82
CONTIG223	35976557_f2_2	7877	21980	198	66
CONTIG2233	10159531_f2_1	7878	21981	1095	365
CONTIG2234	4860307_c3_9	7879	21982	582	194
CONTIG2236	4975827_c3_2	7880	21983	276	92

CONTIG2237	30176277_f1_1	7881	21984	615	205
CONTIG2237	32142192_f2_2	7882	21985	1434	478
CONTIG2238	33391033_f3_1	7883	21986	228	76
CONTIG2238	1985437_c2_2	7884	21987	189	63
CONTIG2239	26350068_f1_1	7885	21988	237	79
CONTIG2239	4770290_c1_3	7886	21989	330	110
CONTIG2240	4775378_f2_3	7887	21990	276	92
CONTIG2240	16806337_c2_5	7888	21991	321	107
CONTIG2241	35364127_f3_4	7889	21992	192	64
CONTIG2241	35207561_c1_6	7890	21993	234	78
CONTIG2242	4486562_f3_1	7891	21994	651	217
CONTIG2243	12578450_f2_1	7892	21995	1134	378
CONTIG2243	35189407_f1_1	7893	21996	237	79
CONTIG2244	23631875_c1_6	7894	21997	192	64
CONTIG2244	26015953_f3_3	7895	21998	183	61
CONTIG2247	29573340_c2_1	7896	21999	306	102
CONTIG225	14556251_c1_5	7897	22000	255	85
CONTIG2251	24507037_f3_4	7898	22001	225	75
CONTIG2251	24392313_f3_3	7899	22002	756	252
CONTIG2253	33213915_c1_4	7900	22003	225	75
CONTIG2253	4731305_f3_2	7901	22004	189	63
CONTIG2255	9771907_c1_3	7902	22005	228	76
CONTIG2255	29507931_f1_1	7903	22006	312	104
CONTIG2257	787885_c3_6	7904	22007	261	87
CONTIG2257	14958161_c3_4	7905	22008	183	61
CONTIG2257	14068841_c3_4	7906	22009	264	88
CONTIG2260	19966925_f1_1	7907	22010	231	77
CONTIG2266	24393800_f1_1	7908	22011	351	117
CONTIG2269	22301377_f2_2	7909	22012	717	239
CONTIG2270	21718762_c1_3	7910	22013	186	62
CONTIG2273	11_f2_3	7911	22014	234	78
CONTIG2273	20113400_f3_5	7912	22015	201	67
CONTIG2273	20884760_f3_6	7913	22016	273	91

CONTIG2274	31379438_f1_1	7914	22017	315	105
CONTIG2274	24337836_c1_4	7915	22018	186	62
CONTIG2274	166277_c2_7	7916	22019	189	63
CONTIG2280	4694031_f2_2	7917	22020	207	69
CONTIG2281	32688525_c3_4	7918	22021	186	62
CONTIG2281	4739043_c3_5	7919	22022	276	92
CONTIG2283	21515682_f3_1	7920	22023	186	62
CONTIG2285	34070250_f2_1	7921	22024	204	68
CONTIG2285	23600055_f1_1	7922	22025	279	93
CONTIG2287	19689132_f2_3	7923	22026	252	84
CONTIG2287	14140637_f1_2	7924	22027	237	79
CONTIG2287	23600062_c2_7	7925	22028	315	105
CONTIG2287	23492762_c3_8	7926	22029	216	72
CONTIG2289	26442317_f3_4	7927	22030	333	111
CONTIG2289	4725300_c1_6	7928	22031	609	203
CONTIG2291	1173128_f1_1	7929	22032	213	71
CONTIG2292	10734425_f2_1	7930	22033	372	124
CONTIG2293	6719050_c3_5	7931	22034	219	73
CONTIG2295	7314055_f2_2	7932	22035	291	97
CONTIG2296	9788937_f1_1	7933	22036	1263	421
CONTIG2298	24656503_c3_4	7934	22037	654	218
CONTIG2299	33694686_c3_3	7935	22038	264	88
CONTIG230	20709436_f3_1	7936	22039	267	89
CONTIG2300	26848467_c3_5	7937	22040	231	77
CONTIG2301	4773285_f1_1	7938	22041	297	99
CONTIG2304	16839067_c3_3	7939	22042	867	289
CONTIG2305	12162950_f1_1	7940	22043	186	62
CONTIG2305	7638_f2_2	7941	22044	204	68
CONTIG2306	3361075_f2_1	7942	22045	234	78
CONTIG2306	1346067_c1_3	7943	22046	213	71
CONTIG2306	6359626_c3_5	7944	22047	336	112
CONTIG2307	4969442_f2_2	7945	22048	186	62
CONTIG2309	4504703_c1_4	7946	22049	252	84

CONTIG2309	14648438_c2_5	7947	22050	67
CONTIG2309	890811_c2_6	7948	22051	624	208
CONTIG2313	24901555_f3_2	7949	22052	74
CONTIG2313	15625300_c2_4	7950	22053	333	111
CONTIG2314	603251_f1_1	7951	22054	636	212
CONTIG2318	21489037_c2_5	7952	22055	207	69
CONTIG2318	41537_c3_7	7953	22056	420	140
CONTIG2319	10548755_c3_3	7954	22057	249	83
CONTIG232	32057936_f3_1	7955	22058	501	167
CONTIG232	21912525_c2_4	7956	22059	207	69
CONTIG2320	5080290_f1_1	7957	22060	195	65
CONTIG2320	12584511_c3_4	7958	22061	198	66
CONTIG2321	14633577_f3_3	7959	22062	264	88
CONTIG2323	3752_c2_6	7960	22063	189	63
CONTIG2324	2386 1683_f3_2	7961	22064	402	134
CONTIG2326	4535066_f3_1	7962	22065	375	125
CONTIG2328	22437562_f3_4	7963	22066	837	279
CONTIG2328	26382938_c1_5	7964	22067	276	92
CONTIG2329	26210813_f2_2	7965	22068	195	65
CONTIG2330	35320812_f3_2	7966	22069	618	206
CONTIG2336	25397052_f2_1	7967	22070	216	72
CONTIG2336	438952_f2_2	7968	22071	186	62
CONTIG2336	6823410_c1_3	7969	22072	861	287
CONTIG234	24823466_c2_4	7970	22073	204	68
CONTIG2340	33984782_f1_1	7971	22074	195	65
CONTIG2340	194631_f3_3	7972	22075	279	93
CONTIG2341	35257050_f3_4	7973	22076	189	63
CONTIG2343	29922650_f2_2	7974	22077	354	118
CONTIG2346	20116286_f3_2	7975	22078	393	131
CONTIG2347	6286_f3_2	7976	22079	321	107
CONTIG2348	32457030_f3_4	7977	22080	438	146
CONTIG2348	34657838_c2_5	7978	22081	273	91
CONTIG2349	13680165_f2_1	7979	22082	231	77

CONTIG2350	4820450_f2_1	7980	22083	663	221
CONTIG2351	8225067_f2_2	7981	22084	237	79
CONTIG2352	29453377_c3_4	7982	22085	357	119
CONTIG2353	33864625_f2_2	7983	22086	270	90
CONTIG2354	21640903_f1_1	7984	22087	456	152
CONTIG2354	1441543_c3_6	7985	22088	432	144
CONTIG2357	15626632_f2_2	7986	22089	255	85
CONTIG2358	4562512_c1_3	7987	22090	570	190
CONTIG2359	22442202_f1_2	7988	22091	288	96
CONTIG2360	4315875_f2_3	7989	22092	597	199
CONTIG2362	27234751_f1_1	7990	22093	276	92
CONTIG2365	7221010_c1_3	7991	22094	318	106
CONTIG2367	20329055_c2_2	7992	22095	606	202
CONTIG2368	26370338_f2_4	7993	22096	216	72
CONTIG2368	26382952_c3_5	7994	22097	495	165
CONTIG237	23910382_c2_2	7995	22098	189	63
CONTIG2371	6098437_c2_4	7996	22099	306	102
CONTIG2373	12993780_f3_1	7997	22100	849	283
CONTIG2374	196875_f3_2	7998	22101	204	68
CONTIG2375	34495328_c3_4	7999	22102	273	91
CONTIG2375	6931552_c3_5	8000	22103	498	166
CONTIG2378	10657587_f2_1	8001	22104	393	131
CONTIG2381	9844058_f2_2	8002	22105	243	81
CONTIG2381	1960888_f3_4	8003	22106	198	66
CONTIG2381	1367142_c1_5	8004	22107	198	66
CONTIG2382	36292_f1_2	8005	22108	231	77
CONTIG2382	21985877_f3_4	8006	22109	369	123
CONTIG2385	6641092_f1_1	8007	22110	189	63
CONTIG2385	36306_f3_2	8008	22111	234	78
CONTIG2386	26384555_f2_1	8009	22112	234	78
CONTIG2387	24648436_f2_2	8010	22113	492	164
CONTIG2387	23835912_f2_3	8011	22114	234	78
CONTIG2387	10650288_c3_5	8012	22115	825	275

CONTIG2388	890937_c1_2	8013	22116	195	65
CONTIG2389	4589530_c3_3	8014	22117	498	166
CONTIG239	1360712_f2_2	8015	22118	249	83
CONTIG239	23925656_c2_4	8016	22119	243	81
CONTIG239	957530_c3_5	8017	22120	189	63
CONTIG2393	19923765_f3_2	8018	22121	207	69
CONTIG2394	1601751.2_c3_7	8019	22122	249	83
CONTIG2395	14566592_f3_2	8020	22123	198	66
CONTIG2396	36351400_c1_2	8021	22124	216	72
CONTIG2397	6062825_f1_2	8022	22125	276	92
CONTIG24	14569436_c3_4	8023	22126	711	237
CONTIG240	22151417_c1_1	8024	22127	192	64
CONTIG2400	3937563_f2_2	8025	22128	492	164
CONTIG2400	34586552_c1_5	8026	22129	228	76
CONTIG2401	21660691_f1_1	8027	22130	228	76
CONTIG2401	10754707_c2_6	8028	22131	381	127
CONTIG2401	34179212_c3_8	8029	22132	189	63
CONTIG2403	24021875_f1_2	8030	22133	210	70
CONTIG2403	26600055_f2_3	8031	22134	189	63
CONTIG2403	2911537_c3_5	8032	22135	312	104
CONTIG2404	4879592_f2_2	8033	22136	258	86
CONTIG2404	25964436_f3_3	8034	22137	273	91
CONTIG2404	23830287_c3_8	8035	22138	246	82
CONTIG2407	12921932_f1_2	8036	22139	204	68
CONTIG2408	22394386_f1_1	8037	22140	963	321
CONTIG2408	24414062_c1_9	8038	22141	186	62
CONTIG2410	6902177_f2_3	8039	22142	189	63
CONTIG2411	25666008_f2_1	8040	22143	285	95
CONTIG2412	24220005_c3_7	8041	22144	243	81
CONTIG2413	23984501_c1_3	8042	22145	207	69
CONTIG2415	36359836_c1_3	8043	22146	483	161
CONTIG2415	835336_c3_4	8044	22147	327	109
CONTIG2416	1990954_c1_4	8045	22148	201	67

CONTIG2419	21485877_f1_1	8046	22149	76	
CONTIG2419	9977177_f2_3	8047	22150	264	88
CONTIG242	22350052_f2_2	8048	22151	480	160
CONTIG2423	23914561_f1_1	8049	22152	192	64
CONTIG2423	35188825_f3_3	8050	22153	201	67
CONTIG2424	828188_f3_1	8051	22154	315	105
CONTIG2428	21914680_f2_1	8056	22159	750	250
CONTIG2425	33257692_f1_1	8052	22155	183	61
CONTIG2425	157535_f3_3	8053	22156	195	65
CONTIG2425	78557_c2_4	8054	22157	198	66
CONTIG2428	22362750_f2_2	8055	22158	285	95
CONTIG2429	116262_f2_2	8057	22160	702	234
CONTIG2430	34586067_c1_2	8058	22161	186	62
CONTIG2431	979656_c2_4	8059	22162	186	62
CONTIG2438	9922578_c2_3	8060	22163	279	93
CONTIG2439	14631513_f3_1	8061	22164	198	66
CONTIG2439	23573462_c3_3	8062	22165	183	61
CONTIG244	16988412_f1_1	8063	22166	225	75
CONTIG244	4698752_c2_3	8064	22167	234	78
CONTIG2440	4194677_f1_1	8065	22168	255	85
CONTIG2440	1047000_f1_2	8066	22169	192	64
CONTIG2440	101412_f1_3	8067	22170	318	106
CONTIG2440	1464712_f2_4	8068	22171	234	78
CONTIG2440	35392568_f3_5	8069	22172	213	71
CONTIG2441	13790888_c2_2	8070	22173	1314	438
CONTIG2442	9938876_f1_2	8071	22174	252	84
CONTIG2442	23929038_f2_3	8072	22175	348	116
CONTIG2442	29313808_f2_4	8073	22176	243	81
CONTIG2443	9878428_c3_4	8074	22177	519	173
CONTIG2450	16988963_f2_3	8075	22178	201	67
CONTIG2450	211056_c2_7	8076	22179	219	73
CONTIG2453	24615637_c3_4	8077	22180	471	157
CONTIG2454	5274187_f1_1	8078	22181	192	64

CONTIG2454	15812882_f2_2	8079	22182	201	67
CONTIG2455	14535885_c2_7	8080	22183	309	103
CONTIG2457	21642031_f1_1	8081	22184	213	71
CONTIG2459	33391925_c1_5	8082	22185	201	67
CONTIG2459	1177342_c3_6	8083	22186	69	69
CONTIG2462	24656575_f1_1	8084	22187	279	93
CONTIG2463	422327_f1_2	8085	22188	198	66
CONTIG2466	22851442_f1_1	8086	22189	273	91
CONTIG2467	31835938_f3_2	8087	22190	408	136
CONTIG2468	30095413_f3_5	8088	22191	267	89
CONTIG2469	29376630_c1_4	8089	22192	210	70
CONTIG2470	976512_c3_7	8090	22193	222	74
CONTIG2471	34003150_f1_1	8091	22194	183	61
CONTIG2471	14632786_f2_3	8092	22195	408	136
CONTIG2475	24104700_f2_1	8093	22196	267	89
CONTIG2475	25478428_c3_2	8094	22197	270	90
CONTIG2478	36220191_f3_4	8095	22198	519	173
CONTIG2479	26562692_f3_1	8096	22199	225	75
CONTIG2480	25431702_f1_1	8097	22200	207	69
CONTIG2481	25595452_f3_4	8098	22201	366	122
CONTIG2482	19939660_c3_3	8099	22202	210	70
CONTIG2483	30125302_c3_5	8100	22203	231	77
CONTIG2485	234702_c2_3	8101	22204	408	136
CONTIG2487	19584388_f3_1	8102	22205	183	61
CONTIG2488	35182776_f2_1	8103	22206	594	198
CONTIG2489	4066011_c3_8	8104	22207	213	71
CONTIG249	1063387_f3_1	8105	22208	198	66
CONTIG2490	34006301_c1_7	8106	22209	378	126
CONTIG2490	35545077_c1_8	8107	22210	279	93
CONTIG2491	798377_f3_5	8108	22211	216	72
CONTIG2491	11838887_f3_6	8109	22212	249	83
CONTIG2493	24615762_c1_5	8110	22213	267	89
CONTIG2493	9789837_c2_6	8111	22214	1164	388

CONTIG2493	23862783_c3_8	8112	22215	531	177
CONTIG2494	22392678_f2_2	8113	22216	237	79
CONTIG2494	10581502_f3_3	8114	22217	198	66
CONTIG2494	14648412_c1_4	8115	22218	312	104
CONTIG2496	266078_c2_6	8116	22219	429	143
CONTIG2497	4494000_f1_1	8117	22220	1185	395
CONTIG2497	36334687_f3_3	8118	22221	183	61
CONTIG2498	19531336_f3_3	8119	22222	216	72
CONTIG2498	6098437_c2_5	8120	22223	306	102
CONTIG2499	24256527_c2_5	8121	22224	984	328
CONTIG2500	4317037_c2_1	8122	22225	378	126
CONTIG250	35179812_c1_5	8125	22228	279	93
CONTIG2500	5251260_f2_2	8123	22226	594	198
CONTIG2501	990632_f3_3	8124	22227	186	62
CONTIG2502	3312_f3_2	8126	22229	252	84
CONTIG2505	20735952_c3_5	8127	22230	285	95
CONTIG2507	1172037_f1_1	8128	22231	204	68
CONTIG2509	14635052_c1_4	8129	22232	291	97
CONTIG2510	26602340_c2_8	8130	22233	186	62
CONTIG2511	24667911_f2_2	8131	22234	282	94
CONTIG2512	35678817_f2_1	8132	22235	321	107
CONTIG2513	625130_f3_2	8133	22236	282	94
CONTIG2514	23992932_f3_2	8134	22237	183	61
CONTIG2516	24414088_c3_3	8135	22238	270	90
CONTIG2518	32132790_c1_3	8136	22239	270	90
CONTIG2518	11719052_c3_5	8137	22240	414	138
CONTIG2519	24414062_f1_1	8138	22241	534	178
CONTIG2519	24412963_f3_2	8139	22242	186	62
CONTIG2520	24823425_c2_5	8140	22243	897	299
CONTIG2520	26345192_f3_1	8141	22244	246	82
CONTIG2521	19542162_c1_6	8142	22245	183	61
CONTIG2523	35740700_f1_1	8143	22246	186	62
CONTIG2529	875017_f1_1	8144	22247	228	76

CONTIG2531	1359392_f1_2	8145	22248	186	62
CONTIG2531	34455288_f3_4	8146	22249	183	61
CONTIG2532	867141_f2_1	8147	22250	513	171
CONTIG2535	22835758_f3_4	8148	22251	201	67
CONTIG2539	4800751_f3_2	8149	22252	363	121
CONTIG2539	12194551_c1_3	8150	22253	312	104
CONTIG254	578155_f2_1	8151	22254	504	168
CONTIG2540	4023577_f3_1	8152	22255	183	61
CONTIG2541	24220965_f3_1	8153	22256	222	74
CONTIG2542	2611517_c2_6	8154	22257	234	78
CONTIG2543	976593_c2_4	8155	22258	183	61
CONTIG2546	6255_f3_5	8156	22259	183	61
CONTIG2546	16883540_c1_6	8157	22260	849	283
CONTIG2547	34189702_c2_4	8158	22261	576	192
CONTIG2547	13834637_c3_5	8159	22262	195	65
CONTIG2548	19728382_c1_5	8160	22263	312	104
CONTIG2557	12783542_c1_4	8161	22264	192	64
CONTIG2559	26380391_f3_1	8162	22265	1818	606
CONTIG256	1035162_f3_1	8163	22266	381	127
CONTIG2560	4884537_f1_1	8164	22267	186	62
CONTIG2560	397800_f3_3	8165	22268	348	116
CONTIG2560	2069627_c3_5	8166	22269	249	83
CONTIG2562	26259681_c2_7	8167	22270	561	187
CONTIG2563	4867327_c1_4	8168	22271	252	84
CONTIG2565	24252312_f2_1	8169	22272	297	99
CONTIG2565	19535152_f3_3	8170	22273	198	66
CONTIG2566	24421875_c1_3	8171	22274	711	237
CONTIG2567	24344126_f1_1	8172	22275	219	73
CONTIG2567	4188150_f1_2	8173	22276	810	270
CONTIG2572	36051257_f2_3	8174	22277	1344	448
CONTIG2572	2344002_c1_4	8175	22278	210	70
CONTIG2572	2220693_c1_7	8176	22279	264	88
CONTIG2574	33362631_c1_5	8177	22280	300	100

CONTIG2576	26594050_f1_2	8178	22281	225	75
CONTIG2576	4298162_c2_3	8179	22282	330	110
CONTIG2577	5948961_f1_1	8180	22283	264	88
CONTIG2577	4307182_c1_2	8181	22284	483	161
CONTIG2578	24495442_c3_6	8182	22285	186	62
CONTIG2579	15668_f3_2	8183	22286	291	97
CONTIG2579	12587805_f3_4	8184	22287	249	83
CONTIG2579	19548501_c3_6	8185	22288	195	65
CONTIG2580	10011687_f3_4	8186	22289	279	93
CONTIG2581	1445137_c2_6	8187	22290	852	284
CONTIG2583	24609786_c1_3	8188	22291	264	88
CONTIG2584	22750637_f1_1	8189	22292	399	133
CONTIG2584	32537502_f3_3	8190	22293	195	65
CONTIG2584	961567_f3_4	8191	22294	342	114
CONTIG2584	24392180_c1_6	8192	22295	240	80
CONTIG2588	14585392_f3_2	8193	22296	192	64
CONTIG2591	6834637_c2_2	8194	22297	942	314
CONTIG2592	4957842_f2_4	8195	22298	186	62
CONTIG2592	12312910_c2_9	8196	22299	249	83
CONTIG2592	13756450_c3_10	8197	22300	471	157
CONTIG2593	5364012_f2_1	8198	22301	240	80
CONTIG2593	4190932_c2_3	8199	22302	201	67
CONTIG2595	20319406_f1_1	8200	22303	210	70
CONTIG2595	4938275_c1_3	8201	22304	183	61
CONTIG2596	2200425_f1_1	8202	22305	1140	380
CONTIG2597	14506905_f3_4	8203	22306	276	92
CONTIG2597	6645252_c3_5	8204	22307	294	98
CONTIG26	25585899_c1_2	8205	22308	279	93
CONTIG2601	21515925_f1_1	8206	22309	495	165
CONTIG2603	24413937_f1_1	8207	22310	219	73
CONTIG2605	12696057_f1_1	8208	22311	246	82
CONTIG2605	26502_f1_2	8209	22312	834	278
CONTIG2607	262_c1_4	8210	22313	198	66

CONTIG2607	30351635_c2_5	8211	22314	195	65
CONTIG2608	23632140_f1_1	8212	22315	183	61
CONTIG2610	29375260_c2_2	8213	22316	189	63
CONTIG2611	6147593_f2_1	8214	22317	225	75
CONTIG2611	25431700_f2_2	8215	22318	186	62
CONTIG2611	24414090_f3_3	8216	22319	258	86
CONTIG2614	34551557_c3_7	8217	22320	231	77
CONTIG2614	5900078_c2_6	8218	22321	720	240
CONTIG2613	2000377_c1_5	8219	22322	579	193
CONTIG2612	6328301_c3_4	8220	22323	276	92
CONTIG2612	29953411_c2_3	8221	22324	357	119
CONTIG2611	34179577_c1_4	8222	22325	285	95
CONTIG2617	22117191_f3_3	8223	22326	279	93
CONTIG2618	15056507_f2_3	8224	22327	489	163
CONTIG2618	9892510_c1_6	8225	22328	264	88
CONTIG2620	1209662_f1_1	8226	22329	411	137
CONTIG2623	4187777_f1_1	8227	22330	189	63
CONTIG2623	24323300_c3_8	8228	22331	279	93
CONTIG2629	26854636_f1_1	8229	22332	231	77
CONTIG2629	24307075_c3_5	8230	22333	1476	492
CONTIG263	15897181_f2_1	8231	22334	183	61
CONTIG263	33284376_c2_2	8232	22335	270	90
CONTIG2634	31772500_f3_2	8233	22336	567	189
CONTIG2634	47353377_f3_3	8234	22337	456	152
CONTIG2636	19843_f2_2	8235	22338	1671	557
CONTIG2636	32136625_c1_6	8236	22339	339	113
CONTIG2637	14540750_f3_2	8237	22340	246	82
CONTIG2638	22448767_c1_3	8238	22341	267	89
CONTIG2639	30346001_f1_1	8239	22342	192	64
CONTIG2639	21642527_c2_5	8240	22343	306	102
CONTIG2641	24235962_f2_2	8241	22344	228	76
CONTIG2641	15742187_c1_4	8242	22345	240	80
CONTIG2642	4892805_f1_1	8243	22346	225	75

CONTIG2643	21490928_f3_1	8244	22347	234	78
CONTIG2645	24492800_c3_5	8245	22348	234	78
CONTIG2646	179010_c1_4	8246	22349	339	113
CONTIG2647	29304032_f1_1	8247	22350	186	62
CONTIG2647	10752257_f3_2	8248	22351	201	67
CONTIG265	2813177_c2_2	8249	22352	540	180
CONTIG2650	4016966_f3_3	8250	22353	228	76
CONTIG2651	4507883_f2_2	8251	22354	201	67
CONTIG2654	9937505_c2_2	8252	22355	609	203
CONTIG2655	5906628_f2_1	8253	22356	279	93
CONTIG2658	24486561_f1_2	8254	22357	264	88
CONTIG266	24064182_f2_2	8255	22358	267	89
CONTIG266	22352160_c3_3	8256	22359	315	105
CONTIG2660	9980442_f1_1	8257	22360	192	64
CONTIG2660	10038428_c2_3	8258	22361	300	100
CONTIG2661	1417502_f2_2	8259	22362	225	75
CONTIG2661	34024193_f3_4	8260	22363	207	69
CONTIG2661	6660917_c2_6	8261	22364	207	69
CONTIG2662	25406332_c2_5	8262	22365	603	201
CONTIG2662	23616337_c2_6	8263	22366	285	95
CONTIG2663	35553150_c1_7	8264	22367	639	213
CONTIG2664	16484760_f3_4	8265	22368	930	310
CONTIG2665	29548427_f2_1	8266	22369	636	212
CONTIG2665	14460951_c2_2	8267	22370	228	76
CONTIG2666	12897187_f1_1	8268	22371	189	63
CONTIG2667	5312827_c3_5	8269	22372	186	62
CONTIG2668	56532_f2_3	8270	22373	237	79
CONTIG2668	4881555_c1_5	8271	22374	195	65
CONTIG2668	24632907_c1_7	8272	22375	198	66
CONTIG2668	25585788_c3_8	8273	22376	219	73
CONTIG2669	24265632_f2_3	8274	22377	234	78
CONTIG267	34020907_f3_2	8275	22378	258	86
CONTIG2671	33985425_c3_4	8276	22379	186	62

CONTIG2673	23437925_f2_2	8277	22380	312	104
CONTIG2682	980000_c3_6	8278	22381	204	68
CONTIG2683	4171177_f1_1	8279	22382	1452	484
CONTIG2683	163425_c3_5	8280	22383	189	63
CONTIG2684	6679702_c3_6	8281	22384	192	64
CONTIG2685	479791_f3_3	8282	22385	609	203
CONTIG2687	1076092_f2_1	8283	22386	462	154
CONTIG2688	34275377_c3_8	8284	22387	300	100
CONTIG2689	33251510_f3_2	8285	22388	201	67
CONTIG2689	6728462_c1_3	8286	22389	285	95
CONTIG2690	178806_c2_4	8287	22390	198	66
CONTIG2691	26594028_f1_1	8288	22391	444	148
CONTIG2692	2848750_f1_1	8289	22392	204	68
CONTIG2693	24343805_f1_1	8290	22393	894	298
CONTIG2693	21757703_c1_2	8291	22394	402	134
CONTIG2695	14650015_c1_6	8292	22395	480	160
CONTIG2695	13941000_c2_9	8293	22396	282	94
CONTIG2697	181283_f1_3	8294	22397	225	75
CONTIG2697	4797015_f3_4	8295	22398	387	129
CONTIG2697	14242155_c3_7	8296	22399	219	73
CONTIG270	954437_c2_1	8297	22400	261	87
CONTIG2700	24303137_f3_1	8298	22401	222	74
CONTIG2701	4117752_c1_1	8299	22402	183	61
CONTIG2703	10323255_f2_3	8300	22403	255	85
CONTIG2703	957750_c3_5	8301	22404	1239	413
CONTIG2705	25410300_f1_1	8302	22405	198	66
CONTIG2707	25392877_f1_1	8303	22406	234	78
CONTIG2707	4725325_c2_5	8304	22407	207	69
CONTIG2712	2906305_c2_3	8305	22408	564	188
CONTIG2712	5969130_c3_4	8306	22409	243	81
CONTIG2715	23945192_f2_1	8307	22410	189	63
CONTIG2715	21760327_c2_5	8308	22411	201	67
CONTIG2717	992187_c3_4	8309	22412	237	79

CONTIG2718	24641580_c1_3	8310	22413	267	89
CONTIG2718	26251930_c1_4	8311	22414	294	98
CONTIG272	87550_f2_3	8312	22415	285	95
CONTIG2723	12679561_c3_1	8313	22416	189	63
CONTIG2724	31520002_f1_1	8314	22417	354	118
CONTIG2725	25506912_f1_1	8315	22418	207	69
CONTIG2725	33398456_c2_3	8316	22419	252	84
CONTIG2728	24495391_f2_2	8317	22420	480	160
CONTIG2728	972627_f2_3	8318	22421	633	211
CONTIG2728	25601505_c1_6	8319	22422	261	87
CONTIG2728	180152_c3_8	8320	22423	207	69
CONTIG2730	1984437_f1_5	8321	22424	243	81
CONTIG2730	4875200_c3_7	8322	22425	240	80
CONTIG2734	35348375_f3_3	8323	22426	249	83
CONTIG2736	6847537_f3_2	8324	22427	228	76
CONTIG2736	24806260_c2_4	8325	22428	234	78
CONTIG2737	187752_c3_5	8326	22429	300	100
CONTIG2739	35830158_f2_1	8327	22430	282	94
CONTIG2740	34171942_f2_1	8328	22431	1290	430
CONTIG2742	3925377_c1_4	8329	22432	288	96
CONTIG2742	4391937_c3_5	8330	22433	255	85
CONTIG2743	11929032_c3_1	8331	22434	1032	344
CONTIG2745	24023515_c1_3	8332	22435	201	67
CONTIG2746	6759652_f3_6	8333	22436	1230	410
CONTIG2746	23907925_f3_7	8334	22437	216	72
CONTIG2746	4977250_c3_10	8335	22438	273	91
CONTIG2748	23473575_f3_5	8336	22439	204	68
CONTIG2749	30207652_f2_2	8337	22440	183	61
CONTIG2749	9808215_c2_6	8338	22441	186	62
CONTIG2750	3204567_f1_1	8339	22442	1428	476
CONTIG2751	3400_f2_2	8340	22443	213	71
CONTIG2751	20320886_c1_5	8341	22444	210	70
CONTIG2753	547200_c1_3	8342	22445	201	67

CONTIG2754	6125402_c2_3	8343	22446	186	62
CONTIG2756	25582056_f2_1	8344	22447	201	67
CONTIG2756	36601503_c3_4	8345	22448	270	90
CONTIG2757	23868800_c1_4	8346	22449	741	247
CONTIG2758	4063377_f2_1	8347	22450	504	168
CONTIG2761	10058137_c3_3	8348	22451	219	73
CONTIG2762	1220056_c1_3	8349	22452	264	88
CONTIG2764	22160028_f2_5	8350	22453	375	125
CONTIG2764	12381718_c1_9	8351	22454	183	61
CONTIG2765	14652300_f3_1	8352	22455	213	71
CONTIG2766	33210752_f3_3	8353	22456	354	118
CONTIG2766	392275_c1_4	8354	22457	282	94
CONTIG2768	29489550_c1_2	8355	22458	213	71
CONTIG2768	4023577_c1_3	8356	22459	183	61
CONTIG2769	189001_c3_4	8357	22460	264	88
CONTIG2770	13867211_c2_1	8358	22461	261	87
CONTIG2770	4197917_c3_3	8359	22462	222	74
CONTIG2771	24617250_c1_4	8360	22463	183	61
CONTIG2771	22707561_c2_5	8361	22464	717	239
CONTIG2772	35798263_f3_2	8362	22465	405	135
CONTIG2772	782818_c1_4	8363	22466	201	67
CONTIG2773	2166340_f2_2	8364	22467	501	167
CONTIG2773	971968_c2_3	8365	22468	939	313
CONTIG2775	2478180_c1_3	8366	22469	243	81
CONTIG2776	24219206_f1_3	8367	22470	213	71
CONTIG2778	4882205_f2_2	8368	22471	363	121
CONTIG2778	6850425_f3_4	8369	22472	258	86
CONTIG278	34412805_f2_1	8370	22473	207	69
CONTIG2786	13864555_f3_1	8371	22474	687	229
CONTIG2787	24399093_f2_2	8372	22475	204	68
CONTIG2788	1992262_f2_2	8373	22476	237	79
CONTIG2788	4533402_c1_5	8374	22477	270	90
CONTIG2789	24226675_f1_1	8375	22478	252	84

CONTIG2790	14489681_f2_2	8376	22479	291	97
CONTIG2790	33469056_c2_5	8377	22480	282	94
CONTIG2792	24492252_f3_4	8378	22481	612	204
CONTIG2792	24424055_c3_6	8379	22482	303	101
CONTIG2793	25563888_f2_2	8380	22483	192	64
CONTIG2793	10626530_f2_4	8381	22484	639	213
CONTIG2796	5975336_f3_3	8382	22485	219	73
CONTIG2796	21532817_c2_6	8383	22486	246	82
CONTIG2799	2813177_c3_5	8384	22487	753	251
CONTIG2801	24876955_c2_12	8385	22488	540	180
CONTIG2803	35736627_f3_2	8386	22489	330	110
CONTIG2803	26448562_f3_3	8387	22490	198	66
CONTIG2803	11725001_c2_6	8388	22491	192	64
CONTIG2807	5126450_f1_1	8389	22492	291	97
CONTIG2807	24786265_f3_2	8390	22493	183	61
CONTIG2810	29772135_c1_2	8391	22494	186	62
CONTIG2813	1173763_f2_3	8392	22495	213	71
CONTIG2814	9797505_f1_1	8393	22496	333	111
CONTIG2816	2343801_f1_7	8394	22497	201	67
CONTIG2817	24892187_f2_1	8395	22498	1713	571
CONTIG2818	24429561_f2_1	8396	22499	1743	581
CONTIG2819	23851415_f1_1	8397	22500	198	66
CONTIG282	2164763_c2_2	8398	22501	486	162
CONTIG2820	10831531_f3_2	8399	22502	282	94
CONTIG2820	24253878_c1_5	8400	22503	222	74
CONTIG2821	24023411_c2_3	8401	22504	1632	544
CONTIG2823	24257887_f1_2	8402	22505	186	62
CONTIG2825	24023262_c1_1	8403	22506	219	73
CONTIG2828	15783540_f1_1	8404	22507	189	63
CONTIG2829	2131260_f2_3	8405	22508	279	93
CONTIG2830	869802_c3_5	8406	22509	183	61
CONTIG2832	10057318_f1_1	8407	22510	834	278
CONTIG2832	4890638_c1_2	8408	22511	285	95

CONTIG					
CONTIG2832	25581410_c2_4	8409	22512	225	75
CONTIG2833	22312555_c2_2	8410	22513	225	75
CONTIG2834	29328182_c3_4	8411	22514	186	62
CONTIG2836	19573300_c3_2	8412	22515	258	86
CONTIG2836	14457751_c3_3	8413	22516	198	66
CONTIG2839	9775303_f3_3	8414	22517	216	72
CONTIG2840	23923912_c2_4	8415	22518	228	76
CONTIG2844	24491252_f3_2	8416	22519	417	139
CONTIG2844	24416500_c2_4	8417	22520	210	70
CONTIG2849	30192162_f1_1	8418	22521	198	66
CONTIG2849	20751328_f1_2	8419	22522	189	63
CONTIG2849	20973136_f3_4	8420	22523	192	64
CONTIG2849	11914187_c1_5	8421	22524	261	87
CONTIG2849	34179687_c3_7	8422	22525	207	69
CONTIG2850	4718800_c1_4	8423	22526	333	111
CONTIG2853	6900025_c2_6	8424	22527	1317	439
CONTIG2854	13679143_f2_1	8425	22528	579	193
CONTIG2854	12_c2_4	8426	22529	198	66
CONTIG2855	3907158_c1_3	8427	22530	687	229
CONTIG2858	10803202_f2_1	8428	22531	234	78
CONTIG2859	22203_f3_2	8429	22532	765	255
CONTIG2860	10937875_f3_1	8430	22533	1140	380
CONTIG2862	3912775_f3_1	8431	22534	270	90
CONTIG2863	9956252_c1_2	8432	22535	231	77
CONTIG2864	24426592_c2_6	8433	22536	207	69
CONTIG2866	4727287_f2_1	8434	22537	201	67
CONTIG2866	7085952_c2_4	8435	22538	249	83
CONTIG2867	23830465_c3_6	8436	22539	231	77
CONTIG2869	972125_c1_5	8437	22540	273	91
CONTIG2869	6812750_c3_8	8438	22541	222	74
CONTIG2871	1989037_f1_1	8439	22542	198	66
CONTIG2873	10235137_f1_1	8440	22543	234	78
CONTIG2873	19693812_f2_4	8441	22544	189	63

CONTIG2874	626453_c1_3	8442	22545	324	108
CONTIG2874	29548525_c3_6	8443	22546	510	170
CONTIG2876	23515677_f1_1	8444	22547	306	102
CONTIG2876	23710015_c2_5	8445	22548	186	62
CONTIG2877	859688_c1_1	8446	22549	810	270
CONTIG2881	14843827_f2_3	8447	22550	291	97
CONTIG2882	21523551_f1_3	8448	22551	228	76
CONTIG2884	30355063_c1_4	8449	22552	306	102
CONTIG2884	21489807_c2_6	8450	22553	393	131
CONTIG2886	6766887_f1_1	8451	22554	237	79
CONTIG2887	4946002_c3_4	8452	22555	333	111
CONTIG2888	25447552_c2_3	8453	22556	231	77
CONTIG2888	11720902_c3_8	8454	22557	192	64
CONTIG2888	11756675_f2_3	8455	22558	204	68
CONTIG2889	23625086_c2_4	8456	22559	306	102
CONTIG2889	9975758_f2_2	8457	22560	213	71
CONTIG289	549053_c2_3	8458	22561	261	87
CONTIG289	10547067_c2_4	8459	22562	192	64
CONTIG2893	22444375_c2_3	8460	22563	189	63
CONTIG2894	14563762_f1_1	8461	22564	306	102
CONTIG2896	24413437_c3_4	8462	22565	201	67
CONTIG2896	25585911_f2_4	8463	22566	243	81
CONTIG2897	24253207_c1_6	8464	22567	249	83
CONTIG2899	21922127_f1_1	8465	22568	423	141
CONTIG2900	34116042_c3_5	8466	22569	201	67
CONTIG2900	9884712_f3_4	8467	22570	336	112
CONTIG2902	4864066_f1_2	8468	22571	387	129
CONTIG2905	14565956_f2_3	8469	22572	216	72
CONTIG2905	21517340_c1_4	8470	22573	222	74
CONTIG2906	25423200_f1_1	8471	22574	216	72
CONTIG2909	1954542_c2_5	8472	22575	189	63
CONTIG2909	25423837_c2_4	8473	22576	192	64
CONTIG291	25423837_c2_4	8474	22577	297	99

CONTIG2913	31910001_f3_4	8475	22578	1077	359
CONTIG2914	4710902_f2_3	8476	22579	1350	450
CONTIG2915	24410912_f2_1	8477	22580	216	72
CONTIG2915	5366075_f3_2	8478	22581	432	144
CONTIG2915	1203430_c3_4	8479	22582	579	193
CONTIG2916	35345437_f3_3	8480	22583	192	64
CONTIG2917	24020186_f3_2	8481	22584	816	272
CONTIG2920	26773550_f3_3	8482	22585	186	62
CONTIG2920	35209458_c2_6	8483	22586	279	93
CONTIG2921	4711530_c1_2	8484	22587	198	66
CONTIG2925	35632836_c3_5	8485	22588	213	71
CONTIG2927	14572182_f2_1	8486	22589	450	150
CONTIG2928	24647188_f1_2	8487	22590	201	67
CONTIG2929	23438918_f1_1	8488	22591	345	115
CONTIG2929	21642187_f2_2	8489	22592	198	66
CONTIG2930	23907528_f3_1	8490	22593	258	86
CONTIG2930	9944751_f3_2	8491	22594	294	98
CONTIG2930	10320337_c2_5	8492	22595	219	73
CONTIG2932	13775307_f2_4	8493	22596	537	179
CONTIG2933	4032650_c3_2	8494	22597	315	105
CONTIG2934	14558257_c3_3	8495	22598	321	107
CONTIG2935	4068752_f3_4	8496	22599	243	81
CONTIG2935	5914177_c3_6	8497	22600	252	84
CONTIG2936	204050_f1_2	8498	22601	240	80
CONTIG2936	2031382_f3_6	8499	22602	210	70
CONTIG2937	19542302_f1_1	8500	22603	405	135
CONTIG2938	1432318_f1_1	8501	22604	1182	394
CONTIG294	32245331_c1_5	8502	22605	261	87
CONTIG2940	39649033_c1_6	8503	22606	183	61
CONTIG2940	29304513_c1_7	8504	22607	219	73
CONTIG2941	19720630_f3_4	8505	22608	321	107
CONTIG2943	24272300_f1_1	8506	22609	1647	549
CONTIG2944	9819555_f1_1	8507	22610	366	122

CONTIG2944	214030_f2_2	8508	22611	282	94
CONTIG2944	11875925_c2_4	8509	22612	228	76
CONTIG2945	29958550_f2_1	8510	22613	1449	483
CONTIG2949	4710342_f3_3	8511	22614	348	116
CONTIG2951	15859462_f2_1	8512	22615	207	69
CONTIG2951	4800257_f2_2	8513	22616	516	172
CONTIG2951	46950649_c1_5	8514	22617	246	82
CONTIG2951	14297137_f2_2	8515	22618	213	71
CONTIG2953	13678425_c2_6	8518	22621	210	70
CONTIG2953	34241387_f3_4	8517	22620	207	69
CONTIG2953	5916266_f2_3	8516	22619	282	94
CONTIG2956	9881952_f2_1	8519	22622	201	67
CONTIG2956	6033188_c2_3	8520	22623	198	66
CONTIG2957	1288127_c1_5	8521	22624	387	129
CONTIG2959	25399066_f2_4	8522	22625	225	75
CONTIG2959	437575_c1_5	8523	22626	390	130
CONTIG296	860877_c3_1	8524	22627	282	94
CONTIG296	14491557_c3_2	8525	22628	231	77
CONTIG2960	1070401_f1_2	8526	22629	264	88
CONTIG2961	25437813_c3_10	8527	22630	243	81
CONTIG2963	1990752_f2_2	8528	22631	246	82
CONTIG2963	11876527_c1_4	8529	22632	267	89
CONTIG2966	26589432_f2_3	8530	22633	192	64
CONTIG2966	4069088_c1_8	8531	22634	210	70
CONTIG2967	23522785_f2_1	8532	22635	384	128
CONTIG2967	5088942_f2_2	8533	22636	189	63
CONTIG2967	16801562_c2_4	8534	22637	201	67
CONTIG2967	21675781_c2_5	8535	22638	222	74
CONTIG2970	13870950_f3_2	8536	22639	219	73
CONTIG2970	36330037_c3_5	8537	22640	228	76
CONTIG2970	13103382_c3_6	8538	22641	381	127
CONTIG2973	968877_c2_3	8539	22642	273	91
CONTIG2973	13673192_c3_7	8540	22643	186	62

CONTIG2974	625635_c2_10	8541	22644	411	137
CONTIG2974	3128177_c3_12	8542	22645	213	71
CONTIG2975	4797792_f2_2	8543	22646	408	136
CONTIG2975	14882877_f2_3	8544	22647	891	297
CONTIG2976	12898438_f1_1	8545	22648	276	92
CONTIG2977	24848137_f2_1	8546	22649	291	97
CONTIG2977	3945437_f3_2	8547	22650	369	123
CONTIG2977	15652_c2_7	8548	22651	207	69
CONTIG2978	2187588_f1_2	8549	22652	246	82
CONTIG2978	29508437_f3_3	8550	22653	186	62
CONTIG2978	4898442_c1_5	8551	22654	183	61
CONTIG2979	36214762_f1_1	8552	22655	183	61
CONTIG2979	23885192_f2_2	8553	22656	432	144
CONTIG298	24822557_c1_4	8554	22657	216	72
CONTIG2982	4495687_c1_5	8555	22658	213	71
CONTIG2982	4772582_c1_6	8556	22659	387	129
CONTIG2982	24300006_c3_9	8557	22660	213	71
CONTIG2982	1985782_c3_10	8558	22661	204	68
CONTIG2983	12617153_f2_1	8559	22662	372	124
CONTIG2986	6150040_c1_4	8560	22663	279	93
CONTIG2986	9844687_c3_8	8561	22664	204	68
CONTIG2988	23839125_f3_7	8562	22665	249	83
CONTIG299	7284530_f1_1	8563	22666	213	71
CONTIG2990	1300932_f1_1	8564	22667	282	94
CONTIG2990	5906703_f2_2	8565	22668	279	93
CONTIG2990	25424125_f3_5	8566	22669	312	104
CONTIG2990	35204693_c2_6	8567	22670	198	66
CONTIG2990	1992328_c3_7	8568	22671	234	78
CONTIG2990	3939077_c3_8	8569	22672	228	76
CONTIG2991	23947261_f2_1	8570	22673	240	80
CONTIG2992	32210786_f2_2	8571	22674	189	63
CONTIG2992	23647307_c1_5	8572	22675	249	83
CONTIG2993	32675341_f3_3	8573	22676	498	166

CONTIG2993	4103827_f3_4	8574	22677	195	65
CONTIG2995	16000_f1_3	8575	22678	192	64
CONTIG2995	2929807_f1_4	8576	22679	249	83
CONTIG2996	23917257_c1_3	8577	22680	219	73
CONTIG2996	1362688_c1_4	8578	22681	252	84
CONTIG2996	36531550_c2_5	8579	22682	234	78
CONTIG2997	6103387_c1_2	8580	22683	237	79
CONTIG2999	22447212_f1_1	8581	22684	219	73
CONTIG2999	24800812_f2_2	8582	22685	225	75
CONTIG2999	5975282_f2_3	8583	22686	249	83
CONTIG2999	23601011_c1_4	8584	22687	198	66
CONTIG3	2375055_c2_1	8585	22688	213	71
CONTIG3	24648377_c3_2	8586	22689	261	87
CONTIG30	30662635_f1_1	8587	22690	222	74
CONTIG30	22365931_f3_2	8588	22691	219	73
CONTIG300	23634450_f2_1	8589	22692	198	66
CONTIG300	6250305_f3_2	8590	22693	222	74
CONTIG3000	11756316_f2_3	8591	22694	324	108
CONTIG3002	3985000_f3_4	8592	22695	708	236
CONTIG3003	6062758_c2_5	8593	22696	228	76
CONTIG3005	1381432_f1_1	8594	22697	195	65
CONTIG3005	4742252_f3_3	8595	22698	219	73
CONTIG3005	24390687_c3_5	8596	22699	276	92
CONTIG3005	10976587_c3_6	8597	22700	189	63
CONTIG3006	19735277_f2_1	8598	22701	294	98
CONTIG301	22457938_c1_3	8599	22702	189	63
CONTIG3010	29461081_c1_6	8600	22703	225	75
CONTIG3011	22692256_c2_7	8601	22704	183	61
CONTIG3011	24025012_c3_9	8602	22705	237	79
CONTIG3013	35176650_f1_2	8603	22706	192	64
CONTIG3013	6897215_f3_6	8604	22707	603	201
CONTIG3019	23995252_c3_4	8605	22708	225	75
CONTIG302	2051426_c3_2	8606	22709	210	70

CONTIG3021	10578430_c3_4	8607	22710	553
CONTIG3022	437692_f1_1	8608	22711	84
CONTIG3022	5084625_f3_5	8609	22712	67
CONTIG3022	32226562_c1_7	8610	22713	66
CONTIG3022	55312_c2_8	8611	22714	100
CONTIG3022	25864057_c3_10	8612	22715	222
CONTIG3023	8632_c1_2	8613	22716	98
CONTIG3024	4742901_f1_1	8614	22717	195
CONTIG3027	6814056_c1_2	8615	22718	78
CONTIG303	194425_f3_1	8616	22719	84
CONTIG303	4096875_c3_2	8617	22720	150
CONTIG3030	16207711_f2_2	8618	22721	80
CONTIG3030	2506875_c3_6	8619	22722	109
CONTIG3031	10282513_c1_4	8620	22723	68
CONTIG3031	10350631_c2_7	8621	22724	62
CONTIG3031	14229192_c3_8	8622	22725	76
CONTIG3031	2366639_c3_9	8623	22726	74
CONTIG3032	36054562_f1_1	8624	22727	74
CONTIG3032	1984842_f2_2	8625	22728	272
CONTIG3035	24617250_f1_1	8626	22729	95
CONTIG3038	4298338_c3_4	8627	22730	145
CONTIG3040	35818775_c2_4	8628	22731	83
CONTIG3040	21775688_f1_1	8629	22732	68
CONTIG3041	24414043_c2_7	8630	22733	72
CONTIG3041	10640632_c2_1	8631	22734	83
CONTIG3042	36617200_c2_2	8632	22735	65
CONTIG3043	12126285_c2_11	8633	22736	192
CONTIG3045	25426255_f2_3	8634	22737	83
CONTIG3045	12301536_c3_6	8635	22738	64
CONTIG3046	34095336_f1_3	8636	22739	72
CONTIG3046	2535878_f1_4	8637	22740	68
CONTIG3046	23626503_f3_6	8638	22741	68
CONTIG3046	14640932_f3_8	8639	22742	100

CONTIG3047	6829525_c2_1	8640	22743	222	74
CONTIG3049	22439007_f2_1	8641	22744	765	255
CONTIG305	26348442_c3_1	8642	22745	186	62
CONTIG3050	4098385_c1_4	8643	22746	285	95
CONTIG3050	24406932_c3_6	8644	22747	225	75
CONTIG3050	195127_c3_7	8645	22748	720	240
CONTIG3053	157763_f2_3	8646	22749	195	65
CONTIG3053	24414688_c2_4	8647	22750	192	64
CONTIG3053	22036662_c2_6	8648	22751	183	61
CONTIG3056	19554788_f1_1	8649	22752	234	78
CONTIG3058	25425767_c2_5	8650	22753	207	69
CONTIG3059	4725262_f3_5	8651	22754	222	74
CONTIG3059	32110067_c1_6	8652	22755	195	65
CONTIG306	16054712_c1_1	8653	22756	426	142
CONTIG3060	32084755_f1_1	8654	22757	201	67
CONTIG3061	23547130_f3_3	8655	22758	195	65
CONTIG3062	36601712_f1_1	8656	22759	228	76
CONTIG3063	22066556_c3_7	8657	22760	234	78
CONTIG3068	14143767_f2_2	8658	22761	891	297
CONTIG307	36042515_f3_2	8659	22762	192	64
CONTIG3071	19687627_f3_2	8660	22763	189	63
CONTIG3072	10054562_c1_5	8661	22764	225	75
CONTIG3076	6094191_c1_2	8662	22765	204	68
CONTIG3076	35166002_c3_4	8663	22766	186	62
CONTIG3078	974038_f2_3	8664	22767	189	63
CONTIG3078	14453405_c3_7	8665	22768	294	98
CONTIG3080	31281306_c3_7	8666	22769	255	85
CONTIG3083	10833567_f1_1	8667	22770	207	69
CONTIG3083	272877_f1_2	8668	22771	744	248
CONTIG3083	16291703_c2_6	8669	22772	621	207
CONTIG3085	4062750_c1_3	8670	22773	261	87
CONTIG3086	14554750_c3_8	8671	22774	246	82
CONTIG3087	22273425_f1_1	8672	22775	222	74

CONTIG3087	26187963_f2_2	8673	22776	249	83
CONTIG309	21679640_c3_2	8674	22777	216	72
CONTIG3090	1298316_f1_1	8675	22778	780	260
CONTIG3092	1198276_f1_1	8676	22779	204	68
CONTIG3092	12691937_c1_4	8677	22780	207	69
CONTIG3092	23913888_c2_6	8678	22781	255	85
CONTIG3093	20709712_f1_2	8679	22782	255	85
CONTIG3094	24413312_f1_1	8680	22783	186	62
CONTIG3094	22832952_f1_2	8681	22784	1008	336
CONTIG3095	3165813_f2_5	8682	22785	399	133
CONTIG3095	433332_f3_3	8683	22786	1032	344
CONTIG3097	13679590_c3_4	8684	22787	237	79
CONTIG3098	25397150_f3_2	8685	22788	234	78
CONTIG3099	23600427_f3_5	8686	22789	528	176
CONTIG3099	22363281_c2_6	8687	22790	240	80
CONTIG310	11173430_f3_1	8688	22791	231	77
CONTIG3102	4535066_c2_2	8689	22792	222	74
CONTIG3104	4460881_f1_2	8690	22793	186	62
CONTIG3104	1074012_f3_5	8691	22794	426	142
CONTIG3105	4097008_f3_6	8692	22795	324	108
CONTIG3106	26290938_f1_2	8693	22796	195	65
CONTIG3106	29688750_c1_9	8694	22797	369	123
CONTIG3108	12694102_f1_1	8695	22798	489	163
CONTIG3108	4535066_f1_2	8696	22799	243	81
CONTIG3108	9769002_f1_3	8697	22800	213	71
CONTIG3108	6642006_f3_4	8698	22801	201	67
CONTIG3109	24019686_f3_2	8699	22802	465	155
CONTIG3109	10831387_c3_5	8700	22803	474	158
CONTIG311	20507192_c1_2	8701	22804	189	63
CONTIG3110	34163962_f2_3	8702	22805	477	159
CONTIG3110	156250_f3_6	8703	22806	213	71
CONTIG3111	21914206_f1_1	8704	22807	186	62
CONTIG3112	4955080_c3_5	8705	22808	591	197

CONTIG3113	13789032_f3_2	8706	22809	891	297
CONTIG3115	957502_f2_1	8707	22810	201	67
CONTIG3116	15784441_f3_3	8708	22811	384	128
CONTIG3117	16797136_c3_8	8709	22812	603	201
CONTIG3118	33714388_c2_2	8710	22813	201	67
CONTIG3120	25423202_c3_2	8711	22814	576	192
CONTIG3121	3939385_f1_1	8712	22815	321	107
CONTIG3121	9788937_f3_9	8713	22816	300	100
CONTIG3121	24426692_f3_10	8714	22817	279	93
CONTIG3121	4801436_f3_11	8715	22818	858	286
CONTIG3121	4957928_c3_13	8716	22819	285	95
CONTIG3123	2166652_f1_1	8717	22820	543	181
CONTIG3123	24431642_f2_2	8718	22821	210	70
CONTIG3123	7047512_c3_5	8719	22822	213	71
CONTIG3124	1260062_c2_5	8720	22823	1461	487
CONTIG3125	36040788_f3_3	8721	22824	312	104
CONTIG3125	19542550_c3_9	8722	22825	183	61
CONTIG3126	10976527_f1_1	8723	22826	636	212
CONTIG3127	6741260_f3_1	8724	22827	225	75
CONTIG3128	10000313_c3_3	8725	22828	576	192
CONTIG3130	22657162_f2_2	8726	22829	195	65
CONTIG3130	547010_c1_3	8727	22830	198	66
CONTIG3130	24220001_c3_6	8728	22831	324	108
CONTIG3131	2915892_f2_2	8729	22832	219	73
CONTIG3131	31901952_c3_3	8730	22833	192	64
CONTIG3134	23452281_f2_2	8731	22834	1068	356
CONTIG3134	24650130_f3_3	8732	22835	264	88
CONTIG3134	24332176_c1_5	8733	22836	195	65
CONTIG3137	16253840_c3_6	8734	22837	1320	440
CONTIG3138	26600777_f2_1	8735	22838	186	62
CONTIG3139	12516512_f3_3	8736	22839	204	68
CONTIG314	35422253_f2_1	8737	22840	234	78
CONTIG314	15709636_f2_2	8738	22841	222	74

CONTIG3141	116300_c2_6	8739	22842	282	94
CONTIG3142	15100027_c1_4	8740	22843	384	128
CONTIG3146	22661076_f2_1	8741	22844	258	86
CONTIG3146	29478785_c1_2	8742	22845	240	80
CONTIG3146	34180300_c2_3	8743	22846	243	81
CONTIG3147	5937512_f3_5	8744	22847	195	65
CONTIG3148	2597817_c2_6	8745	22848	279	93
CONTIG3148	3937761_c3_7	8746	22849	303	101
CONTIG3149	16620305_f3_1	8747	22850	249	83
CONTIG315	16803817_c2_1	8748	22851	186	62
CONTIG3150	19729640_f2_2	8749	22852	318	106
CONTIG3150	13006503_f2_3	8750	22853	186	62
CONTIG3150	22828136_f3_4	8751	22854	264	88
CONTIG3150	20329638_c3_8	8752	22855	195	65
CONTIG3150	24238593_c3_7	8753	22856	207	69
CONTIG3150	4459705_c2_6	8754	22857	195	65
CONTIG3151	23476718_c3_9	8755	22858	636	212
CONTIG3151	21643775_f1_1	8756	22859	189	63
CONTIG3152	4687950_c3_4	8757	22860	219	73
CONTIG3153	1067693_f1_1	8758	22861	342	114
CONTIG3154	26351686_f1_2	8759	22862	210	70
CONTIG3154	6742042_c1_3	8760	22863	240	80
CONTIG3155	23944152_f2_3	8761	22864	186	62
CONTIG3155	562760_c2_4	8762	22865	192	64
CONTIG3156	2929542_c2_4	8763	22866	225	75
CONTIG3157	14648442_c2_6	8764	22867	408	136
CONTIG3157	9945932_c3_7	8765	22868	204	68
CONTIG3158	29539510_f1_1	8766	22869	264	88
CONTIG3158	838575_f2_3	8767	22870	267	89
CONTIG3158	10938377_f3_5	8768	22871	195	65
CONTIG316	16803817_f3_5	8769	22872	186	62
CONTIG3160	16806392_f1_1	8770	22873	201	67
CONTIG3160	13961557_f1_2	8771	22874	285	95

CONTIG3161	24492187_c3_3	8772	22875	318	106
CONTIG3162	821090_f1_1	8773	22876	588	196
CONTIG3162	4019631_f2_2	8774	22877	339	113
CONTIG3162	24220316_c3_3	8775	22878	201	67
CONTIG3164	4115680_c3_6	8776	22879	354	118
CONTIG3165	33397581_c2_1	8777	22880	2001	667
CONTIG3167	26646887_c2_6	8778	22881	279	93
CONTIG317	5320152_c1_2	8779	22882	183	61
CONTIG3170	24392556_f3_1	8780	22883	216	72
CONTIG3172	1382778_f3_3	8781	22884	240	80
CONTIG3172	23625830_c1_6	8782	22885	186	62
CONTIG3174	22461562_f3_1	8783	22886	219	73
CONTIG3175	24492135_f3_2	8784	22887	225	75
CONTIG3176	35392200_c3_5	8785	22888	444	148
CONTIG3180	14629655_c1_7	8786	22889	228	76
CONTIG3180	4808507_c1_8	8787	22890	270	90
CONTIG3180	26283378_c3_16	8788	22891	255	85
CONTIG3181	4790962_c1_4	8789	22892	471	157
CONTIG3182	7314050_f3_4	8790	22893	321	107
CONTIG3184	24334687_c2_8	8791	22894	192	64
CONTIG3185	20409687_f2_2	8792	22895	267	89
CONTIG3185	3142175_c1_3	8793	22896	309	103
CONTIG3185	3937533_c3_5	8794	22897	189	63
CONTIG3186	12937788_f3_1	8795	22898	237	79
CONTIG3187	26213875_f3_4	8796	22899	240	80
CONTIG3188	24494127_f1_1	8797	22900	567	189
CONTIG3188	14941002_f2_2	8798	22901	570	190
CONTIG319	41666651_f3_1	8799	22902	288	96
CONTIG3190	9928753_c1_6	8800	22903	396	132
CONTIG3193	2988902_c3_8	8801	22904	591	197
CONTIG3194	782535_f1_2	8802	22905	222	74
CONTIG3195	22117162_c3_1	8803	22906	243	81
CONTIG3196	22461063_c1_6	8804	22907	234	78

CONTIG3199	34406700_f1_1	8805	22908	186	62
CONTIG3199	2820377_f1_2	8806	22909	234	78
CONTIG3199	25942308_c2_8	8807	22910	693	231
CONTIG32	22948767_f1_1	8808	22911	270	90
CONTIG3200	3990763_f2_3	8809	22912	327	109
CONTIG3200	1051967_f2_1	8810	22913	363	121
CONTIG3201	26376078_c3_9	8811	22914	438	146
CONTIG3202	25397187_f3_1	8812	22915	225	75
CONTIG3203	14223750_c1_2	8813	22916	1152	384
CONTIG3203	34179756_c3_3	8814	22917	210	70
CONTIG3204	33461626_c3_5	8815	22918	204	68
CONTIG3209	29488537_f3_2	8816	22919	213	71
CONTIG3211	4297215_c1_7	8817	22920	1485	495
CONTIG3212	24789037_f3_3	8818	22921	285	95
CONTIG3213	16053375_c1_2	8819	22922	252	84
CONTIG3218	6647762_c1_5	8820	22923	222	74
CONTIG3218	26755280_c1_7	8821	22924	435	145
CONTIG3218	36448452_c2_8	8822	22925	201	67
CONTIG3219	25395662_f1_1	8823	22926	201	67
CONTIG3219	10031510_c3_8	8824	22927	585	195
CONTIG322	14564567_f2_1	8825	22928	714	238
CONTIG3220	24015680_c2_4	8826	22929	231	77
CONTIG3222	26822293_f3_7	8827	22930	201	67
CONTIG3222	34198462_c3_11	8828	22931	354	118
CONTIG3225	5993802_f3_2	8829	22932	240	80
CONTIG3227	1019096_c1_3	8830	22933	240	80
CONTIG3227	23603463_c2_7	8831	22934	225	75
CONTIG3228	1441332_f1_1	8832	22935	288	96
CONTIG3228	3956537_f1_2	8833	22936	267	89
CONTIG3229	31295207_c3_7	8834	22937	207	69
CONTIG3230	25423885_f1_1	8835	22938	312	104
CONTIG3230	157500_f1_2	8836	22939	525	175
CONTIG3230	4692152_f2_3	8837	22940	237	79

CONTIG3230	594175_f3_4	8838	22941	246	82
CONTIG3230	29533140_c3_6	8839	22942	324	108
CONTIG3231	22657635_f1_1	8840	22943	720	240
CONTIG3235	25556255_c3_4	8841	22944	189	63
CONTIG3235	30707575_c3_5	8842	22945	183	61
CONTIG3237	21618957_f1_1	8843	22946	309	103
CONTIG3238	24490927_f2_2	8844	22947	225	75
CONTIG3238	16209750_f3_3	8845	22948	189	63
CONTIG3239	34664018_f2_3	8846	22949	186	62
CONTIG3240	34033450_f2_2	8847	22950	201	67
CONTIG3240	34572068_f2_3	8848	22951	201	67
CONTIG3240	34064378_f3_4	8849	22952	261	87
CONTIG3240	6645012_c2_6	8850	22953	204	68
CONTIG3240	2132807_c3_7	8851	22954	492	164
CONTIG3242	9944505_f3_2	8852	22955	648	216
CONTIG3243	6048402_c2_3	8853	22956	279	93
CONTIG3244	22308161_f1_1	8854	22957	567	189
CONTIG3246	20444002_f3_1	8855	22958	210	70
CONTIG3247	25938966_f3_1	8856	22959	354	118
CONTIG3247	14586580_f3_2	8857	22960	309	103
CONTIG3248	4818878_c2_6	8858	22961	669	223
CONTIG3249	24804681_f2_2	8859	22962	219	73
CONTIG325	24098875_f3_2	8860	22963	519	173
CONTIG3250	1456275_f1_1	8861	22964	204	68
CONTIG3250	33994057_c1_3	8862	22965	378	126
CONTIG3250	4192163_c2_5	8863	22966	264	88
CONTIG3251	24070342_f2_2	8864	22967	183	61
CONTIG3252	20489501_c1_5	8865	22968	201	67
CONTIG3253	26366262_c3_6	8866	22969	231	77
CONTIG3254	393760_f1_1	8867	22970	201	67
CONTIG3255	13867937_c2_4	8868	22971	744	248
CONTIG3256	1204643_f3_3	8869	22972	216	72
CONTIG3259	24324062_c2_6	8870	22973	717	239

CONTIG3259	26209702_c3_7	8871	22974	291	97
CONTIG3260	34620313_f2_1	8872	22975	186	62
CONTIG3261	995381l_c1_3	8873	22976	453	151
CONTIG3261	23562885_c3_5	8874	22977	288	96
CONTIG3262	243830_f1_3	8875	22978	201	67
CONTIG3263	14221962_f3_1	8876	22979	204	68
CONTIG3264	3365937_c2_5	8877	22980	1683	561
CONTIG3266	3126912_c1_1	8878	22981	225	75
CONTIG3266	6760300_c1_3	8879	22982	252	84
CONTIG3268	32205055_c2_6	8880	22983	207	69
CONTIG3270	24095687_f1_1	8881	22984	519	173
CONTIG3270	26253563_f3_3	8882	22985	333	111
CONTIG3270	26564010_c2_6	8883	22986	753	251
CONTIG3271	10751637_f1_1	8884	22987	189	63
CONTIG3271	14859680_f2_2	8885	22988	1149	383
CONTIG3272	35585312_c2_3	8886	22989	183	61
CONTIG3272	4875002_c2_4	8887	22990	183	61
CONTIG3272	32227312_c3_5	8888	22991	222	74
CONTIG3274	9765636_f3_5	8889	22992	288	96
CONTIG3276	6755465_f3_2	8890	22993	1707	569
CONTIG3278	4394531_f1_1	8891	22994	192	64
CONTIG3278	1179042_c3_5	8892	22995	192	64
CONTIG3279	20520311_f3_3	8893	22996	195	65
CONTIG3280	13945257_f3_5	8894	22997	183	61
CONTIG3281	4453762_f3_3	8895	22998	243	81
CONTIG3281	820131_f2_4	8896	22999	1170	390
CONTIG3282	7866225_c1_6	8897	23000	204	68
CONTIG3282	15038911_c1_7	8898	23001	231	77
CONTIG3284	22113827_f1_1	8899	23002	186	62
CONTIG3285	29501677_f2_3	8900	23003	216	72
CONTIG3285	5969017_c2_6	8901	23004	201	67
CONTIG3285	22928518_c3_8	8902	23005	183	61
CONTIG3286	35360256_f1_2	8903	23006	192	64

CONTIG3286	19689125_f1_3	8904	23007	396	132
CONTIG3286	4532817_f3_4	8905	23008	228	76
CONTIG3288	822135_c1_1	8906	23009	1107	369
CONTIG3288	819436_c3_3	8907	23010	210	70
CONTIG3290	6835887_c3_3	8908	23011	1176	392
CONTIG3291	4116658_f2_2	8909	23012	339	113
CONTIG3293	1346910_f2_1	8910	23013	1680	560
CONTIG3294	9885830_f3_2	8911	23014	279	93
CONTIG3296	391925_c2_7	8912	23015	189	63
CONTIG3297	24801063_c1_7	8913	23016	279	93
CONTIG3298	1409657_c2_2	8914	23017	879	293
CONTIG3299	30089638_f3_3	8915	23018	183	61
CONTIG3300	4711937_c1_6	8916	23019	240	80
CONTIG3301	4142508_c3_3	8917	23020	861	287
CONTIG3303	22900762_f1_1	8918	23021	201	67
CONTIG3303	5972127_f2_3	8919	23022	228	76
CONTIG3305	35429578_f3_4	8920	23023	354	118
CONTIG3305	4711657_c3_10	8921	23024	210	70
CONTIG3306	3306375_c1_3	8922	23025	213	71
CONTIG3307	25423561_c1_4	8923	23026	2064	688
CONTIG3309	23494793_f2_1	8924	23027	228	76
CONTIG331	16970461_c3_1	8925	23028	585	195
CONTIG3310	35156540_c2_6	8926	23029	357	119
CONTIG3311	29688750_f3_6	8927	23030	369	123
CONTIG3313	58557_c1_8	8928	23031	216	72
CONTIG3314	960336_f1_1	8929	23032	201	67
CONTIG3314	26365927_c1_6	8930	23033	234	78
CONTIG3314	4189077_c2_10	8931	23034	1188	396
CONTIG3316	30556530_c1_2	8932	23035	702	234
CONTIG3317	3611013_f1_1	8933	23036	201	67
CONTIG3317	33859576_f3_5	8934	23037	267	89
CONTIG3318	792137_f3_4	8935	23038	387	129
CONTIG3319	6735133_f2_1	8936	23039	1386	462

CONTIG332	10830193_f1_1	8937	23040	303	101
CONTIG3320	29558215_c3_5	8938	23041	225	75
CONTIG3321	6834385_f1_2	8939	23042	204	68
CONTIG3321	11727325_c1_3	8940	23043	207	69
CONTIG3322	1990652_f2_2	8941	23044	216	72
CONTIG3324	35948255_c2_5	8942	23045	186	62
CONTIG3325	1368832_f1_1	8943	23046	390	130
CONTIG3325	31343892_f1_2	8944	23047	204	68
CONTIG3325	13861555_f2_5	8945	23048	204	68
CONTIG3325	34173155_f2_6	8946	23049	336	112
CONTIG3326	23440840_f1_1	8947	23050	252	84
CONTIG3326	9970428_f2_2	8948	23051	198	66
CONTIG3326	16444452_f2_4	8949	23052	186	62
CONTIG3327	33502750_f1_1	8950	23053	984	328
CONTIG3328	23672193_f1_1	8951	23054	246	82
CONTIG3329	1288452_c3_5	8952	23055	759	253
CONTIG3331	391257_f1_1	8953	23056	273	91
CONTIG3331	13832790_f1_2	8954	23057	201	67
CONTIG3331	2033207_c3_5	8955	23058	192	64
CONTIG3331	6681326_c3_6	8956	23059	498	166
CONTIG3332	4745462_f2_2	8957	23060	198	66
CONTIG3332	26382942_c3_8	8958	23061	228	76
CONTIG3334	19645050_f3_2	8959	23062	210	70
CONTIG3336	24648432_c1_2	8960	23063	561	187
CONTIG3336	80377_c3_5	8961	23064	318	106
CONTIG3337	5867277_f1_1	8962	23065	480	160
CONTIG3337	4304650_f3_3	8963	23066	351	117
CONTIG3338	14250285_f2_1	8964	23067	1185	395
CONTIG3338	4336556_f3_2	8965	23068	1662	554
CONTIG3338	4094052_c1_3	8966	23069	264	88
CONTIG3338	9970678_c3_5	8967	23070	255	85
CONTIG3339	24022257_f2_2	8968	23071	456	152
CONTIG3341	804686_c1_3	8969	23072	495	165

CONTIG3342	14537901_c3_9	8970	23073	333	111
CONTIG3343	157790_f1_1	8971	23074	648	216
CONTIG3344	35322153_c1_2	8972	23075	207	69
CONTIG3344	25398442_f2_2	8973	23076	186	62
CONTIG3346	582800_c3_4	8974	23077	267	89
CONTIG3347	14640812_f3_5	8975	23078	189	63
CONTIG3347	16525262_f3_6	8976	23079	1269	423
CONTIG3350	23906392_f1_2	8977	23080	267	89
CONTIG3350	4413436_f2_4	8978	23081	432	144
CONTIG3350	23476002_f3_5	8979	23082	186	62
CONTIG3350	4172517_c1_7	8980	23083	192	64
CONTIG3350	39805_c3_8	8981	23084	186	62
CONTIG3351	24408432_c3_4	8982	23085	195	65
CONTIG3351	813875_c3_5	8983	23086	195	65
CONTIG3352	49976_c3_4	8984	23087	507	169
CONTIG3354	4703876_f3_5	8985	23088	186	62
CONTIG3355	23989186_c1_2	8986	23089	858	286
CONTIG3356	17311_c2_6	8987	23090	1743	581
CONTIG3357	6851688_c3_5	8988	23091	246	82
CONTIG3358	35422942_c3_4	8989	23092	1239	413
CONTIG3359	36621096_c3_10	8990	23093	1065	355
CONTIG3360	35159378_f3_4	8991	23094	672	224
CONTIG3361	12377337_c1_3	8992	23095	186	62
CONTIG3362	23469553_f3_6	8993	23096	618	206
CONTIG3362	19625163_c1_7	8994	23097	1158	386
CONTIG3363	1250_f3_8	8995	23098	183	61
CONTIG3363	1406282_f3_9	8996	23099	207	69
CONTIG3365	7062827_c1_1	8997	23100	282	94
CONTIG3365	24399056_c3_2	8998	23101	255	85
CONTIG3365	12540877_c3_4	8999	23102	210	70
CONTIG3366	10351064_c1_4	9000	23103	234	78
CONTIG3366	7226387_c3_8	9001	23104	195	65
CONTIG3367	23675265_f3_6	9002	23105	240	80

CONTIG3368	14727287_c2_4	9003	23106	660	220
CONTIG3369	2391916_f2_2	9004	23107	234	78
CONTIG337	13065655_f3_1	9005	23108	210	70
CONTIG337	526877_c3_5	9006	23109	192	64
CONTIG3370	24782752_f3_5	9007	23110	219	73
CONTIG3371	250692_c3_7	9008	23111	186	62
CONTIG3372	812635_c1_6	9009	23112	195	65
CONTIG3372	23714028_c1_7	9010	23113	231	77
CONTIG3373	2376403_c3_9	9011	23114	213	71
CONTIG3372	14069386_f2_2	9012	23115	321	107
CONTIG3376	26765750_c2_3	9013	23116	345	115
CONTIG3376	4334427_c3_7	9014	23117	246	82
CONTIG3378	20526382_f3_2	9015	23118	1659	553
CONTIG3378	19570952_c1_3	9016	23119	291	97
CONTIG3379	1569430_f3_3	9017	23120	219	73
CONTIG338	6432_f2_2	9018	23121	363	121
CONTIG3380	187957_f2_2	9019	23122	192	64
CONTIG3382	25595387_c3_7	9020	23123	222	74
CONTIG3383	4351532_c1_3	9021	23124	396	132
CONTIG3389	13725137_f2_1	9022	23125	384	128
CONTIG339	4307625_c2_2	9023	23126	189	63
CONTIG3391	21676562_f1_1	9024	23127	249	83
CONTIG3391	36119552_f2_3	9025	23128	204	68
CONTIG3391	16101501_f3_4	9026	23129	201	67
CONTIG3392	1203126_f1_1	9027	23130	222	74
CONTIG3392	26445257_f3_3	9028	23131	1413	471
CONTIG3394	5890877_f2_3	9029	23132	336	112
CONTIG3394	23472552_f2_4	9030	23133	186	62
CONTIG3394	3177_f2_5	9031	23134	297	99
CONTIG3395	24316530_f3_3	9032	23135	231	77
CONTIG3395	2531627_c2_7	9033	23136	255	85
CONTIG3396	6048182_f1_1	9034	23137	1908	636
CONTIG3397	12931313_f1_2	9035	23138	498	166

CONTIG3398	23828567_f1_1	9036	23139	327	109
CONTIG3398	29734633_f3_3	9037	23140	900	300
CONTIG3398	788942_c2_5	9038	23141	639	213
CONTIG3398	10196877_c3_6	9039	23142	660	220
CONTIG3399	20949127_c1_4	9040	23143	336	112
CONTIG34	22366577_c1_2	9041	23144	522	174
CONTIG340	24417203_f1_1	9042	23145	240	80
CONTIG340	4789632_f2_2	9043	23146	186	62
CONTIG3400	33781562_c2_6	9044	23147	204	68
CONTIG3400	5878125_c3_9	9045	23148	192	64
CONTIG3401	4885913_f1_1	9046	23149	216	72
CONTIG3401	22343762_c2_4	9047	23150	186	62
CONTIG3402	21493932_f2_4	9048	23151	477	159
CONTIG3404	24252186_f3_2	9049	23152	237	79
CONTIG3405	15820262_f3_4	9050	23153	246	82
CONTIG3406	5116262_f3_4	9051	23154	192	64
CONTIG3406	25423406_c2_8	9052	23155	201	67
CONTIG3408	23673450_c1_7	9053	23156	195	65
CONTIG3409	4531507_c2_3	9054	23157	558	186
CONTIG3410	25547932_f1_1	9055	23158	324	108
CONTIG3410	24503192_f3_7	9056	23159	279	93
CONTIG3410	21663135_c3_13	9057	23160	186	62
CONTIG3411	813762_f1_1	9058	23161	219	73
CONTIG3411	23945132_c1_6	9059	23162	279	93
CONTIG3412	1385813_f2_2	9060	23163	264	88
CONTIG3414	23866411_f1_1	9061	23164	402	134
CONTIG3414	17040877_f2_2	9062	23165	186	62
CONTIG3414	24885965_c1_8	9063	23166	333	111
CONTIG3416	35718762_c2_9	9064	23167	201	67
CONTIG3417	21761015_f1_1	9065	23168	252	84
CONTIG3417	16906915_f3_2	9066	23169	192	64
CONTIG3417	29866292_c3_5	9067	23170	198	66
CONTIG3418	235265_c3_3	9068	23171	294	98

CONTIG3419	33252018_f2_3	9069	23172	189	63
CONTIG3419	4303531_f2_4	9070	23173	339	113
CONTIG3420	35255176_c1_3	9071	23174	186	62
CONTIG3422	23479566_f3_2	9072	23175	264	88
CONTIG3423	29736250_f1_1	9073	23176	222	74
CONTIG3423	5270436_c1_6	9074	23177	189	63
CONTIG3423	33395312_c3_8	9075	23178	216	72
CONTIG3424	24491061_c2_4	9076	23179	192	64
CONTIG343	1375 0317_f1_1	9077	23180	495	165
CONTIG343	4176678_c2_4	9078	23181	285	95
CONTIG3431	54775_c1_2	9079	23182	1170	390
CONTIG3431	4100817_c3_4	9080	23183	198	66
CONTIG3431	898261_c3_5	9081	23184	255	85
CONTIG3432	24414056_c1_10	9082	23185	204	68
CONTIG3433	2913930_f2_1	9083	23186	219	73
CONTIG3435	25469653_c3_2	9084	23187	1671	557
CONTIG3436	35162837_c1_5	9085	23188	192	64
CONTIG3436	34022717_c1_6	9086	23189	279	93
CONTIG3438	7057025_f2_1	9087	23190	561	187
CONTIG344	10196957_f3_1	9088	23191	321	107
CONTIG3440	14742187_c3_10	9089	23192	732	244
CONTIG3442	19533312_c1_4	9090	23193	183	61
CONTIG3442	1993 7876_c3_5	9091	23194	489	163
CONTIG3443	14878436_c3_4	9092	23195	309	103
CONTIG3444	12212777_f1_2	9093	23196	228	76
CONTIG3444	6050717_f3_5	9094	23197	942	314
CONTIG3445	10828550_f3_2	9095	23198	282	94
CONTIG3447	25993837_f1_1	9096	23199	336	112
CONTIG3447	3132692_f2_2	9097	23200	2100	700
CONTIG3447	6814078_f3_7	9098	23201	726	242
CONTIG3449	34464410_c3_1	9099	23202	333	111
CONTIG3450	24507276_c1_3	9100	23203	891	297
CONTIG3452	1446050_c1_5	9101	23204	621	207

CONTIG3454	32537662_f1_1	9102	23205	195	65
CONTIG3454	4882811_f2_3	9103	23206	255	85
CONTIG3454	19734441_c1_5	9104	23207	195	65
CONTIG3455	22664567_c2_5	9105	23208	1326	442
CONTIG3457	4095313_f2_5	9106	23209	528	176
CONTIG3457	1463912_c1_11	9107	23210	780	260
CONTIG3458	21881592_c1_8	9108	23211	585	195
CONTIG3461	22946885_f1_1	9109	23212	192	64
CONTIG3461	970327_c3_13	9110	23213	504	168
CONTIG3464	32664032_f2_2	9111	23214	189	63
CONTIG3464	23469050_f3_3	9112	23215	222	74
CONTIG3464	10978462_c2_7	9113	23216	756	252
CONTIG3466	29454825_c2_2	9114	23217	231	77
CONTIG3467	34385313_f3_1	9115	23218	219	73
CONTIG3467	1381257_c3_4	9116	23219	237	79
CONTIG3468	444135_c2_7	9117	23220	186	62
CONTIG3468	9800817_c3_8	9118	23221	195	65
CONTIG3469	21687825_f3_3	9119	23222	198	66
CONTIG3470	4895010_c2_6	9120	23223	330	110
CONTIG3471	22554712_f3_3	9121	23224	201	67
CONTIG3473	16595900_c2_4	9122	23225	903	301
CONTIG3476	398502_f1_2	9123	23226	249	83
CONTIG3476	4312510_f2_3	9124	23227	201	67
CONTIG3476	25425651_f2_5	9125	23228	891	297
CONTIG3476	16039665_c3_7	9126	23229	186	62
CONTIG3477	5941937_f1_1	9127	23230	186	62
CONTIG3479	4298302_c2_9	9128	23231	225	75
CONTIG348	21675277_f3_3	9129	23232	258	86
CONTIG3481	33398535_f2_3	9130	23233	234	78
CONTIG3481	5194640_c1_4	9131	23234	600	200
CONTIG3481	9843750_c3_6	9132	23235	669	223
CONTIG3483	10970305_f2_2	9133	23236	1149	383
CONTIG3484	16446961_f1_1	9134	23237	204	68

CONTIG3484	4882826_f1_2	9135	23238	186	62
CONTIG3484	4901577_f2_4	9136	23239	195	65
CONTIG3484	23953550_c1_5	9137	23240	201	67
CONTIG3484	26564212_c3_8	9138	23241	201	67
CONTIG3485	3322163_c2_3	9139	23242	894	298
CONTIG3487	400075_f2_2	9140	23243	213	71
CONTIG3487	31453450_f3_3	9141	23244	240	80
CONTIG3488	3989050_f2_2	9142	23245	183	61
CONTIG3488	1964127_c3_5	9143	23246	219	73
CONTIG3489	23928375_f3_3	9144	23247	231	77
CONTIG3490	567311_f1_2	9145	23248	309	103
CONTIG3492	12110777_f1_1	9146	23249	237	79
CONTIG3492	24709461_f3_5	9147	23250	396	132
CONTIG3492	1353153_c2_6	9148	23251	210	70
CONTIG3493	5861062_f2_1	9149	23252	288	96
CONTIG3493	14625252_c3_6	9150	23253	207	69
CONTIG3494	23454702_f1_3	9151	23254	213	71
CONTIG3494	29507800_f2_4	9152	23255	1167	389
CONTIG3494	29879715_f2_5	9153	23256	264	88
CONTIG3495	13941876_f1_2	9154	23257	660	220
CONTIG3495	5319205_f2_3	9155	23258	243	81
CONTIG3495	1677042_c2_6	9156	23259	186	62
CONTIG3496	5985880_c3_6	9157	23260	198	66
CONTIG3497	24901562_f3_4	9158	23261	189	63
CONTIG3497	9939775_f3_5	9159	23262	231	77
CONTIG3498	6831590_c2_10	9160	23263	720	240
CONTIG350	14735908_f3_1	9161	23264	219	73
CONTIG3500	42192_c1_9	9162	23265	219	73
CONTIG3500	25679637_c1_10	9163	23266	264	88
CONTIG3500	5080392_c3_15	9164	23267	192	64
CONTIG3501	1260_c2_4	9165	23268	216	72
CONTIG3501	26751507_c3_5	9166	23269	267	89
CONTIG3502	16179038_f1_1	9167	23270	534	178

CONTIG3502	29410688_f3_2	9168	23271	363	121
CONTIG3502	15647802_c2_4	9169	23272	306	102
CONTIG3502	20600755_c3_5	9170	23273	255	85
CONTIG3502	31251510_c3_6	9171	23274	237	79
CONTIG3503	1178175_f2_2	9172	23275	243	81
CONTIG3503	22281427_c2_4	9173	23276	225	75
CONTIG3507	14178787_c2_4	9174	23277	1368	456
CONTIG3508	3937925_f2_2	9175	23278	264	88
CONTIG3508	23907675_f2_4	9176	23279	204	68
CONTIG3509	9765650_c3_7	9177	23280	195	65
CONTIG3509	87510_f2_4	9178	23281	198	66
CONTIG3509	24241000_c1_6	9179	23282	246	82
CONTIG351	22268751_c3_2	9180	23283	234	78
CONTIG3512	26690933_f3_5	9181	23284	237	79
CONTIG3513	36503931_f3_4	9182	23285	255	85
CONTIG3513	23992640_f3_5	9183	23286	360	120
CONTIG3513	15079412_c1_6	9184	23287	219	73
CONTIG3513	20488843_c2_8	9185	23288	198	66
CONTIG3514	33472953_f3_2	9186	23289	1260	420
CONTIG3516	29335937_f1_4	9187	23290	243	81
CONTIG3516	20017067_f3_5	9188	23291	264	88
CONTIG3518	21566262_f1_1	9189	23292	219	73
CONTIG3519	24015938_c3_7	9190	23293	198	66
CONTIG352	25578900_c3_2	9191	23294	369	123
CONTIG3520	12598437_c1_6	9192	23295	1374	458
CONTIG3520	22890637_c3_9	9193	23296	630	210
CONTIG3522	24609450_c3_7	9194	23297	1380	460
CONTIG3525	15627178_f3_6	9195	23298	393	131
CONTIG3525	12632277_c2_9	9196	23299	183	61
CONTIG3528	6290638_f2_4	9197	23300	198	66
CONTIG3529	9928812_f3_1	9198	23301	219	73
CONTIG3530	10553132_c2_5	9199	23302	183	61
CONTIG3531	24815807_f3_2	9200	23303	192	64

CONTIG3534	35336718_c2_3	9201	23304	210	70
CONTIG3536	16796918_f2_2	9202	23305	309	103
CONTIG3537	6647665_c1_3	9203	23306	192	64
CONTIG3538	11900015_c1_4	9204	23307	195	65
CONTIG3539	24225437_c1_7	9205	23308	201	67
CONTIG354	23475012_c2_2	9206	23309	372	124
CONTIG3540	3943762_f1_4	9207	23310	198	66
CONTIG3540	32212751_f3_6	9208	23311	708	236
CONTIG3545	174041_c2_8	9209	23312	234	78
CONTIG3545	21520255_f3_6	9210	23313	612	204
CONTIG3545	32319555_c3_9	9211	23314	195	65
CONTIG3546	24808128_f3_3	9212	23315	291	97
CONTIG3546	1452928_c2_8	9213	23316	198	66
CONTIG3548	26776681_f2_3	9214	23317	234	78
CONTIG3548	600702_c2_9	9215	23318	195	65
CONTIG355	26343950_f1_1	9216	23319	213	71
CONTIG3551	25580010_f1_1	9217	23320	237	79
CONTIG3551	23437575_c2_6	9218	23321	1230	410
CONTIG3552	13720930_c2_5	9219	23322	189	63
CONTIG3552	1417502_c3_7	9220	23323	225	75
CONTIG3553	29578450_f1_1	9221	23324	246	82
CONTIG3553	4024063_f1_3	9222	23325	207	69
CONTIG3553	3912681_f2_8	9223	23326	726	242
CONTIG3553	1484313_f3_9	9224	23327	249	83
CONTIG3553	584717_c1_14	9225	23328	186	62
CONTIG3553	30115840_c3_17	9226	23329	213	71
CONTIG3553	3921900_c3_18	9227	23330	237	79
CONTIG3554	6058466_f3_3	9228	23331	1014	338
CONTIG3554	3187001_c1_5	9229	23332	207	69
CONTIG3556	26613300_c2_3	9230	23333	204	68
CONTIG3557	10962801_f2_1	9231	23334	687	229
CONTIG3557	12617151_f2_3	9232	23335	216	72
CONTIG3558	5084476_f1_2	9233	23336	204	68

CONTIG3559	31726635_f2_2	9234	23337	258	86
CONTIG3559	24633428_c3_4	9235	23338	189	63
CONTIG356	2849050_f3_2	9236	23339	282	94
CONTIG356	33707012_c3_5	9237	23340	225	75
CONTIG3561	21525450_f1_1	9238	23341	234	78
CONTIG3562	9924035_f3_3	9239	23342	327	109
CONTIG3562	16601702_c1_5	9240	23343	189	63
CONTIG3563	24422250_f1_1	9241	23344	201	67
CONTIG3563	1053550_f2_5	9242	23345	294	98
CONTIG3563	897307_f3_6	9243	23346	183	61
CONTIG3563	5898300_c3_11	9244	23347	753	251
CONTIG3563	24329181_c3_13	9245	23348	216	72
CONTIG3565	19564668_c1_6	9246	23349	519	173
CONTIG3565	24100055_c2_7	9247	23350	468	156
CONTIG3566	24424052_f2_5	9248	23351	183	61
CONTIG3567	1415955_f3_1	9249	23352	219	73
CONTIG3567	899086_f3_2	9250	23353	201	67
CONTIG357	4101013_c2_1	9251	23354	762	254
CONTIG3572	175327_f1_1	9252	23355	222	74
CONTIG3572	868885_c1_3	9253	23356	216	72
CONTIG3573	1225015_c2_5	9254	23357	195	65
CONTIG3574	30173381_f1_1	9255	23358	261	87
CONTIG3576	12504807_f1_1	9256	23359	846	282
CONTIG3577	30703432_f1_1	9257	23360	213	71
CONTIG3579	4781505_f1_1	9258	23361	216	72
CONTIG3579	805425_f2_3	9259	23362	201	67
CONTIG3581	25426563_c3_7	9260	23363	1566	522
CONTIG3583	2225827_f1_1	9261	23364	705	235
CONTIG3583	29969386_c1_7	9262	23365	303	101
CONTIG3584	22008450_f2_4	9263	23366	222	74
CONTIG3584	25595388_c3_9	9264	23367	192	64
CONTIG3585	23640913_f1_2	9265	23368	195	65
CONTIG3585	4062752_f2_3	9266	23369	204	68

CONTIG3585	24414090_f3_5	9267	23370	258	86
CONTIG3585	6678811_c1_7	9268	23371	312	104
CONTIG3585	19688805_c2_10	9269	23372	198	66
CONTIG3585	1378135_c3_11	9270	23373	183	61
CONTIG3586	20984678_f1_1	9271	23374	1812	604
CONTIG3587	24500290_f3_5	9272	23375	267	89
CONTIG3587	20320942_f3_6	9273	23376	222	74
CONTIG3588	23480027_f2_2	9274	23377	525	175
CONTIG3589	11817135_c1_4	9275	23378	189	63
CONTIG3589	812518_c3_5	9276	23379	219	73
CONTIG3590	26307752_c1_3	9277	23380	201	67
CONTIG3594	4766015_f3_3	9278	23381	249	83
CONTIG3594	10552000_c1_5	9279	23382	189	63
CONTIG3595	34257885_c1_7	9280	23383	273	91
CONTIG3595	29687500_c2_8	9281	23384	222	74
CONTIG3597	4335287_c2_3	9282	23385	336	112
CONTIG3598	24409750_f3_3	9283	23386	189	63
CONTIG3599	23679836_c3_4	9284	23387	219	73
CONTIG36	20007635_f3_2	9285	23388	258	86
CONTIG36	24417183_c1_3	9286	23389	276	92
CONTIG3600	26209676_c1_4	9287	23390	285	95
CONTIG3600	23470318_c3_6	9288	23391	282	94
CONTIG3601	626317_f2_3	9289	23392	246	82
CONTIG3601	34197135_f3_5	9290	23393	192	64
CONTIG3601	1406937_c3_9	9291	23394	453	151
CONTIG3602	2347262_f3_2	9292	23395	258	86
CONTIG3602	21518800_c1_3	9293	23396	252	84
CONTIG3602	5313137_c2_4	9294	23397	183	61
CONTIG3604	22479755_c3_8	9295	23398	246	82
CONTIG3605	33359763_f2_2	9296	23399	267	89
CONTIG3606	5270252_f2_1	9297	23400	231	77
CONTIG3607	23437508_c1_3	9298	23401	234	78
CONTIG3608	2925875_f1_1	9299	23402	243	81

CONTIG3608	4020011_f1_2	9300	23403	309	103
CONTIG3608	4147762_c1_8	9301	23404	351	117
CONTIG3609	1963937_c2_8	9302	23405	201	67
CONTIG3609	24632907_c3_10	9303	23406	195	65
CONTIG3610	6289127_c1_5	9304	23407	270	90
CONTIG3612	25469055_f3_4	9305	23408	183	61
CONTIG3612	24355143_f3_6	9306	23409	216	72
CONTIG3612	1206930_c2_9	9307	23410	564	188
CONTIG3612	33993900_c3_10	9308	23411	444	148
CONTIG3613	35647032_f3_2	9309	23412	201	67
CONTIG3614	450026_f2_2	9310	23413	1656	552
CONTIG3617	6678751_c2_3	9311	23414	666	222
CONTIG3617	10166402_c2_4	9312	23415	207	69
CONTIG3618	20344152_c2_4	9313	23416	588	196
CONTIG3619	30276532_f2_3	9314	23417	219	73
CONTIG362	2189566_f3_1	9315	23418	948	316
CONTIG3620	6641913_c2_3	9316	23419	186	62
CONTIG3622	20734806_f3_1	9317	23420	546	182
CONTIG3622	32069713_c3_4	9318	23421	213	71
CONTIG3623	26214000_c2_7	9319	23422	255	85
CONTIG3624	24502175_c3_5	9320	23423	228	76
CONTIG3626	17049168_f3_2	9321	23424	531	177
CONTIG3628	6921942_c3_4	9322	23425	207	69
CONTIG3629	6050088_c1_4	9323	23426	186	62
CONTIG3629	16579130_c2_5	9324	23427	510	170
CONTIG3630	1203142_f1_1	9325	23428	183	61
CONTIG3630	25953403_c2_4	9326	23429	186	62
CONTIG3631	34172188_f1_1	9327	23430	357	119
CONTIG3631	1006902_f2_2	9328	23431	1038	346
CONTIG3634	6928125_f3_4	9329	23432	228	76
CONTIG3634	2147252_c1_8	9330	23433	186	62
CONTIG3634	23875277_c2_9	9331	23434	300	100
CONTIG3636	287561_c1_5	9332	23435	312	104

CONTIG3636	6837588_c1_7	9333	23436	570	190
CONTIG3638	10976436_f3_3	9334	23437	192	64
CONTIG3640	26353267_c1_7	9335	23438	315	105
CONTIG3643	19539838_c1_4	9336	23439	825	275
CONTIG3644	20395010_f2_1	9337	23440	225	75
CONTIG3644	10546927_f3_2	9338	23441	195	65
CONTIG3644	11135876_c3_4	9339	23442	195	65
CONTIG3646	10578180_f3_1	9340	23443	222	74
CONTIG3646	24744378_c3_2	9341	23444	474	158
CONTIG3647	11522828_f2_2	9342	23445	243	81
CONTIG3649	12707802_c3_8	9343	23446	246	82
CONTIG365	11756938_f2_1	9344	23447	474	158
CONTIG3650	14068967_f1_1	9345	23448	1335	445
CONTIG3650	14500828_c3_2	9346	23449	189	63
CONTIG3652	10946908_f3_1	9347	23450	207	69
CONTIG3653	15636287_f3_5	9348	23451	186	62
CONTIG3659	22445186_c2_5	9349	23452	234	78
CONTIG3660	4145252_c1_4	9350	23453	228	76
CONTIG3661	10722160_c3_6	9351	23454	249	83
CONTIG3663	24610763_f1_1	9352	23455	1269	423
CONTIG3666	24037765_c1_3	9353	23456	255	85
CONTIG3668	5119077_c2_7	9354	23457	528	176
CONTIG3668	7110066_c3_9	9355	23458	246	82
CONTIG3669	24423377_f3_5	9356	23459	183	61
CONTIG3671	29494455_f1_1	9357	23460	258	86
CONTIG3671	984802_f2_2	9358	23461	183	61
CONTIG3672	423761_f3_3	9359	23462	276	92
CONTIG3673	31289057_f1_3	9360	23463	198	66
CONTIG3673	32225926_f2_4	9361	23464	225	75
CONTIG3675	33850338_c2_1	9362	23465	1065	355
CONTIG3677	33208150_f2_1	9363	23466	294	98
CONTIG3677	4723278_f3_3	9364	23467	438	146
CONTIG3677	14316656_c2_5	9365	23468	189	63

CONTIG3677	10558467_c3_7	9366	23469	249	83
CONTIG3678	6054038_f1_1	9367	23470	288	96
CONTIG3678	822338_f1_2	9368	23471	201	67
CONTIG3678	23444677_c2_5	9369	23472	201	67
CONTIG3681	14079686_f1_1	9370	23473	249	83
CONTIG3682	209717_c3_10	9371	23474	186	62
CONTIG3683	24017026_f3_2	9372	23475	219	73
CONTIG3685	22925127_f3_3	9373	23476	186	62
CONTIG3685	25500312_c2_4	9374	23477	183	61
CONTIG3686	22031575_f1_1	9375	23478	906	302
CONTIG3688	23941502_f3_2	9376	23479	633	211
CONTIG3689	4421937_f3_3	9377	23480	330	110
CONTIG3691	35807755_f2_1	9378	23481	444	148
CONTIG3691	234576_f3_3	9379	23482	354	118
CONTIG3691	9850437_c1_4	9380	23483	1263	421
CONTIG3692	79653_c2_6	9381	23484	615	205
CONTIG3693	24313893_c1_3	9382	23485	279	93
CONTIG3694	34008436_f2_2	9383	23486	237	79
CONTIG3694	16839700_c3_8	9384	23487	834	278
CONTIG3695	10594392_f2_4	9385	23488	222	74
CONTIG3695	35354827_c2_7	9386	23489	738	246
CONTIG3697	26562530_f2_3	9387	23490	189	63
CONTIG3698	24064632_f3_4	9388	23491	261	87
CONTIG3701	93_c2_6	9389	23492	183	61
CONTIG3704	24470063_c2_4	9390	23493	561	187
CONTIG3705	5094636_f1_1	9391	23494	681	227
CONTIG3705	14879378_f2_3	9392	23495	195	65
CONTIG3708	23444752_c1_6	9393	23496	186	62
CONTIG3709	34174031_f2_3	9394	23497	213	71
CONTIG3710	19665683_c2_8	9395	23498	1194	398
CONTIG3710	14720327_c2_9	9396	23499	186	62
CONTIG3712	87561_c2_6	9397	23500	195	65
CONTIG3712	4328937_c2_7	9398	23501	738	246

CONTIG3714	9959385_f1_1	9399	23502	201	67
CONTIG3714	23988762_c2_4	9400	23503	255	85
CONTIG3714	1692600_c3_5	9401	23504	207	69
CONTIG3715	20082160_c3_7	9402	23505	240	80
CONTIG3716	259386_c3_9	9403	23506	390	130
CONTIG3717	5078200_c1_5	9404	23507	243	81
CONTIG3717	34381502_c1_7	9405	23508	297	99
CONTIG3718	4687575_f3_5	9406	23509	243	81
CONTIG3718	1060933_c1_7	9407	23510	327	109
CONTIG3720	22445177_c1_4	9408	23511	393	131
CONTIG3720	10819003_c1_5	9409	23512	282	94
CONTIG3720	24339051_c2_6	9410	23513	612	204
CONTIG3721	24414012_f1_1	9411	23514	279	93
CONTIG3723	5972252_f3_4	9412	23515	195	65
CONTIG3727	4821942_f2_3	9413	23516	318	106
CONTIG3727	176892_f3_5	9414	23517	189	63
CONTIG3728	34579626_f2_2	9415	23518	198	66
CONTIG3728	20390926_c1_5	9416	23519	249	83
CONTIG3728	22078552_c2_7	9417	23520	201	67
CONTIG3728	19953140_c3_10	9418	23521	285	95
CONTIG3729	24093840_f2_3	9419	23522	213	71
CONTIG3730	2910812_f1_1	9420	23523	216	72
CONTIG3730	13680192_f1_2	9421	23524	225	75
CONTIG3730	1972127_f3_7	9422	23525	183	61
CONTIG3730	36532887_c1_9	9423	23526	213	71
CONTIG3730	21928137_c2_10	9424	23527	207	69
CONTIG3731	9843930_f2_8	9425	23528	210	70
CONTIG3731	2110306_c2_15	9426	23529	444	148
CONTIG3732	23844008_f1_3	9427	23530	309	103
CONTIG3732	11723200_c1_4	9428	23531	207	69
CONTIG3735	2770337_f2_6	9429	23532	543	181
CONTIG3735	20350808_c1_11	9430	23533	189	63
CONTIG3737	11225691_f2_1	9431	23534	279	93

CONTIG3738	978425_f3_3	9432	23535	936	312
CONTIG3738	21881687_c3_8	9433	23536	186	62
CONTIG3739	240803_f1_1	9434	23537	456	152
CONTIG3740	870902_c3_9	9435	23538	216	72
CONTIG3741	4680_f3_2	9436	23539	198	66
CONTIG3744	11722632_f1_1	9437	23540	192	64
CONTIG3744	24511525_f3_3	9438	23541	183	61
CONTIG3745	10164025_c2_6	9439	23542	228	76
CONTIG3746	14273588_f3_5	9440	23543	183	61
CONTIG3746	24782806_f3_6	9441	23544	441	147
CONTIG3746	1660937_c1_7	9442	23545	195	65
CONTIG3747	25972187_f1_1	9443	23546	969	323
CONTIG3747	22368885_f2_5	9444	23547	465	155
CONTIG3747	35335900_f3_7	9445	23548	255	85
CONTIG3748	3913387_f3_4	9446	23549	234	78
CONTIG3748	4569427_c2_7	9447	23550	198	66
CONTIG3748	3906562_c2_9	9448	23551	213	71
CONTIG3750	11900015_f2_2	9449	23552	195	65
CONTIG3750	29945875_c1_5	9450	23553	198	66
CONTIG3750	19922010_c3_7	9451	23554	204	68
CONTIG3753	7038877_c1_6	9452	23555	189	63
CONTIG3753	13755017_c1_7	9453	23556	273	91
CONTIG3753	15662_c2_8	9454	23557	306	102
CONTIG3753	31346883_c3_11	9455	23558	192	64
CONTIG3754	276878_f1_1	9456	23559	1014	338
CONTIG3755	25406702_c2_8	9457	23560	192	64
CONTIG3755	25974012_c2_10	9458	23561	228	76
CONTIG3756	5086087_c2_6	9459	23562	219	73
CONTIG3757	24617213_f2_1	9460	23563	750	250
CONTIG3759	4098132_f3_4	9461	23564	1440	480
CONTIG3760	30588277_f1_1	9462	23565	216	72
CONTIG3760	4745287_c1_3	9463	23566	186	62
CONTIG3760	29486313_c1_5	9464	23567	204	68

CONTIG3760	14063150_c3_6	9465	23568	267	89
CONTIG3761	6097512_f2_2	9466	23569	222	74
CONTIG3761	35156256_f3_3	9467	23570	216	72
CONTIG3761	3017817_c2_9	9468	23571	222	74
CONTIG3761	12539000_c3_11	9469	23572	186	62
CONTIG3764	881910_f3_3	9470	23573	261	87
CONTIG3764	3369142_c1_5	9471	23574	246	82
CONTIG3765	14095443_f1_1	9472	23575	240	80
CONTIG3770	24615680_c3_5	9473	23576	204	68
CONTIG3771	22070202_f3_6	9474	23577	204	68
CONTIG3773	178_f1_1	9475	23578	189	63
CONTIG3773	12912588_f3_5	9476	23579	228	76
CONTIG3774	14455175_c3_6	9479	23582	216	72
CONTIG3774	24647250_f1_1	9478	23581	195	65
CONTIG3773	6664050_c1_6	9477	23580	243	81
CONTIG3777	23990877_f1_1	9480	23583	189	63
CONTIG3777	13962833_c2_5	9481	23584	1155	385
CONTIG3779	14176537_c2_8	9482	23585	246	82
CONTIG378	986038_f2_1	9483	23586	294	98
CONTIG3780	4306537_c2_5	9484	23587	531	177
CONTIG3782	235700_c1_4	9485	23588	732	244
CONTIG3783	2548377_c3_9	9486	23589	243	81
CONTIG3785	10838882_f1_1	9487	23590	711	237
CONTIG3787	23444382_f1_1	9488	23591	306	102
CONTIG3789	882937_f2_2	9489	23592	342	114
CONTIG3790	33782837_f2_2	9490	23593	261	87
CONTIG3791	30275337_f3_3	9491	23594	294	98
CONTIG3792	23828302_f1_1	9492	23595	450	150
CONTIG3792	29501590_f2_6	9493	23596	195	65
CONTIG3793	32428956_f3_2	9494	23597	1386	462
CONTIG3795	22065900_c1_4	9495	23598	195	65
CONTIG3796	11812626_f1_1	9496	23599	720	240
CONTIG3797	9770668_f3_4	9497	23600	1029	343

CONTIG3797	29336006_c1_5	9498	23601	88
CONTIG3798	10815812_f2_3	9499	23602	356
CONTIG3799	176562_c1_5	9500	23603	1068
CONTIG380	557885_c3_3	9501	23604	82
CONTIG3800	3536725_f1_1	9502	23605	306
CONTIG3802	23632818_c1_7	9503	23606	258
CONTIG3802	34392052_c2_11	9504	23607	189
CONTIG3802	53326_c2_12	9505	23608	67
CONTIG3804	813802_f3_3	9506	23609	70
CONTIG3804	25603436_c3_8	9507	23610	789
CONTIG3804	23650702_f3_4	9508	23611	263
CONTIG3805	785432_f3_4	9509	23612	86
CONTIG3806	22891426_f3_7	9510	23613	71
CONTIG3807	991682_c2_8	9511	23614	80
CONTIG3808	24250753_f2_2	9512	23615	225
CONTIG3808	35179626_c2_5	9513	23616	75
CONTIG3808	15109700_c3_6	9514	23617	97
CONTIG3809	24335937_f2_3	9515	23618	80
CONTIG3809	813801_f3_5	9516	23619	105
CONTIG3815	19921875_f1_1	9517	23620	69
CONTIG3815	1968753_c3_6	9518	23621	91
CONTIG3816	1179632_f2_1	9519	23622	74
CONTIG3816	861267_c1_4	9520	23623	74
CONTIG3816	197152_c3_6	9521	23624	99
CONTIG3817	14226562_f2_2	9522	23625	262
CONTIG3819	22445312_f2_2	9523	23626	609
CONTIG382	31257682_f3_1	9524	23627	63
CONTIG382	34180438_c2_2	9525	23628	62
CONTIG3822	23859437_f2_2	9526	23629	63
CONTIG3822	1542_c2_3	9527	23630	72
CONTIG3823	665942_f1_2	9528	23631	66
CONTIG3823	4062535_f1_3	9529	23632	64
CONTIG3823	1117376_f2_4	9530	23633	61

CONTIG3823	5908406_c1_8	9531	23634	195	65
CONTIG3824	24298782_c1_4	9532	23635	186	62
CONTIG3824	11829516_c2_6	9533	23636	315	105
CONTIG3824	5159633_c3_9	9534	23637	189	63
CONTIG3824	30131937_c3_10	9535	23638	195	65
CONTIG3825	21516433_f3_5	9536	23639	573	191
CONTIG3828	31414568_f1_1	9537	23640	204	68
CONTIG3829	19551557_f2_2	9538	23641	819	273
CONTIG383	19532511_f2_2	9539	23642	282	94
CONTIG3830	10972936_c1_3	9540	23643	321	107
CONTIG3830	20322165_c3_5	9541	23644	369	123
CONTIG3832	157037_c2_9	9542	23645	210	70
CONTIG3833	23866250_f3_7	9543	23646	282	94
CONTIG3835	13671877_c1_3	9544	23647	225	75
CONTIG3835	5897083_c2_6	9545	23648	267	89
CONTIG3835	22265635_c3_7	9546	23649	231	77
CONTIG3836	13673175_f1_1	9547	23650	1203	401
CONTIG3837	33406575_f1_2	9548	23651	198	66
CONTIG3837	50_f3_4	9549	23652	237	79
CONTIG3837	14221875_c1_6	9550	23653	420	140
CONTIG3838	19695265_c1_1	9551	23654	189	63
CONTIG3839	4882875_f1_2	9552	23655	306	102
CONTIG3839	21875375_c2_6	9553	23656	210	70
CONTIG3840	24619177_f2_2	9554	23657	246	82
CONTIG3840	406302_f2_3	9555	23658	201	67
CONTIG3840	10980181_c2_5	9556	23659	231	77
CONTIG3842	34550127_f1_3	9557	23660	201	67
CONTIG3842	20400300_f2_5	9558	23661	660	220
CONTIG3844	35736025_c3_5	9559	23662	279	93
CONTIG3845	4102152_f1_1	9560	23663	192	64
CONTIG3845	20398307_f2_2	9561	23664	183	61
CONTIG3845	4176285_c1_3	9562	23665	369	123
CONTIG3847	12303188_f1_2	9563	23666	183	61

CONTIG3847	134677_f1_5	9564	23667	241	
CONTIG3847	23443312_f3_9	9565	23668	195	65
CONTIG3847	19798830_c3_14	9566	23669	201	67
CONTIG3849	35392001_f2_2	9567	23670	780	260
CONTIG3849	2162818_f2_3	9568	23671	426	142
CONTIG3849	19569575_c2_10	9569	23672	192	64
CONTIG385	24398276_c1_3	9570	23673	225	75
CONTIG3851	489135_f2_4	9571	23674	231	77
CONTIG3851	22112537_f2_5	9572	23675	1056	352
CONTIG3853	14453155_c3_8	9573	23676	195	65
CONTIG3854	29330015_f2_4	9574	23677	195	65
CONTIG3854	14882663_c1_8	9575	23678	297	99
CONTIG3856	14553805_f2_2	9576	23679	267	89
CONTIG3858	4719637_c3_7	9577	23680	966	322
CONTIG386	14975680_f3_1	9578	23681	240	80
CONTIG3860	973375_f1_2	9579	23682	195	65
CONTIG3861	10757840_c2_8	9580	23683	252	84
CONTIG3862	24223127_f2_4	9581	23684	189	63
CONTIG3862	782751_c1_5	9582	23685	324	108
CONTIG3864	21526436_c2_7	9583	23686	921	307
CONTIG3865	656378_f1_1	9584	23687	225	75
CONTIG3866	19722787_f3_1	9585	23688	1626	542
CONTIG3867	34182837_c1_3	9586	23689	195	65
CONTIG3867	5939062_f2_2	9587	23690	330	110
CONTIG3869	80062_c1_4	9588	23691	189	63
CONTIG3869	179625_c1_2	9589	23692	243	81
CONTIG387	4688161_c1_3	9590	23693	201	67
CONTIG3872	24234775_c3_5	9591	23694	222	74
CONTIG3872	11805457_f2_2	9592	23695	303	101
CONTIG3872	23460952_c2_6	9593	23696	297	99
CONTIG3872	23689513_c3_7	9594	23697	183	61
CONTIG3874	110683_c3_8	9595	23698	291	97
CONTIG3874	21485967_f3_3	9596	23699	219	73

CONTIG3876	2548753_f1_2	9597	23700	213	71
CONTIG3876	835000_f1_3	9598	23701	198	66
CONTIG3876	1197008_f3_6	9599	23702	297	99
CONTIG3876	23632951_c3_9	9600	23703	192	64
CONTIG3877	24687555_f2_1	9601	23704	207	69
CONTIG3877	9801307_f2_2	9602	23705	291	97
CONTIG3877	4866637_f3_3	9603	23706	186	62
CONTIG3877	3944053_c1_5	9604	23707	297	99
CONTIG3877	4882700_c2_6	9605	23708	219	73
CONTIG3877	2913961_c3_7	9606	23709	192	64
CONTIG3879	5890675_f1_2	9607	23710	783	261
CONTIG3879	29580040_c2_3	9608	23711	297	99
CONTIG388	24062838_c3_3	9609	23712	192	64
CONTIG3881	23632336_f3_3	9610	23713	342	114
CONTIG3881	13851510_c2_5	9611	23714	228	76
CONTIG3882	25992278_f1_2	9612	23715	201	67
CONTIG3884	11726576_f3_7	9613	23716	186	62
CONTIG3885	179576_c3_4	9614	23717	258	86
CONTIG3885	25428261_c3_5	9615	23718	579	193
CONTIG3886	6729632_c2_3	9616	23719	273	91
CONTIG3887	19580380_f3_3	9617	23720	189	63
CONTIG3887	13787786_c2_4	9618	23721	195	65
CONTIG3888	13707187_c1_2	9619	23722	387	129
CONTIG3888	10352000_c1_3	9620	23723	774	258
CONTIG3888	6917952_c2_4	9621	23724	186	62
CONTIG389	24697050_f1_2	9622	23725	309	103
CONTIG3890	26600750_f3_3	9623	23726	186	62
CONTIG3891	24298452_f1_2	9624	23727	189	63
CONTIG3891	300_c1_7	9625	23728	195	65
CONTIG3891	593837_c3_13	9626	23729	219	73
CONTIG3894	1447182_c2_6	9627	23730	321	107
CONTIG3896	26380391_f1_1	9628	23731	234	78
CONTIG3896	4147762_c2_9	9629	23732	351	117

CONTIG3897	26437767_c1_2	9630	23733	294	98
CONTIG3897	16585912_c2_3	9631	23734	237	79
CONTIG3897	36330062_c3_4	9632	23735	198	66
CONTIG3898	29495332_c2_4	9633	23736	219	73
CONTIG3900	2771010_f2_3	9634	23737	522	174
CONTIG3902	84650_f3_4	9635	23738	204	68
CONTIG3902	4511502_c1_8	9636	23739	192	64
CONTIG3902	2660903_c2_10	9637	23740	201	67
CONTIG3903	35407805_c3_6	9638	23741	219	73
CONTIG3904	33237767_f3_3	9639	23742	1212	404
CONTIG3904	4101561_c2_5	9640	23743	273	91
CONTIG3905	804151_c3_7	9641	23744	420	140
CONTIG3907	605078_c2_3	9642	23745	195	65
CONTIG3908	14562657_f1_1	9643	23746	573	191
CONTIG3908	24240950_f2_2	9644	23747	1113	371
CONTIG3908	14507942_f3_3	9645	23748	216	72
CONTIG3908	2464641_f1_1	9646	23749	273	91
CONTIG3909	6070255_c1_5	9647	23750	753	251
CONTIG3909	6734752_f2_2	9648	23751	504	168
CONTIG3909	2625317_f2_3	9649	23752	594	198
CONTIG3909	4472502_f3_5	9650	23753	255	85
CONTIG3911	23594017_c1_4	9651	23754	240	80
CONTIG3911	4298828_c3_5	9652	23755	219	73
CONTIG3912	2931377_f1_1	9653	23756	183	61
CONTIG3912	19729787_f3_2	9654	23757	207	69
CONTIG3912	22462510_f3_3	9655	23758	225	75
CONTIG3913	25569552_f3_6	9656	23759	1137	379
CONTIG3917	3915677_c1_4	9657	23760	216	72
CONTIG3919	21675305_f2_1	9658	23761	219	73
CONTIG3919	30156300_f3_3	9659	23762	258	86
CONTIG3919	470300_c3_7	9660	23763	1116	372
CONTIG392	3519481_f1_2	9661	23764	219	73
CONTIG3922	24657885_f2_2	9662	23765	207	69

CONTIG3922	500010_f3_5	9663	23766	198	66
CONTIG3922	2440537_c1_6	9664	23767	234	78
CONTIG3926	878405_f1_1	9665	23768	234	78
CONTIG3927	22072340_f1_2	9666	23769	831	277
CONTIG3928	31757160_c2_4	9667	23770	219	73
CONTIG393	24395207_f3_2	9668	23771	189	63
CONTIG3932	6140902_f2_2	9669	23772	1188	396
CONTIG3935	23945430_f2_3	9670	23773	222	74
CONTIG3935	14566686_c2_7	9671	23774	201	67
CONTIG3936	32243750_f2_1	9672	23775	195	65
CONTIG3936	21742000_f3_3	9673	23776	195	65
CONTIG394	25475652_f3_4	9674	23777	189	63
CONTIG3937	23535786_f3_2	9675	23778	252	84
CONTIG3937	6100628_c2_6	9676	23779	504	168
CONTIG3938	6140877_f1_2	9677	23780	264	88
CONTIG394	10734386_f1_2	9678	23781	237	79
CONTIG394	23835760_f2_3	9679	23782	597	199
CONTIG3940	5254758_c1_12	9680	23783	237	79
CONTIG3940	26366506_c1_13	9681	23784	549	183
CONTIG3940	24823590_c3_14	9682	23785	183	61
CONTIG3942	20968927_f2_3	9683	23786	285	95
CONTIG3942	35625000_f3_6	9684	23787	414	138
CONTIG3943	589160_f1_1	9685	23788	510	170
CONTIG3943	30507817_c2_4	9686	23789	204	68
CONTIG3944	23835313_f1_1	9687	23790	258	86
CONTIG3944	5891430_f2_2	9688	23791	1371	457
CONTIG395	7054577_f2_1	9689	23792	225	75
CONTIG395	5908507_c3_3	9690	23793	252	84
CONTIG3950	29511305_c2_5	9691	23794	240	80
CONTIG3951	23484662_f3_3	9692	23795	210	70
CONTIG3953	13313286_c1_5	9693	23796	204	68
CONTIG3953	188901_c2_6	9694	23797	903	301
CONTIG3958	12522787_c2_6	9695	23798	480	160

CONTIG3959	26835937_c1_7	9696	23799	264	88
CONTIG3959	10003402_c2_8	9697	23800	213	71
CONTIG396	25439062_f3_1	9698	23801	183	61
CONTIG3960	6022700_c1_3	9699	23802	216	72
CONTIG3960	29531587_c1_4	9700	23803	234	78
CONTIG3961	24006591_c3_7	9701	23804	282	94
CONTIG3962	9939752_f2_1	9702	23805	579	193
CONTIG3963	2783177_f1_2	9703	23806	204	68
CONTIG3966	6447076_f2_1	9704	23807	207	69
CONTIG3967	4742012_f3_4	9705	23808	381	127
CONTIG397	4509400_f3_1	9706	23809	195	65
CONTIG3970	24401875_f3_9	9707	23810	468	156
CONTIG3971	21682713_f2_2	9708	23811	231	77
CONTIG3971	14237508_c2_3	9709	23812	240	80
CONTIG3971	19736712_c3_4	9710	23813	213	71
CONTIG3973	33625012_f3_4	9711	23814	240	80
CONTIG3973	16668552_c2_6	9712	23815	324	108
CONTIG3975	24299012_f1_1	9713	23816	690	230
CONTIG3975	2928202_f1_3	9714	23817	690	230
CONTIG3976	1969010_c3_7	9715	23818	225	75
CONTIG3977	24095392_f2_3	9716	23819	183	61
CONTIG3978	13832550_f2_4	9717	23820	297	99
CONTIG3979	4489135_f1_2	9718	23821	213	71
CONTIG398	239502_c2_2	9719	23822	195	65
CONTIG3980	24001932_f2_1	9720	23823	183	61
CONTIG3980	627002_c2_4	9721	23824	195	65
CONTIG3981	32683326_f1_1	9722	23825	699	233
CONTIG3981	25396950_f1_2	9723	23826	282	94
CONTIG3981	23926703_f2_4	9724	23827	225	75
CONTIG3981	21994032_f3_5	9725	23828	1650	550
CONTIG3981	24609380_c3_14	9726	23829	216	72
CONTIG3982	30274037_c3_7	9727	23830	438	146
CONTIG3983	5892550_f2_2	9728	23831	195	65

CONTIG3983	33770160_c3_6	9729	23832	234	78
CONTIG3984	15781513_f1_1	9730	23833	192	64
CONTIG3984	2834561_f2_2	9731	23834	306	102
CONTIG3984	2117626_f2_4	9732	23835	222	74
CONTIG3984	9882818_c1_6	9733	23836	993	331
CONTIG3985	2202_f2_2	9734	23837	990	330
CONTIG3985	36338443_f3_4	9735	23838	375	125
CONTIG3985	25394712_c1_10	9736	23839	195	65
CONTIG3986	1953437_f1_2	9737	23840	189	63
CONTIG3986	24421915_f1_3	9738	23841	204	68
CONTIG3986	26382813_c1_8	9739	23842	381	127
CONTIG3987	24062510_c1_4	9740	23843	186	62
CONTIG3987	81637_c2_6	9741	23844	213	71
CONTIG3988	22386538_c1_1	9742	23845	183	61
CONTIG3988	859807_c1_2	9743	23846	183	61
CONTIG3989	29945875_f1_1	9744	23847	204	68
CONTIG3989	656377_c2_3	9745	23848	234	78
CONTIG399	787660_c1_2	9746	23849	228	76
CONTIG3990	21991425_f2_1	9747	23850	258	86
CONTIG3990	24879718_c3_7	9748	23851	1056	352
CONTIG3991	29487760_f1_1	9749	23852	201	67
CONTIG3991	4103441_c1_8	9750	23853	195	65
CONTIG3992	24414188_f1_1	9751	23854	1065	355
CONTIG3992	23553390_f3_3	9752	23855	240	80
CONTIG3993	4765556_c1_4	9753	23856	189	63
CONTIG3993	21683162_c2_7	9754	23857	237	79
CONTIG3994	4095006_c1_5	9755	23858	279	93
CONTIG3995	4695177_c1_9	9756	23859	369	123
CONTIG3995	1350337_c2_11	9757	23860	189	63
CONTIG3997	25898453_c1_5	9758	23861	474	158
CONTIG3999	21750003_c1_4	9759	23862	186	62
CONTIG3999	23641036_c2_5	9760	23863	252	84
CONTIG4001	36410906_f2_6	9761	23864	204	68

CONTIG4003	36524037_f2_3	9762	23865	252	84
CONTIG4005	29878388_f1_2	9763	23866	1014	338
CONTIG4005	23626952_c2_5	9764	23867	198	66
CONTIG4005	24255251_c2_6	9765	23868	243	81
CONTIG4008	20188786_c3_8	9766	23869	333	111
CONTIG4006	29569562_f2_3	9767	23870	255	85
CONTIG4006	33210762_c1_5	9768	23871	273	91
CONTIG4006	5283142_c2_6	9769	23872	1074	358
CONTIG4007	19730037_c3_7	9770	23873	258	86
CONTIG4008	25990687_c1_7	9771	23874	186	62
CONTIG4009	10635927_f1_1	9772	23875	195	65
CONTIG4009	5111551_f2_4	9773	23876	240	80
CONTIG4009	4790967_c3_7	9774	23877	231	77
CONTIG401	33837903_c3_9	9775	23878	243	81
CONTIG401	6816555_c3_3	9776	23879	192	64
CONTIG4010	6817265_f3_1	9777	23880	1263	421
CONTIG4012	33209687_c3_3	9778	23881	225	75
CONTIG4013	30275688_c1_2	9779	23882	369	123
CONTIG4013	14537687_c3_4	9780	23883	204	68
CONTIG4016	23875885_f2_3	9781	23884	189	63
CONTIG4016	21695160_f3_6	9782	23885	345	115
CONTIG4016	3926552_c1_9	9783	23886	558	186
CONTIG4016	25556700_c2_14	9784	23887	261	87
CONTIG4016	192052_c3_15	9785	23888	282	94
CONTIG4017	33407813_f3_5	9786	23889	189	63
CONTIG402	10725025_c3_2	9787	23890	213	71
CONTIG4020	6023427_f2_2	9788	23891	279	93
CONTIG4020	22708393_f3_3	9789	23892	243	81
CONTIG4020	1970450_c3_5	9790	23893	183	61
CONTIG4021	24410686_f3_9	9791	23894	243	81
CONTIG4022	15712778_f1_2	9792	23895	198	66
CONTIG4024	21729675_c2_5	9793	23896	198	66
CONTIG4026	24640937_c1_6	9794	23897	441	147

CONTIG4027	23569437_c1_6	9795	23898	198	66
CONTIG4029	26570150_c1_6	9796	23899	225	75
CONTIG403	23609452_f1_1	9797	23900	186	62
CONTIG403	12269651_f1_2	9798	23901	216	72
CONTIG403	24429592_c1_3	9799	23902	189	63
CONTIG4030	22542587_f1_1	9800	23903	246	82
CONTIG4030	29339678_c1_2	9801	23904	243	81
CONTIG4030	30109676_c1_3	9802	23905	204	68
CONTIG4032	3959652_c2_3	9803	23906	549	183
CONTIG4033	33242877_c2_4	9804	23907	1596	532
CONTIG4035	5960328_f2_1	9805	23908	240	80
CONTIG4037	20898387_c3_4	9806	23909	243	81
CONTIG4038	19585812_f1_1	9807	23910	198	66
CONTIG4038	16522807_f1_2	9808	23911	876	292
CONTIG4039	207762_f2_6	9809	23912	243	81
CONTIG404	204840_f2_2	9810	23913	213	71
CONTIG4040	20391950_c1_3	9811	23914	225	75
CONTIG4041	23479753_f1_1	9812	23915	240	80
CONTIG4042	4381307_f1_2	9813	23916	216	72
CONTIG4042	6768753_f3_3	9814	23917	258	86
CONTIG4042	821925_f3_4	9815	23918	186	62
CONTIG4042	19173313_c3_7	9816	23919	1317	439
CONTIG4043	13756250_f3_3	9817	23920	279	93
CONTIG4043	860015_c3_7	9818	23921	204	68
CONTIG4044	26641533_c2_4	9819	23922	222	74
CONTIG4045	12766918_f3_4	9820	23923	204	68
CONTIG4045	34258387_f3_5	9821	23924	222	74
CONTIG4045	24644178_c2_9	9822	23925	189	63
CONTIG4047	35804715_f2_4	9823	23926	249	83
CONTIG4047	33204068_c3_7	9824	23927	285	95
CONTIG4048	23444001_c3_4	9825	23928	198	66
CONTIG4053	24039140_f2_1	9826	23929	237	79
CONTIG4053	29533143_f2_3	9827	23930	288	96

CONTIG4055	24657687_c1_6	9828	23931	1515	505
CONTIG4056	30179516_c2_6	9829	23932	249	83
CONTIG4057	4485062_f1_1	9830	23933	222	74
CONTIG4057	9875292_c3_6	9831	23934	198	66
CONTIG4057	23475050_c3_7	9832	23935	1266	422
CONTIG4058	29334787_f2_1	9833	23936	167	
CONTIG4058	4767503_f2_2	9834	23937	1473	491
CONTIG4058	30475887_f3_3	9835	23938	375	125
CONTIG4059	12932067_c2_3	9836	23939	183	61
CONTIG406	6818926_f1_1	9837	23940	231	77
CONTIG4061	9772143_f2_5	9838	23941	234	78
CONTIG4062	25876680_c1_5	9839	23942	204	68
CONTIG4062	20580275_c3_8	9840	23943	237	79
CONTIG4063	5250252_f3_4	9841	23944	366	122
CONTIG4063	24410887_c2_5	9842	23945	255	85
CONTIG4063	30751563_c3_6	9843	23946	216	72
CONTIG4066	204088_f2_1	9844	23947	246	82
CONTIG4067	20425776_f1_1	9845	23948	234	78
CONTIG4067	34554013_c3_7	9846	23949	288	96
CONTIG4068	5260903_f3_2	9847	23950	228	76
CONTIG4068	23939062_c2_4	9848	23951	231	77
CONTIG4069	16798428_f1_2	9849	23952	183	61
CONTIG4069	2188800_f2_3	9850	23953	255	85
CONTIG4069	23626536_c2_7	9851	23954	183	61
CONTIG4069	34573462_c2_8	9852	23955	273	91
CONTIG4072	4976587_c1_10	9853	23956	195	65
CONTIG4073	22351551_f2_1	9854	23957	192	64
CONTIG4073	19537512_c1_2	9855	23958	1269	423
CONTIG4075	970392_f1_2	9856	23959	228	76
CONTIG4075	12502251_c2_12	9857	23960	192	64
CONTIG4075	13863808_c2_13	9858	23961	225	75
CONTIG4076	65530_c3_6	9859	23962	1164	388
CONTIG4078	782965_c1_6	9860	23963	1335	445

CONTIG4078	6428555_c2_7	9861	23964	630	210
CONTIG4082	4066375_f2_2	9862	23965	297	99
CONTIG4082	24335963_f3_3	9863	23966	186	62
CONTIG4083	14257812_c1_3	9864	23967	318	106
CONTIG4085	14298500_f1_1	9865	23968	870	290
CONTIG4086	26965_f3_5	9866	23969	339	113
CONTIG4087	954507_f1_1	9867	23970	420	140
CONTIG4088	10973410_f2_5	9868	23971	1800	600
CONTIG4088	25675628_c1_11	9869	23972	195	65
CONTIG4089	14156568_c2_9	9870	23973	315	105
CONTIG4089	33470762_c3_13	9871	23974	273	91
CONTIG409	21520252_c2_2	9872	23975	213	71
CONTIG409	4729638_c3_3	9873	23976	249	83
CONTIG4091	13866567_f3_5	9874	23977	396	132
CONTIG4092	14728562_f2_3	9875	23978	354	118
CONTIG4093	14266576_f2_2	9876	23979	219	73
CONTIG4094	14350035_f2_3	9877	23980	276	92
CONTIG4096	10972187_f3_5	9878	23981	423	141
CONTIG4096	24236401_c3_12	9879	23982	183	61
CONTIG4099	24481951_c1_5	9880	23983	234	78
CONTIG4099	23944552_c3_12	9881	23984	315	105
CONTIG41	20525007_f2_1	9882	23985	198	66
CONTIG41	22460953_c2_2	9883	23986	279	93
CONTIG4100	3937766_f3_5	9884	23987	198	66
CONTIG4100	34667938_c3_13	9885	23988	288	96
CONTIG4101	14150050_f2_4	9886	23989	342	114
CONTIG4101	29960200_c3_8	9887	23990	435	145
CONTIG4102	23443760_f2_1	9888	23991	489	163
CONTIG4103	35160337_f1_1	9889	23992	297	99
CONTIG4103	6644092_f2_3	9890	23993	219	73
CONTIG4104	13837762_c3_11	9891	23994	243	81
CONTIG4105	9801453_f1_1	9892	23995	186	62
CONTIG4105	4103378_c2_7	9893	23996	234	78

CONTIG4105	22476512_c2_8	9894	23997	225	75
CONTIG4107	4797155_c1_3	9895	23998	372	124
CONTIG4108	23926683_f2_4	9896	23999	246	82
CONTIG4108	26570458_f3_6	9897	24000	189	63
CONTIG4108	2783400_c1_8	9898	24001	201	67
CONTIG4109	25582682_f2_4	9899	24002	228	76
CONTIG4109	31532167_c1_5	9900	24003	243	81
CONTIG4112	4797752_c3_5	9901	24004	186	62
CONTIG4115	4460135_f3_2	9902	24005	183	61
CONTIG4116	24413883_f2_1	9903	24006	378	126
CONTIG4118	25661042_c1_8	9904	24007	1431	477
CONTIG4119	23941927_f3_1	9905	24008	720	240
CONTIG4119	16500_c1_2	9906	24009	237	79
CONTIG4119	25672215_c3_5	9907	24010	186	62
CONTIG412	585002_f3_1	9908	24011	321	107
CONTIG4120	4890693_f2_3	9909	24012	240	80
CONTIG4120	5898400_f3_4	9910	24013	525	175
CONTIG4121	4335312_f1_1	9911	24014	189	63
CONTIG4121	26203388_f1_2	9912	24015	927	309
CONTIG4121	176538_f3_4	9913	24016	204	68
CONTIG4123	23859437_f1_1	9914	24017	186	62
CONTIG4123	2402078_f3_3	9915	24018	183	61
CONTIG4123	4179708_f3_4	9916	24019	183	61
CONTIG4124	26350001_f2_3	9917	24020	411	137
CONTIG4125	30157938_f2_5	9918	24021	192	64
CONTIG4126	22460012_c2_7	9919	24022	396	132
CONTIG4127	22270931_f2_2	9920	24023	576	192
CONTIG4127	135906_c3_6	9921	24024	288	96
CONTIG4128	978575_f2_2	9922	24025	783	261
CONTIG4128	187507_c1_7	9923	24026	255	85
CONTIG4128	25438431_c3_8	9924	24027	456	152
CONTIG4130	31367137_f1_3	9925	24028	183	61
CONTIG4131	12610660_c2_9	9926	24029	183	61

CONTIG4133	3917078_f1_2	9927	24030	204	68
CONTIG4133	1954385_f1_3	9928	24031	246	82
CONTIG4133	20317067_f2_4	9929	24032	195	65
CONTIG4134	35647042_c2_6	9930	24033	189	63
CONTIG4134	14063127_f2_1	9931	24034	933	311
CONTIG4134	175011_f3_4	9932	24035	762	254
CONTIG4134	6697302_c2_6	9933	24036	234	78
CONTIG4135	30573550_f1_3	9934	24037	183	61
CONTIG4135	22268763_c1_5	9935	24038	312	104
CONTIG4135	10945277_c1_6	9936	24039	213	71
CONTIG4139	4150912_c1_7	9937	24040	249	83
CONTIG4140	10019187_c2_10	9938	24041	1143	381
CONTIG4142	14860306_c1_5	9939	24042	348	116
CONTIG4145	34173513_c3_4	9940	24043	705	235
CONTIG4145	970087_f1_1	9941	24044	291	97
CONTIG4145	502290_f2_2	9942	24045	603	201
CONTIG4146	15641627_c3_8	9943	24046	240	80
CONTIG4146	24411052_c2_8	9944	24047	573	191
CONTIG4147	33439635_c3_9	9945	24048	189	63
CONTIG4148	2937750_c3_7	9946	24049	528	176
CONTIG4148	14647177_f1_1	9947	24050	189	63
CONTIG415	197655_f3_3	9948	24051	276	92
CONTIG4150	4898411_c3_6	9949	24052	273	91
CONTIG4150	10423577_f2_4	9950	24053	189	63
CONTIG4151	910905_c1_12	9951	24054	339	113
CONTIG4151	2229817_f1_1	9952	24055	204	68
CONTIG4152	36620465_c1_5	9953	24056	207	69
CONTIG4152	16531300_f2_4	9954	24057	306	102
CONTIG4153	25392127_f2_5	9955	24058	240	80
CONTIG4154	24250017_f3_2	9956	24059	1317	439
CONTIG4155	23553887_c1_5	9957	24060	282	94
CONTIG4155	4806883_f2_1	9958	24061	240	80
	43183333_c3_4	9959	24062	192	64

CONTIG4157	11135787_f1_1	9960	24063	684	228
CONTIG4157	35235325_c3_6	9961	24064	183	61
CONTIG4158	25515912_f2_2	9962	24065	225	75
CONTIG416	32610817_f1_1	9963	24066	726	242
CONTIG4160	4723300_f2_2	9964	24067	672	224
CONTIG4161	2125012_f1_5	9965	24068	213	71
CONTIG4161	30714465_f3_9	9966	24069	210	70
CONTIG4162	14459637_c1_9	9967	24070	582	194
CONTIG4162	4882275_c2_11	9968	24071	672	224
CONTIG4163	34182826_c3_13	9969	24072	576	192
CONTIG4163	23634705_c2_5	9970	24073	234	78
CONTIG4164	25503431_f1_1	9971	24074	927	309
CONTIG4164	11910662_c3_9	9972	24075	384	128
CONTIG4165	20413450_f2_1	9973	24076	282	94
CONTIG4165	12985688_c1_5	9974	24077	183	61
CONTIG4165	4064013_c1_6	9975	24078	969	323
CONTIG4166	2063331_f1_1	9976	24079	186	62
CONTIG4166	24642181_f2_2	9977	24080	489	163
CONTIG4166	14191876_f2_3	9978	24081	372	124
CONTIG4166	10743800_f3_4	9979	24082	603	201
CONTIG4166	3390675_c2_8	9980	24083	189	63
CONTIG4167	26443753_f2_4	9981	24084	294	98
CONTIG4167	22345560_f3_6	9982	24085	231	77
CONTIG4168	36117062_f2_2	9983	24086	228	76
CONTIG4168	1211562_c2_5	9984	24087	711	237
CONTIG4170	798583_f3_2	9985	24088	1437	479
CONTIG4171	22851686_f2_1	9986	24089	279	93
CONTIG4171	9964802_f3_4	9987	24090	216	72
CONTIG4171	10743825_c1_6	9988	24091	228	76
CONTIG4173	24412912_c1_8	9989	24092	318	106
CONTIG4174	6063552_f3_4	9990	24093	201	67
CONTIG4174	26822574_c1_6	9991	24094	282	94
CONTIG4175	34063915_c3_6	9992	24095	432	144

CONTIG4175	34551687_c3_7	9993	24096	390	130
CONTIG4176	25582518_f2_2	9994	24097	195	65
CONTIG4179	14962631_c1_4	9995	24098	225	75
CONTIG418	10045286_f3_2	9996	24099	201	67
CONTIG418	600142_c3_3	9997	24100	534	178
CONTIG418	9767660_c1_6	9998	24101	243	81
CONTIG4180	14064750_c1_7	9999	24102	294	98
CONTIG4181	5103203_c2_6	10000	24103	186	62
CONTIG4185	22870642_f1_3	10001	24104	210	70
CONTIG4185	26619155_f3_5	10002	24105	195	65
CONTIG4185	35159468_c1_6	10003	24106	204	68
CONTIG4186	26460817_f3_1	10004	24107	918	306
CONTIG4186	6049205_c3_4	10005	24108	192	64
CONTIG4191	14319703_c2_6	10006	24109	258	86
CONTIG4192	14532180_f3_1	10007	24110	663	221
CONTIG4192	23910900_c1_2	10008	24111	744	248
CONTIG4192	23448375_c3_3	10009	24112	462	154
CONTIG4193	5870300_f1_4	10010	24113	189	63
CONTIG4193	24644627_c3_10	10011	24114	228	76
CONTIG4193	33786302_c3_11	10012	24115	441	147
CONTIG4194	21534011_f3_4	10013	24116	258	86
CONTIG4194	28219636_c1_5	10014	24117	1275	425
CONTIG4195	34409803_c2_5	10015	24118	246	82
CONTIG4196	22069655_c1_4	10016	24119	207	69
CONTIG4197	24484375_c2_6	10017	24120	1302	434
CONTIG4198	4705326_c3_8	10018	24121	183	61
CONTIG420	33782212_f1_1	10019	24122	585	195
CONTIG420	1178913_c3_5	10020	24123	450	150
CONTIG4200	36132162_c3_8	10021	24124	735	245
CONTIG4202	14882625_f3_5	10022	24125	1296	432
CONTIG4202	11879125_c2_8	10023	24126	285	95
CONTIG4202	5100260_c3_11	10024	24127	201	67
CONTIG4203	2929568_f3_3	10025	24128	195	65

CONTIG4204	35729666_f1_1	10026	24129	210	70
CONTIG4204	23479650_c1_3	10027	24130	228	76
CONTIG4205	16898513_c1_3	10028	24131	366	122
CONTIG4206	46900_f1_1	10029	24132	240	80
CONTIG4208	24798380_c2_9	10030	24133	270	90
CONTIG4208	23484437_c3_10	10031	24134	204	68
CONTIG4209	31329512_c3_6	10032	24135	696	232
CONTIG421	23634390_c2_5	10033	24136	333	111
CONTIG4210	21603427_f2_3	10034	24137	246	82
CONTIG4210	24612557_c3_10	10035	24138	774	258
CONTIG4211	20110306_c2_2	10036	24139	927	309
CONTIG4212	11023327_f2_1	10037	24140	2151	717
CONTIG4213	32221927_f1_1	10038	24141	1281	427
CONTIG4213	1056557_f1_2	10039	24142	531	177
CONTIG4214	24807927_f1_3	10040	24143	267	89
CONTIG4216	14245938_f2_3	10041	24144	276	92
CONTIG4217	20365825_f1_1	10042	24145	222	74
CONTIG4217	2950275_c1_4	10043	24146	240	80
CONTIG4217	14237508_c1_5	10044	24147	279	93
CONTIG4219	819086_c1_2	10045	24148	795	265
CONTIG4219	20347152_c3_3	10046	24149	1167	389
CONTIG422	25572075_c3_4	10047	24150	558	186
CONTIG4220	390927_f3_1	10048	24151	225	75
CONTIG4222	4719767_f2_6	10049	24152	201	67
CONTIG4222	24844202_c2_12	10050	24153	240	80
CONTIG4223	2050012_f1_1	10051	24154	189	63
CONTIG4223	21531550_f1_2	10052	24155	198	66
25	6640925_f2_1	10053	24156	249	83
	31304507_f3_2	10054	24157	936	312
	25396931_c2_4	10055	24158	189	63
	23984625_c3_5	10056	24159	477	159
	29484438_f1_1	10057	24160	195	65
	2537553_f3_3	10058	24161	312	104

CONTIG4227	25391316_c2_7	10059	24162	222	74
CONTIG4228	34610255_f3_6	10060	24163	807	269
CONTIG4228	30111343_c1_7	10061	24164	207	69
CONTIG4229	4710761_f2_1	10062	24165	462	154
CONTIG423	23679677_f2_1	10063	24166	201	67
CONTIG423	22297187_c3_2	10064	24167	216	72
CONTIG4230	3944692_f1_1	10065	24168	576	192
CONTIG4232	23540676_f1_3	10066	24169	210	70
CONTIG4232	4721408_f2_4	10067	24170	186	62
CONTIG4233	23867002_c1_2	10068	24171	828	276
CONTIG4233	10554750_c3_6	10069	24172	213	71
CONTIG4235	867775_f3_5	10070	24173	207	69
CONTIG4235	24020285_c3_7	10071	24174	240	80
CONTIG4236	47137_c2_5	10072	24175	1452	484
CONTIG4237	24398505_c1_4	10073	24176	213	71
CONTIG4237	11204691_c1_6	10074	24177	246	82
CONTIG4239	13085917_f3_3	10075	24178	210	70
CONTIG4239	15819062_c2_4	10076	24179	186	62
CONTIG4239	12772677_c3_5	10077	24180	240	80
CONTIG4240	33595882_c3_3	10078	24181	195	65
CONTIG4241	4101075_c2_7	10079	24182	183	61
CONTIG4241	34581257_c2_9	10080	24183	186	62
CONTIG4241	26367212_c3_11	10081	24184	204	68
CONTIG4242	5469035_f1_2	10082	24185	180	60
CONTIG4242	11963542_f3_4	10083	24186	315	105
CONTIG4242	33241625_f3_5	10084	24187	210	70
CONTIG4243	988252_c1_4	10085	24188	216	72
CONTIG4244	21991530_f1_1	10086	24189	402	134
CONTIG4244	24798193_f2_2	10087	24190	213	71
CONTIG4244	13866682_f3_4	10088	24191	216	72
CONTIG4244	25564812_c1_7	10089	24192	246	82
CONTIG4244	14459525_c3_13	10090	24193	183	61
CONTIG4245	26672055_f2_4	10091	24194	189	63

CONTIG4245	26448468_c2_13	10092	24195	225	75
CONTIG4246	26380312_c3_7	10093	24196	288	96
CONTIG4247	6369081_f3_2	10094	24197	267	89
CONTIG4247	469375_c3_6	10095	24198	237	79
CONTIG4248	5891561_f3_3	10096	24199	1605	535
CONTIG4248	36133277_c2_4	10097	24200	411	137
CONTIG4248	4067592_c2_5	10098	24201	216	72
CONTIG4249	4742076_f2_4	10099	24202	312	104
CONTIG4249	26595305_f2_5	10100	24203	729	243
CONTIG4250	32562_f1_1	10101	24204	363	121
CONTIG4253	25391017_f3_4	10102	24205	987	329
CONTIG4254	1351436_f1_1	10103	24206	237	79
CONTIG4254	822638_f2_2	10104	24207	207	69
CONTIG4254	14745312_f2_3	10105	24208	258	86
CONTIG4255	22042150_f1_1	10106	24209	297	99
CONTIG4255	30133385_f1_3	10107	24210	363	121
CONTIG4256	21484431_c1_4	10108	24211	258	86
CONTIG4256	4071015_c2_8	10109	24212	195	65
CONTIG4258	23959763_f3_1	10110	24213	273	91
CONTIG4258	16835825_c2_5	10111	24214	345	115
CONTIG4259	25674157_f1_1	10112	24215	225	75
CONTIG4259	19798126_f2_3	10113	24216	351	117
CONTIG4259	839068_f3_4	10114	24217	1851	617
CONTIG4259	25469805_c3_7	10115	24218	222	74
CONTIG4259	22462936_c3_13	10116	24219	216	72
CONTIG426	9819500_f1_1	10117	24220	222	74
CONTIG4262	33254501_f1_1	10118	24221	183	61
CONTIG4263	969062_f1_2	10119	24222	282	94
CONTIG4263	31735425_f2_3	10120	24223	198	66
CONTIG4263	12376293_c1_5	10121	24224	216	72
CONTIG4263	162590_c1_7	10122	24225	186	62
CONTIG4264	35235005_f1_1	10123	24226	294	98
CONTIG4266	36110812_f1_1	10124	24227	186	62

CONTIG4266	36074156_c2_5	10125	24228	231	77
CONTIG4268	22078517_c2_9	10126	24229	201	67
CONTIG4269	25664001_c1_2	10127	24230	219	73
CONTIG427	423261_f2_1	10128	24231	378	126
CONTIG427	24300006_c2_3	10129	24232	243	81
CONTIG4271	401655_f3_5	10130	24233	195	65
CONTIG4271	35188825_c2_6	10131	24234	195	65
CONTIG4272	32063462_c1_4	10132	24235	726	242
CONTIG4273	32531558_c1_8	10133	24236	828	276
CONTIG4273	9765628_c3_11	10134	24237	1017	339
CONTIG4274	23537831_c2_9	10135	24238	192	64
CONTIG4275	13859626_c1_6	10136	24239	1182	394
CONTIG4275	6250305_c3_8	10137	24240	225	75
CONTIG4278	1368877_f2_3	10138	24241	192	64
CONTIG4278	35399086_f3_4	10139	24242	186	62
CONTIG428	19620463_c1_4	10140	24243	186	62
CONTIG4282	4896927_c1_7	10141	24244	234	78
CONTIG4283	21932625_f2_2	10142	24245	363	121
CONTIG4283	35676576_f3_3	10143	24246	537	179
CONTIG4283	20351625_c3_12	10144	24247	450	150
CONTIG4284	15625458_f2_2	10145	24248	219	73
CONTIG4284	3927_f3_4	10146	24249	195	65
CONTIG4284	2036825_c1_5	10147	24250	192	64
CONTIG4285	24306588_f3_2	10148	24251	207	69
CONTIG4285	23648937_c2_7	10149	24252	273	91
CONTIG4285	10631250_c2_8	10150	24253	210	70
CONTIG4287	11807825_f2_3	10151	24254	237	79
CONTIG4287	4187830_c2_9	10152	24255	528	176
CONTIG4288	9846900_f1_1	10153	24256	204	68
CONTIG4288	19926260_c2_5	10154	24257	201	67
CONTIG4289	12782393_f3_3	10155	24258	237	79
CONTIG4289	15888_c2_6	10156	24259	222	74
CONTIG429	29456300_c1_2	10157	24260	360	120

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CONTIG429	16446937_c3_3	10158	24261	417	139
CONTIG4290	34236641_f1_1	10159	24262	183	61
CONTIG4290	22445890_f2_3	10160	24263	198	66
CONTIG4290	79682_f3_5	10161	24264	255	85
CONTIG4291	6689200_f3_6	10162	24265	186	62
CONTIG4291	4173188_f3_7	10163	24266	249	83
CONTIG4292	14531261_f3_2	10164	24267	267	89
CONTIG4292	21517025_c2_3	10165	24268	312	104
CONTIG4292	6921961_c3_6	10166	24269	207	69
CONTIG4293	34424200_c3_7	10167	24270	246	82
CONTIG4293	24853305_f1_2	10168	24271	183	61
CONTIG4293	4875057_f2_3	10169	24272	444	148
CONTIG4294	1734453_c2_5	10170	24273	375	125
CONTIG4295	21770762_c2_7	10171	24274	366	122
CONTIG4295	568937_c3_11	10172	24275	210	70
CONTIG4296	390640_c3_5	10173	24276	237	79
CONTIG4297	25581700_f3_3	10174	24277	219	73
CONTIG4297	12626537_c1_5	10175	24278	369	123
CONTIG4301	3243902_f1_1	10176	24279	273	91
CONTIG4304	33205001_f3_5	10177	24280	336	112
CONTIG4305	3392_f2_1	10178	24281	225	75
CONTIG4305	35205453_c2_5	10179	24282	246	82
CONTIG4306	3964802_f1_1	10180	24283	201	67
CONTIG4308	24297176_c2_8	10181	24284	600	200
CONTIG4308	24501702_c3_9	10182	24285	1044	348
CONTIG4309	24876880_f1_2	10183	24286	207	69
CONTIG4309	14556318_c1_6	10184	24287	207	69
CONTIG4309	23828250_c2_8	10185	24288	246	82
CONTIG4310	24227252_c1_5	10186	24289	261	87
CONTIG4310	1219286_c3_10	10187	24290	630	210
CONTIG4311	26206283_f3_6	10188	24291	192	64
CONTIG4312	4478406_c3_8	10189	24292	204	68
CONTIG4313	426567_f1_2	10190	24293	234	78

CONTIG4313	23486578_c2_6	10191	24294	237	79
CONTIG4314	33203551_f3_4	10192	24295	198	66
CONTIG4314	819075_c2_5	10193	24296	231	77
CONTIG4315	9803276_c2_10	10194	24297	201	67
CONTIG4315	25548251_c2_11	10195	24298	246	82
CONTIG4316	16056937_f3_1	10196	24299	219	73
CONTIG4318	34195461_c1_4	10197	24300	285	95
CONTIG4319	14563152_f2_2	10198	24301	240	80
CONTIG4321	23628387_f3_6	10199	24302	627	209
CONTIG4321	22539136_f3_7	10200	24303	210	70
CONTIG4322	23647586_c2_4	10201	24304	246	82
CONTIG4323	35203432_f1_1	10202	24305	228	76
CONTIG4323	30272157_f3_3	10203	24306	273	91
CONTIG4324	23475300_c1_8	10204	24307	690	230
CONTIG4326	4509567_f2_3	10205	24308	189	63
CONTIG4326	20161567_f3_7	10206	24309	213	71
CONTIG4326	29532775_c3_11	10207	24310	207	69
CONTIG4329	5896900_c3_2	10208	24311	261	87
CONTIG4332	4962542_c2_9	10209	24312	288	96
CONTIG4333	25585902_c3_8	10210	24313	324	108
CONTIG4336	24492063_f1_2	10211	24314	198	66
CONTIG4336	24647675_c2_9	10212	24315	198	66
CONTIG4337	24433757_f1_1	10213	24316	183	61
CONTIG4337	16414000_c3_10	10214	24317	558	186
CONTIG4338	14852192_f3_4	10215	24318	213	71
CONTIG4338	14453132_c2_9	10216	24319	249	83
CONTIG4338	36454062_c3_11	10217	24320	204	68
CONTIG4339	882817_f3_4	10218	24321	234	78
CONTIG434	33713410_f1_1	10219	24322	192	64
CONTIG4340	5288910_f1_1	10220	24323	663	221
CONTIG4341	34459687_c1_4	10221	24324	222	74
CONTIG4342	24505052_f2_1	10222	24325	222	74
CONTIG4343	15861703_f2_1	10223	24326	189	63

CONTIG4343	6343827_c1_4	10224	24327	243	81
CONTIG4343	22457687_c3_7	10225	24328	204	68
CONTIG4345	14843758_f1_1	10226	24329	183	61
CONTIG4345	32664087_f2_5	10227	24330	663	221
CONTIG4345	24303300_c1_8	10228	24331	240	80
CONTIG4346	24265837_c2_4	10229	24332	192	64
CONTIG4347	23614662_f1_3	10230	24333	258	86
CONTIG4347	9773376_f1_4	10231	24334	201	67
CONTIG4349	23867135_c1_4	10232	24335	189	63
CONTIG4351	4180277_f2_1	10233	24336	261	87
CONTIG4352	23447188_f3_6	10234	24337	255	85
CONTIG4353	193757_c2_4	10235	24338	204	68
CONTIG4353	34187800_c2_5	10236	24339	255	85
CONTIG4353	9881556_c3_6	10237	24340	258	86
CONTIG4354	32475877_c3_7	10238	24341	321	107
CONTIG4355	984385_c2_7	10239	24342	258	86
CONTIG4356	3303577_f1_2	10240	24343	207	69
CONTIG4356	10718911_c2_8	10241	24344	264	88
CONTIG4359	24414838_f1_2	10242	24345	294	98
CONTIG4360	23538553_f2_2	10243	24346	213	71
CONTIG4361	22438255_f2_6	10244	24347	198	66
CONTIG4362	33845250_f1_3	10245	24348	297	99
CONTIG4362	24413912_c2_6	10246	24349	1686	562
CONTIG4363	14587552_f2_3	10247	24350	501	167
CONTIG4364	4119786_f1_1	10248	24351	204	68
CONTIG4364	33984687_c1_5	10249	24352	198	66
CONTIG4364	174041_c2_6	10250	24353	249	83
CONTIG4366	4003135_c2_7	10251	24354	309	103
CONTIG4366	16796925_c2_3	10252	24355	207	69
CONTIG4368	23548453_f1_1	10253	24356	204	68
CONTIG4369	4137_c1_6	10254	24357	210	70
CONTIG4369	29313936_c2_9	10255	24358	261	87
CONTIG4369	14101427_c3_13	10256	24359	270	90

CONTIG4373	31262_c1_2	10257	24360	228	76
CONTIG4373	1486381l_c2_6	10258	24361	183	61
CONTIG4373	11145290_c3_8	10259	24362	183	61
CONTIG4376	25437631_c1_6	10260	24363	1875	625
CONTIG4376	22284563_c1_7	10261	24364	183	61
CONTIG4376	24495327_c2_10	10262	24365	273	91
CONTIG4377	23835058_f3_4	10263	24366	555	185
CONTIG4378	20312766_c2_7	10264	24367	201	67
CONTIG4379	287516_c2_4	10265	24368	195	65
CONTIG4380	31250462_f2_1	10266	24369	225	75
CONTIG4380	30756262_c2_4	10267	24370	267	89
CONTIG4380	10718766_c3_5	10268	24371	273	91
CONTIG4381	36562812_f2_1	10269	24372	237	79
CONTIG4381	34026550_c2_4	10270	24373	219	73
CONTIG4381	14064002_c3_6	10271	24374	267	89
CONTIG4381	10975886_c3_7	10272	24375	189	63
CONTIG4383	13125050_c1_9	10273	24376	468	156
CONTIG4383	165936_c2_10	10274	24377	483	161
CONTIG4388	22400262_c2_4	10275	24378	348	116
CONTIG4389	7033206_c1_3	10276	24379	270	90
CONTIG4389	20117012_c2_5	10277	24380	198	66
CONTIG439	24475061_c2_5	10278	24381	195	65
CONTIG4390	26445212_c2_9	10279	24382	192	64
CONTIG4392	7087885_c1_4	10280	24383	246	82
CONTIG4393	23943937_c2_9	10281	24384	198	66
CONTIG4394	2120187_c3_8	10282	24385	462	154
CONTIG4395	390680_f1_1	10283	24386	201	67
CONTIG4395	14475035_c3_12	10284	24387	1674	558
CONTIG4396	2750181_c2_9	10285	24388	231	77
CONTIG4401	9765625_c2_4	10286	24389	426	142
CONTIG4401	829000_c3_5	10287	24390	1251	417
CONTIG4403	9819155_f1_2	10288	24391	210	70
CONTIG4403	30080288_c1_11	10289	24392	216	72

CONTIG4403	12367178_c1_15	10290	24393	243	81
CONTIG4404	1171927_f1_1	10291	24394	210	70
CONTIG4407	5915677_f3_4	10292	24395	189	63
CONTIG4407	3944442_c3_10	10293	24396	204	68
CONTIG4408	32203213_f2_1	10294	24397	210	70
CONTIG4408	4720277_c1_4	10295	24398	510	170
CONTIG4408	24256253_c2_6	10296	24399	240	80
CONTIG4408	1261281_c3_7	10297	24400	534	178
CONTIG4409	14957812_c3_7	10298	24401	219	73
CONTIG4410	23541656_f2_2	10299	24402	222	74
CONTIG4411	14736430_f2_5	10300	24403	342	114
CONTIG4413	33392177_c3_6	10301	24404	192	64
CONTIG4414	1416317_f2_2	10302	24405	252	84
CONTIG4416	35642642_f2_4	10303	24406	201	67
CONTIG4416	30183578_c2_9	10304	24407	984	328
CONTIG4416	21562877_c2_10	10305	24408	207	69
CONTIG4416	12517010_c2_11	10306	24409	189	63
CONTIG4417	26345280_f3_6	10307	24410	522	174
CONTIG4417	26362717_c1_8	10308	24411	957	319
CONTIG4417	19689035_c1_9	10309	24412	213	71
CONTIG4417	36361550_c3_12	10310	24413	282	94
CONTIG4418	12297510_f1_3	10311	24414	771	257
CONTIG4418	2929561_f2_4	10312	24415	231	77
CONTIG4418	5084686_f3_7	10313	24416	189	63
CONTIG4419	1272137_c1_6	10314	24417	1413	471
CONTIG4420	14641181_f1_3	10315	24418	198	66
CONTIG4420	12675261_c1_5	10316	24419	204	68
CONTIG4422	10740802_c2_7	10317	24420	807	269
CONTIG4422	9964087_c2_10	10318	24421	198	66
CONTIG4423	398441_f1_1	10319	24422	351	117
CONTIG4424	24414212_c1_5	10320	24423	183	61
CONTIG4425	23634627_f1_3	10321	24424	201	67
CONTIG4425	9776950_f2_4	10322	24425	186	62

CONTIG4426	34000078_f3_6	10323	24426	192	64
CONTIG4429	4101702_c2_5	10324	24427	285	95
CONTIG4432	13884508_c1_9	10325	24428	270	90
CONTIG4433	24023912_c1_6	10326	24429	216	72
CONTIG4433	35329512_c2_8	10327	24430	183	61
CONTIG4434	5104767_f2_3	10328	24431	195	65
CONTIG4434	15823587_c3_6	10329	24432	258	86
CONTIG4435	36223427_f1_1	10330	24433	201	67
CONTIG4436	4178780_f2_4	10331	24434	597	199
CONTIG4436	960811_f2_5	10332	24435	216	72
CONTIG4436	14531511_c3_11	10333	24436	246	82
CONTIG4437	14553300_f1_2	10334	24437	420	140
CONTIG4437	12284661_f2_5	10335	24438	372	124
CONTIG4438	14720641_f2_1	10336	24439	207	69
CONTIG4439	6645138_c3_9	10337	24440	834	278
CONTIG444	1032510_f2_1	10338	24441	186	62
CONTIG4440	32595135_f3_4	10339	24442	1515	505
CONTIG4443	23612777_f1_1	10340	24443	1614	538
CONTIG4444	24020436_f3_4	10341	24444	261	87
CONTIG4444	36539078_c3_5	10342	24445	396	132
CONTIG4445	24412507_f2_2	10343	24446	189	63
CONTIG4445	20343752_f2_4	10344	24447	276	92
CONTIG4445	3417287_f3_5	10345	24448	183	61
CONTIG4445	10_c3_8	10346	24449	198	66
CONTIG4450	5350285_c2_8	10347	24450	249	83
CONTIG4450	19725156_c3_10	10348	24451	261	87
CONTIG4452	23461561_c1_8	10349	24452	363	121
CONTIG4452	31363453_c2_11	10350	24453	345	115
CONTIG4454	3909575_c2_2	10351	24454	249	83
CONTIG4455	13800181_c3_3	10352	24455	189	63
CONTIG4456	23676627_f2_3	10353	24456	252	84
CONTIG4456	633541_f3_4	10354	24457	276	92
CONTIG4457	21964768_f1_2	10355	24458	246	82

CONTIG4457	290676_c3_12	10356	24459	390	130
CONTIG4459	22676451_f3_3	10357	24460	234	78
CONTIG4459	6850192_c1_5	10358	24461	327	109
CONTIG4459	47878_c2_6	10359	24462	198	66
CONTIG4459	24332892_c2_8	10360	24463	192	64
CONTIG4459	24416015_c3_10	10361	24464	258	86
CONTIG446	29428127_f2_1	10362	24465	267	89
CONTIG4461	13947681_f2_2	10363	24466	186	62
CONTIG4463	1353133_c1_1	10364	24467	240	80
CONTIG4466	24334407_f2_2	10365	24468	495	165
CONTIG4466	26345307_c2_6	10366	24469	225	75
CONTIG4467	6484385_f1_1	10367	24470	282	94
CONTIG4467	33392762_f3_4	10368	24471	222	74
CONTIG4467	4550705_c3_8	10369	24472	1218	406
CONTIG4468	36505_f3_5	10370	24473	918	306
CONTIG4469	26367187_f1_2	10371	24474	276	92
CONTIG447	4708281_f2_1	10372	24475	768	256
CONTIG4470	15863761_f3_2	10373	24476	240	80
CONTIG4470	47812_c2_6	10374	24477	207	69
CONTIG4470	4070341_c3_7	10375	24478	291	97
CONTIG4471	35349012_f3_3	10376	24479	195	65
CONTIG4471	4491257_c1_5	10377	24480	552	184
CONTIG4471	26571050_c2_6	10378	24481	291	97
CONTIG4471	883555_c2_7	10379	24482	354	118
CONTIG4471	25430427_c3_10	10380	24483	189	63
CONTIG4473	11025707_f2_2	10381	24484	1638	546
CONTIG4475	1070887_c2_7	10382	24485	897	299
CONTIG4475	7800_c3_12	10383	24486	204	68
CONTIG4477	34642090_c2_3	10384	24487	210	70
CONTIG4477	34258442_c3_5	10385	24488	672	224
CONTIG4478	34187942_f1_1	10386	24489	183	61
CONTIG4478	14667567_f3_4	10387	24490	180	60
CONTIG4478	1204818_c1_5	10388	24491	183	61

CONTIG4479	23626512_c3_4	10389	24492	2358	786
CONTIG448	26441303_c1_2	10390	24493	789	263
CONTIG4480	25585151_f1_2	10391	24494	195	65
CONTIG4480	10657805_f2_3	10392	24495	183	61
CONTIG4480	656252_f2_4	10393	24496	225	75
CONTIG4481	715_c3_13	10394	24497	249	83
CONTIG4483	979832_f3_11	10395	24498	198	66
CONTIG4483	627_c1_12	10396	24499	231	77
CONTIG4483	12915962_c2_16	10397	24500	606	202
CONTIG4483	23552163_c2_17	10398	24501	216	72
CONTIG4484	36116402_f3_3	10399	24502	192	64
CONTIG4484	14643812_c3_6	10400	24503	186	62
CONTIG4485	4111650_f2_4	10401	24504	288	96
CONTIG4485	11126926_c3_7	10402	24505	231	77
CONTIG4485	10446062_c3_8	10403	24506	189	63
CONTIG4488	6933260_f3_1	10404	24507	210	70
CONTIG4488	53806_c2_3	10405	24508	516	172
CONTIG4490	22052216_f3_2	10406	24509	249	83
CONTIG4490	34692_c3_7	10407	24510	291	97
CONTIG4491	23714687_f1_1	10408	24511	294	98
CONTIG4491	34173311_c1_3	10409	24512	630	210
CONTIG4492	34179665_f3_2	10410	24513	186	62
CONTIG4492	21738888_c2_7	10411	24514	321	107
CONTIG4493	25421925_f2_4	10412	24515	405	135
CONTIG4493	36605468_f3_6	10413	24516	183	61
CONTIG4493	5110268_c3_17	10414	24517	231	77
CONTIG4494	6667160_f1_2	10415	24518	363	121
CONTIG4495	5104826_c2_6	10416	24519	216	72
CONTIG4496	4413885_c1_4	10417	24520	222	74
CONTIG4496	34620311_c2_5	10418	24521	198	66
CONTIG4497	14630200_f2_2	10419	24522	213	71
CONTIG4497	4892177_f2_3	10420	24523	246	82
CONTIG4497	4891280_f3_5	10421	24524	213	71

CONTIG4497	953177_c3_9	10422	24525	405	135
CONTIG4499	31454761_f3_9	10423	24526	192	64
CONTIG45	30126926_c2_2	10424	24527	183	61
CONTIG45	117805_c3_3	10425	24528	315	105
CONTIG450	22037558_f1_1	10426	24529	216	72
CONTIG4500	89378_f2_2	10427	24530	219	73
CONTIG4500	24304635_c2_9	10428	24531	276	92
CONTIG4500	20392175_f1_2	10429	24532	186	62
CONTIG4501	10251077_f1_3	10430	24533	195	65
CONTIG4501	13068766_c1_7	10431	24534	237	79
CONTIG4501	14492010_c3_13	10432	24535	189	63
CONTIG4503	32245467_c1_6	10433	24536	552	184
CONTIG4503	20024035_c3_7	10434	24537	1239	413
CONTIG4505	5350840_c2_10	10435	24538	258	86
CONTIG4506	19531262_f3_11	10436	24539	282	94
CONTIG4509	156553_f3_3	10437	24540	225	75
CONTIG451	20413430_f3_2	10438	24541	300	100
CONTIG4510	3915910_c2_4	10439	24542	219	73
CONTIG4512	25822831_f3_5	10440	24543	216	72
CONTIG4512	9796950_c1_6	10441	24544	201	67
CONTIG4514	579555_f2_6	10442	24545	207	69
CONTIG4515	36228151_f1_1	10443	24546	195	65
CONTIG4517	46958_f2_6	10444	24547	183	61
CONTIG4517	24657650_f3_7	10445	24548	1302	434
CONTIG4517	242787_c1_9	10446	24549	195	65
CONTIG4518	1363755_f2_1	10447	24550	861	287
CONTIG452	444687_c3_3	10448	24551	264	88
CONTIG452	4865752_c3_5	10449	24552	195	65
CONTIG4521	237937_f3_3	10450	24553	279	93
CONTIG4522	33213412_f2_2	10451	24554	270	90
CONTIG4523	19694050_f2_1	10452	24555	192	64
CONTIG4523	16421912_c3_6	10453	24556	210	70
CONTIG4525	29303427_f1_1	10454	24557	1836	612

CONTIG4525	2660262_c3_7	10455	24558	186	62
CONTIG4526	35392508_f2_4	10456	24559	237	79
CONTIG4527	14586062_c3_11	10457	24560	246	82
CONTIG4528	26367306_c3_12	10458	24561	900	300
CONTIG453	22459385_f2_2	10459	24562	183	61
CONTIG4531	3318827_f2_6	10460	24563	201	67
CONTIG4531	15642686_c1_8	10461	24564	207	69
CONTIG4534	21641930_f2_3	10462	24565	210	70
CONTIG4534	9777127_f2_4	10463	24566	387	129
CONTIG4534	24510188_f2_5	10464	24567	552	184
CONTIG4535	1195907_c3_12	10465	24568	192	64
CONTIG4536	829712_f1_1	10466	24569	219	73
CONTIG4536	7032138_c3_8	10467	24570	216	72
CONTIG4537	2829802_f3_4	10468	24571	219	73
CONTIG4537	6329502_c3_8	10469	24572	405	135
CONTIG4538	15789752_c1_3	10470	24573	198	66
CONTIG4539	4073412_f2_3	10471	24574	969	323
CONTIG4539	6836425_c1_10	10472	24575	228	76
CONTIG4539	25400936_c2_14	10473	24576	225	75
CONTIG4540	1386583 0_f3_4	10474	24577	291	97
CONTIG4540	5115927_f3_5	10475	24578	318	106
CONTIG4541	23640926_c1_5	10476	24579	240	80
CONTIG4541	35353382_c2_8	10477	24580	960	320
CONTIG4542	30129843_f2_1	10478	24581	237	79
CONTIG4542	35314125_c2_4	10479	24582	231	77
CONTIG4542	21679687_c3_5	10480	24583	297	99
CONTIG4543	10625432_f2_3	10481	24584	318	106
CONTIG4544	33242186_c1_2	10482	24585	192	64
CONTIG4545	24647500_c3_5	10483	24586	708	236
CONTIG4549	26563942_f2_1	10484	24587	267	89
CONTIG4550	1173552_f3_2	10485	24588	255	85
CONTIG4550	24410666_c2_3	10486	24589	192	64
CONTIG4551	796900_f2_5	10487	24590	762	254

CONTIG4551	814457_f3_7	10488	24591	186	62
CONTIG4552	25666067_f3_10	10489	24592	195	65
CONTIG4552	33699002_c1_11	10490	24593	207	69
CONTIG4552	9954032_c2_15	10491	24594	642	214
CONTIG4554	29296893_f1_1	10492	24595	627	209
CONTIG4554	23469081_f2_4	10493	24596	231	77
CONTIG4556	1211516_f3_6	10494	24597	234	78
CONTIG4556	30581500_c2_8	10495	24598	204	68
CONTIG4557	5086537_c2_8	10496	24599	279	93
CONTIG4558	6913151_f1_1	10497	24600	1023	341
CONTIG4558	1647213_f3_5	10498	24601	195	65
CONTIG4560	5360192_f3_3	10499	24602	414	138
CONTIG4561	24239061_f2_2	10500	24603	201	67
CONTIG4561	13675252_f2_4	10501	24604	207	69
CONTIG4565	21722756_c2_6	10502	24605	375	125
CONTIG4565	24800877_c3_7	10503	24606	627	209
CONTIG4566	24666067_f1_1	10504	24607	231	77
CONTIG4567	22070286_f2_1	10505	24608	216	72
CONTIG4568	4740717_f1_1	10506	24609	237	79
CONTIG4568	22539075_c2_8	10507	24610	1062	354
CONTIG4568	13883577_c3_9	10508	24611	270	90
CONTIG4569	11877175_f3_2	10509	24612	273	91
CONTIG4569	12383582_c3_6	10510	24613	183	61
CONTIG4569	24665927_c3_7	10511	24614	411	137
CONTIG4571	24218753_f1_1	10512	24615	195	65
CONTIG4571	7986052_c1_4	10513	24616	186	62
CONTIG4572	213535_f3_2	10514	24617	270	90
CONTIG4572	29692680_c2_3	10515	24618	183	61
CONTIG4572	3004843_c2_4	10516	24619	183	61
CONTIG4574	31287811_c1_6	10517	24620	210	70
CONTIG4575	3907677_c1_5	10518	24621	255	85
CONTIG4575	23835952_c3_10	10519	24622	456	152
CONTIG4576	4073552_f2_5	10520	24623	246	82

CONTIG4576	10978433_f3_6	10521	24624	231	77
CONTIG4577	20756528_f3_2	10522	24625	243	81
CONTIG4577	164000_f3_3	10523	24626	240	80
CONTIG4578	34632692_f1_1	10524	24627	1005	335
CONTIG4578	176567_f3_6	10525	24628	315	105
CONTIG4579	267887_f1_1	10526	24629	258	86
CONTIG4579	24271916_f2_2	10527	24630	933	311
CONTIG4579	24026885_f2_3	10528	24631	195	65
CONTIG4579	32128750_c2_7	10529	24632	192	64
CONTIG4580	15035438_c3_7	10530	24633	663	221
CONTIG4582	4564377_f2_1	10531	24634	183	61
CONTIG4582	12673437_c2_4	10532	24635	390	130
CONTIG4583	1180262_c1_2	10533	24636	339	113
CONTIG4584	30470040_f1_1	10534	24637	201	67
CONTIG4584	860327_f2_4	10535	24638	237	79
CONTIG4584	29533135_c1_6	10536	24639	216	72
CONTIG4584	5121010_c3_10	10537	24640	222	74
CONTIG4585	6848752_c1_9	10538	24641	1206	402
CONTIG4585	1257843_c3_11	10539	24642	360	120
CONTIG4587	23707925_c2_6	10540	24643	210	70
CONTIG4588	12617031_f1_2	10541	24644	357	119
CONTIG4588	35991688_c1_5	10542	24645	252	84
CONTIG4589	19691885_c2_5	10543	24646	204	68
CONTIG459	24409392_f1_1	10544	24647	219	73
CONTIG4590	20495686_f1_2	10545	24648	315	105
CONTIG4590	20350337_f2_4	10546	24649	297	99
CONTIG4590	1617063_f3_5	10547	24650	213	71
CONTIG4590	3275_f3_6	10548	24651	198	66
CONTIG4590	5115811_c2_8	10549	24652	225	75
CONTIG4590	4695933_c3_9	10550	24653	213	71
CONTIG4591	1609687_c1_3	10551	24654	210	70
CONTIG4591	24413951_c1_4	10552	24655	189	63
CONTIG4591	2772637_c3_10	10553	24656	186	62

CONTIG4592	25468792_c1_5	10554	24657	666	222
CONTIG4594	24229561_f2_3	10555	24658	603	201
CONTIG4596	9870156_c3_12	10556	24659	345	115
CONTIG4597	24089055_f1_2	10557	24660	252	84
CONTIG4597	20189415_f3_6	10558	24661	282	94
CONTIG4598	16604678_c1_6	10559	24662	198	66
CONTIG4599	35656506_f2_2	10560	24663	261	87
CONTIG4599	167630_f3_3	10561	24664	255	85
CONTIG46	26445285_c2_2	10562	24665	261	87
CONTIG460	34164218_c2_1	10563	24666	207	69
CONTIG4600	36539177_c2_3	10564	24667	195	65
CONTIG4602	26382938_c2_5	10565	24668	330	110
CONTIG4603	3302280_f2_3	10566	24669	213	71
CONTIG4603	22679566_f3_5	10567	24670	300	100
CONTIG4604	39062_f2_3	10568	24671	1014	338
CONTIG4604	24617807_f2_4	10569	24672	234	78
CONTIG4605	10835942_f2_2	10570	24673	375	125
CONTIG4605	24426553_f3_5	10571	24674	225	75
CONTIG4605	188760_c2_10	10572	24675	231	77
CONTIG4606	29429687_f3_5	10573	24676	297	99
CONTIG4606	6054502_c1_6	10574	24677	195	65
CONTIG4608	9766512_f1_3	10575	24678	297	99
CONTIG4608	4953405_f2_4	10576	24679	258	86
CONTIG4608	4860702_c3_10	10577	24680	246	82
CONTIG4609	30167502_f1_2	10578	24681	192	64
CONTIG4609	972942_f3_7	10579	24682	207	69
CONTIG4609	2926502_c2_15	10580	24683	243	81
CONTIG461	26281687_c2_4	10581	24684	777	259
CONTIG4610	46961_f1_2	10582	24685	264	88
CONTIG4610	13836052_f2_3	10583	24686	384	128
CONTIG4610	24303503_c1_5	10584	24687	264	88
CONTIG4610	14492175_c1_6	10585	24688	186	62
CONTIG4615	10413382_f3_3	10586	24689	345	115

CONTIG4615	23454050_f3_4	10587	24690	183	61
CONTIG4615	30556257_f3_6	10588	24691	186	62
CONTIG4616	970262_c1_5	10589	24692	192	64
CONTIG4616	20955000_c2_8	10590	24693	237	79
CONTIG4619	4890700_f3_5	10591	24694	189	63
CONTIG462	984636_f2_2	10592	24695	312	104
CONTIG4620	1181325_f2_5	10593	24696	198	66
CONTIG4621	1606596_f2_2	10594	24697	774	258
CONTIG4621	19960300_f2_3	10595	24698	501	167
CONTIG4622	6285306_f1_2	10596	24699	525	175
CONTIG4623	34485682_f1_2	10597	24700	195	65
CONTIG4623	3306262_f2_3	10598	24701	441	147
CONTIG4623	23960010_c1_6	10599	24702	183	61
CONTIG4623	23995626_c1_7	10600	24703	336	112
CONTIG4625	4877182_f1_1	10601	24704	183	61
CONTIG4625	34011592_c3_9	10602	24705	255	85
CONTIG4626	31328317_f2_1	10603	24706	186	62
CONTIG4628	23948450_f2_1	10604	24707	183	61
CONTIG4628	4475312_c1_2	10605	24708	216	72
CONTIG4628	625075_c3_4	10606	24709	279	93
CONTIG4629	14642142_f1_1	10607	24710	228	76
CONTIG4629	33484692_c2_8	10608	24711	291	97
CONTIG4630	5866432_c1_7	10609	24712	231	77
CONTIG4631	956640_f3_5	10610	24713	225	75
CONTIG4631	23957887_c3_11	10611	24714	255	85
CONTIG4632	30251942_c2_9	10612	24715	255	85
CONTIG4633	25422512_c2_9	10613	24716	204	68
CONTIG4633	4722125_c3_11	10614	24717	192	64
CONTIG4633	6031563_c3_12	10615	24718	192	64
CONTIG4634	24320307_f2_1	10616	24719	453	151
CONTIG4635	3912750_f1_2	10617	24720	384	128
CONTIG4636	12900099_c1_3	10618	24721	183	61
CONTIG4636	1053763_c3_8	10619	24722	192	64

CONTIG464	10005175_f2_1	10620	24723	297	99
CONTIG4640	876312_f1_1	10621	24724	756	252
CONTIG4640	30115937_c1_7	10622	24725	708	236
CONTIG4642	20321910_f2_3	10623	24726	186	62
CONTIG4642	24093812_f2_4	10624	24727	351	117
CONTIG4642	23468786_f3_7	10625	24728	270	90
CONTIG4642	25397135_c2_9	10626	24729	186	62
CONTIG4643	4064186_f2_3	10627	24730	294	98
CONTIG4643	2773428_c3_7	10628	24731	225	75
CONTIG4644	26853527_f1_1	10629	24732	228	76
CONTIG4644	26368818_f3_7	10630	24733	1806	602
CONTIG4644	20703930_c3_12	10631	24734	252	84
CONTIG4644	3994200_c3_13	10632	24735	186	62
CONTIG4645	6678467_f1_1	10633	24736	288	96
CONTIG4645	24422151_c1_7	10634	24737	273	91
CONTIG4647	23443761_f2_2	10635	24738	258	86
CONTIG4647	5292812_f2_3	10636	24739	243	81
CONTIG4647	26287532_f3_6	10637	24740	255	85
CONTIG4647	11876300_c2_7	10638	24741	867	289
CONTIG4647	859680_c3_8	10639	24742	840	280
CONTIG4649	3912761_c2_8	10640	24743	222	74
CONTIG4650	21758462_f3_6	10641	24744	279	93
CONTIG4650	1284692_c1_7	10642	24745	213	71
CONTIG4650	19742706_c1_8	10643	24746	201	67
CONTIG4651	33831687_c3_5	10644	24747	348	116
CONTIG4652	7069687_f1_1	10645	24748	465	155
CONTIG4652	35205312_f2_3	10646	24749	204	68
CONTIG4652	24882188_f2_5	10647	24750	1008	336
CONTIG4653	7039182_f1_2	10648	24751	237	79
CONTIG4654	33401587_f3_7	10649	24752	219	73
CONTIG4657	1429657_c1_8	10650	24753	192	64
CONTIG4658	29332176_f1_1	10651	24754	393	131
CONTIG4659	4034635_f2_3	10652	24755	543	181

CONTIG4659	24022207_f3_5	10653	24756	192	64
CONTIG4659	6772075_c2_6	10654	24757	294	98
CONTIG4660	26594806_f3_7	10655	24758	963	321
CONTIG4661	25820875_c2_4	10656	24759	243	81
CONTIG4661	2439383_f1_1	10657	24760	348	116
CONTIG4663	26345452_f3_5	10658	24761	471	157
CONTIG4663	32289566_c1_10	10659	24762	195	65
CONTIG4663	29925662_c2_14	10660	24763	252	84
CONTIG4663	5959453_c3_15	10661	24764	237	79
CONTIG4664	23400_c2_7	10662	24765	261	87
CONTIG4665	36226661_c2_12	10663	24766	1752	584
CONTIG4666	24475676_f1_3	10664	24767	213	71
CONTIG4666	32620691_c1_12	10665	24768	285	95
CONTIG4667	34049067_c3_10	10666	24769	204	68
CONTIG467	33400317_c3_1	10667	24770	183	61
CONTIG4668	551937_f1_1	10668	24771	243	81
CONTIG4669	1195186_c2_6	10669	24772	186	62
CONTIG4669	26041308_c2_6	10670	24773	189	63
CONTIG4670	26269625_c2_7	10671	24774	678	226
CONTIG4670	25520275_c1_7	10672	24775	495	165
CONTIG4671	14276437_f1_2	10673	24776	228	76
CONTIG4671	10978377_f2_1	10674	24777	324	108
CONTIG4671	20595178_f3_3	10675	24778	192	64
CONTIG4672	23867177_c3_12	10676	24779	219	73
CONTIG4673	9772578_f3_4	10677	24780	189	63
CONTIG4673	22063426_c2_7	10678	24781	237	79
CONTIG4676	6851413_c3_10	10679	24782	204	68
CONTIG4676	26350317_f3_2	10680	24783	273	91
CONTIG4678	10272590_f3_3	10681	24784	186	62
CONTIG4680	25398318_c3_7	10682	24785	186	62
CONTIG4680	14726502_f3_6	10683	24786	189	63
CONTIG4680	6908280_f2_3	10684	24787	195	65
CONTIG4680	14161511_f2_4	10685	24788	216	72

CONTIG4680	21662938_c2_10	10686	24789	909	303
CONTIG4680	26658510_c2_11	10687	24790	1074	358
CONTIG4681	13775302_c3_3	10688	24791	216	72
CONTIG4682	20595252_f2_2	10689	24792	183	61
CONTIG4682	25581377_f3_5	10690	24793	240	80
CONTIG4683	4300002_f3_2	10691	24794	204	68
CONTIG4686	2037807_f1_2	10692	24795	234	78
CONTIG4686	2070378_f3_4	10693	24796	183	61
CONTIG4688	1417921 8_c2_6	10694	24797	321	107
CONTIG4687	24313925_f3_7	10695	24798	504	168
CONTIG4687	2378762_c1_8	10696	24799	198	66
CONTIG4688	1707632_c1_6	10697	24800	294	98
CONTIG4688	1016293 7_c1_7	10698	24801	186	62
CONTIG4689	35673427_f3_6	10699	24802	189	63
CONTIG4690	36574038_f3_4	10700	24803	228	76
CONTIG4690	4064400_c1_6	10701	24804	387	129
CONTIG4690	21721906_c2_8	10702	24805	198	66
CONTIG4691	24485912_f2_3	10703	24806	342	114
CONTIG4692	6093783_c2_6	10704	24807	243	81
CONTIG4693	25390718_c2_3	10705	24808	204	68
CONTIG4694	23642126_f2_2	10706	24809	1980	660
CONTIG4695	2915807_f1_1	10707	24810	258	86
CONTIG4695	25414501_f2_3	10708	24811	294	98
CONTIG4695	33398390_f3_4	10709	24812	189	63
CONTIG4695	34062510_f3_5	10710	24813	204	68
CONTIG4695	19970375_c3_8	10711	24814	282	94
CONTIG4696	6752202_f3_5	10712	24815	306	102
CONTIG4696	3242816_c1_6	10713	24816	249	83
CONTIG4698	35156550_c1_3	10714	24817	213	71
CONTIG4698	822181_c1_4	10715	24818	228	76
CONTIG4699	19726562_f2_3	10716	24819	183	61
CONTIG4699	15938_f2_4	10717	24820	219	73
CONTIG47	23929512_f2_3	10718	24821	276	92

CONTIG47	3183587_c2_7	10719	24822	198	66
CONTIG470	2869788_f1_1	10720	24823	690	230
CONTIG4700	36610890_f3_5	10721	24824	204	68
CONTIG4701	26359385_c1_6	10722	24825	351	117
CONTIG4701	20194375_c3_13	10723	24826	222	74
CONTIG4703	2381300_f2_3	10724	24827	246	82
CONTIG4703	31906517_f2_6	10725	24828	213	71
CONTIG4703	12578130_f3_7	10726	24829	216	72
CONTIG4704	1048280_c2_7	10727	24830	888	296
CONTIG4705	23634510_f3_5	10728	24831	690	230
CONTIG4706	22048176_f1_1	10729	24832	435	145
CONTIG4707	19584410_f1_1	10730	24833	246	82
CONTIG4707	26839217_c2_6	10731	24834	195	65
CONTIG4708	24008385_c3_8	10732	24835	930	310
CONTIG4708	23515905_c2_4	10733	24836	243	81
CONTIG4709	14259688_f3_9	10734	24837	270	90
CONTIG471	23359388_f2_1	10735	24838	291	97
CONTIG4710	7304543_f1_1	10736	24839	183	61
CONTIG4710	33798562_c3_5	10737	24840	294	98
CONTIG4710	21995462_c3_7	10738	24841	585	195
CONTIG4712	40750_f2_2	10739	24842	198	66
CONTIG4713	33437880_c2_6	10740	24843	324	108
CONTIG4714	10820307_f3_5	10741	24844	297	99
CONTIG4714	23625000_c1_6	10742	24845	207	69
CONTIG4715	2928275_c1_7	10743	24846	369	123
CONTIG4715	663567_f2_4	10744	24847	216	72
CONTIG4716	15914193_f3_8	10745	24848	198	66
CONTIG4716	25390701_f1_3	10746	24849	210	70
CONTIG4716	24004752_f3_6	10747	24850	192	64
CONTIG4717	14628127_c1_8	10748	24851	297	99
CONTIG4720	33245255_c2_6	10749	24852	243	81
CONTIG4720	116588_f1_1	10750	24853	333	111
CONTIG4720	1438826_f2_3	10751	24854	294	98

CONTIG4720	32226562_c1_9	10752	24855	198	66
CONTIG4720	3017287_c2_10	10753	24856	906	302
CONTIG4722	26214192_f2_2	10754	24857	279	93
CONTIG4722	17041563_f2_2	10755	24858	198	66
CONTIG4722	10725005_c3_10	10756	24859	189	63
CONTIG4724	5937660_f2_2	10757	24860	375	125
CONTIG4724	36220656_f2_3	10758	24861	246	82
CONTIG4725	24226553_f2_3	10759	24862	225	75
CONTIG4726	24298432_f2_2	10760	24863	186	62
CONTIG4726	3313825_f2_3	10761	24864	570	190
CONTIG4727	3323762_f2_2	10762	24865	261	87
CONTIG4728	4492303_c2_8	10763	24866	822	274
CONTIG4728	34274188_c3_14	10764	24867	282	94
CONTIG4728	35157000_c2_11	10765	24868	753	251
CONTIG4729	24414042_c1_7	10766	24869	513	171
CONTIG4729	35943775_c3_13	10767	24870	261	87
CONTIG4730	24722817_f3_6	10768	24871	294	98
CONTIG4731	5266890_f1_2	10769	24872	297	99
CONTIG4731	16803177_f2_6	10770	24873	204	68
CONTIG4731	2829427_c1_11	10771	24874	609	203
CONTIG4732	21570262_f1_3	10772	24875	207	69
CONTIG4732	4425805_f2_5	10773	24876	201	67
CONTIG4733	4339688_f1_1	10774	24877	183	61
CONTIG4733	178528_f2_3	10775	24878	417	139
CONTIG4734	21890902_c2_8	10776	24879	255	85
CONTIG4734	5163180_c2_9	10777	24880	243	81
CONTIG4736	21673300_f2_3	10778	24881	759	253
CONTIG4738	24033_f1_2	10779	24882	201	67
CONTIG4738	32109457_c2_7	10780	24883	234	78
CONTIG4738	22300262_c2_8	10781	24884	315	105
CONTIG4739	2034403_c3_5	10782	24885	201	67
CONTIG4740	22850053_f2_7	10783	24886	186	62
CONTIG4742	19648385_f2_2	10784	24887	702	234

CONTIG4742	4070938_c3_9	10785	24888	258	86
CONTIG4743	36570311_f1_1	10786	24889	225	75
CONTIG4743	35972153_f1_2	10787	24890	219	73
CONTIG4743	29922180_c3_8	10788	24891	195	65
CONTIG4744	26444562_c3_6	10789	24892	261	87
CONTIG4745	26444807_f2_2	10790	24893	198	66
CONTIG4746	14253805_f3_4	10791	24894	252	84
CONTIG4746	26912513_c3_12	10792	24895	483	161
CONTIG4747	1562701 5_c3_13	10793	24896	198	66
CONTIG4747	24401410_f1_3	10794	24897	192	64
CONTIG4748	5865918_f3_4	10795	24898	282	94
CONTIG4748	24433535_c1_8	10796	24899	237	79
CONTIG475	1076107 8_c2_1	10797	24900	186	62
CONTIG4750	23629450_f2_4	10798	24901	201	67
CONTIG4753	12112877_f1_2	10799	24902	249	83
CONTIG4754	32038937_f1_1	10800	24903	219	73
CONTIG4754	22317055_c3_7	10801	24904	186	62
CONTIG4756	11814425_f2_3	10802	24905	204	68
CONTIG4756	836638_c1_11	10803	24906	357	119
CONTIG4757	4095052_c2_6	10804	24907	204	68
CONTIG4757	24022825_c3_8	10805	24908	228	76
CONTIG4759	34160783_f2_6	10806	24909	297	99
CONTIG4759	15930_c2_14	10807	24910	990	330
CONTIG476	13851630_c3_1	10808	24911	555	185
CONTIG4760	23836052_f3_2	10809	24912	225	75
CONTIG4761	24395305_f3_3	10810	24913	222	74
CONTIG4761	21673825_f3_4	10811	24914	264	88
CONTIG4762	12988307_f2_2	10812	24915	354	118
CONTIG4762	23835408_f3_7	10813	24916	279	93
CONTIG4762	14848427_f3_8	10814	24917	534	178
CONTIG4762	5129681_f3_9	10815	24918	213	71
CONTIG4763	2735890_f1_2	10816	24919	336	112
CONTIG4764	20431588_c3_8	10817	24920	312	104

CONTIG4764	197000_c3_13	10818	24921	186	62
CONTIG4765	429561_f1_1	10819	24922	204	68
CONTIG4765	8406313_c3_9	10820	24923	369	123
CONTIG4765	21492755_c3_10	10821	24924	186	62
CONTIG4766	5877300_f2_3	10822	24925	1407	469
CONTIG4766	14251561_c2_6	10823	24926	219	73
CONTIG4767	14744000_c3_7	10824	24927	192	64
CONTIG4769	13942887_c2_9	10825	24928	669	223
CONTIG4770	24239425_f2_3	10826	24929	276	92
CONTIG4771	4017751_f2_3	10827	24930	183	61
CONTIG4771	12553127_c1_7	10828	24931	189	63
CONTIG4771	10745287_c2_8	10829	24932	186	62
CONTIG4771	815650_c2_11	10830	24933	186	62
CONTIG4772	23703501_c1_7	10831	24934	249	83
CONTIG4773	30661566_f1_1	10832	24935	195	65
CONTIG4775	4116262_c1_6	10833	24936	342	114
CONTIG4776	22157551_f1_1	10834	24937	225	75
CONTIG4777	22766257_c1_5	10835	24938	246	82
CONTIG4777	2395002_c2_8	10836	24939	195	65
CONTIG4778	10212505_f1_1	10837	24940	186	62
CONTIG478	33685937_c2_1	10838	24941	321	107
CONTIG4782	1568I712_f1_1	10839	24942	279	93
CONTIG4783	23866081_c2_5	10840	24943	195	65
CONTIG4785	33204402_c2_7	10841	24944	195	65
CONTIG4785	12672557_c3_10	10842	24945	372	124
CONTIG4786	35360340_c2_7	10843	24946	225	75
CONTIG4788	24615837_f1_1	10844	24947	1527	509
CONTIG4788	34180337_f3_4	10845	24948	879	293
CONTIG4789	22268751_f3_6	10846	24949	234	78
CONTIG4789	23837757_c2_10	10847	24950	204	68
CONTIG4790	24609505_f1_2	10848	24951	237	79
CONTIG4790	22454677_c2_10	10849	24952	255	85
CONTIG4791	4797751_c1_3	10850	24953	624	208

CONTIG4793	22437626_f3_3	10851	24954	264	88
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CONTIG4794	13788893_f1_1	10853	24956	264	88
CONTIG4795	6385751_f3_4	10854	24957	855	285
CONTIG4796	7084682_f3_1	10855	24958	192	64
CONTIG4798	26376941_f3_5	10856	24959	408	136
CONTIG4800	9938253_f3_4	10857	24960	306	102
CONTIG4801	36564093_f2_4	10858	24961	222	74
CONTIG4802	26015953_c2_10	10859	24962	183	61
CONTIG4803	4300031_f2_4	10860	24963	249	83
CONTIG4803	21662790_c2_9	10861	24964	195	65
CONTIG4804	1953375_f1_2	10862	24965	339	113
CONTIG4804	14484763_f3_6	10863	24966	204	68
CONTIG4805	16888_c2_8	10864	24967	195	65
CONTIG4806	14564125_c2_5	10865	24968	504	168
CONTIG4806	23473465_c1_10	10866	24969	825	275
CONTIG4807	12_f2_4	10867	24970	222	74
CONTIG4807	1210937_f3_6	10868	24971	324	108
CONTIG4807	30736075_c1_9	10869	24972	198	66
CONTIG4808	24255432_c1_6	10870	24973	318	106
CONTIG4808	797305_c2_9	10871	24974	330	110
CONTIG4809	23863125_f1_2	10872	24975	300	100
CONTIG4809	3906578_f2_4	10873	24976	348	116
CONTIG4809	14629375_f2_5	10874	24977	186	62
CONTIG4809	7087588_c2_9	10875	24978	357	119
CONTIG481	31562_f2_1	10876	24979	240	80
CONTIG4811	21975306_f2_3	10877	24980	303	101
CONTIG4811	14333136_f3_4	10878	24981	219	73
CONTIG4811	26422086_f3_8	10879	24982	198	66
CONTIG4812	15647692_c1_5	10880	24983	1029	343
CONTIG4812	1172182_c3_10	10881	24984	366	122
CONTIG4812	33331680_c3_11	10882	24985	222	74
CONTIG4813	14657887_c1_7	10883	24986	225	75

CONTIG4813	34195312_c3_10	10884	24987	183	61
CONTIG4814	16833126_f1_1	10885	24988	945	315
CONTIG4815	24335802_f1_1	10886	24989	1197	399
CONTIG4815	23915913_f3_7	10887	24990	243	81
CONTIG4815	33250013_c1_8	10888	24991	183	61
CONTIG4816	29563753_f1_2	10889	24992	273	91
CONTIG4816	19808541_f3_5	10890	24993	186	62
CONTIG4816	2150377_c1_6	10891	24994	672	224
CONTIG4816	19704500_c1_7	10892	24995	270	90
CONTIG4817	23445882_f1_2	10893	24996	192	64
CONTIG4817	4726525_c1_5	10894	24997	204	68
CONTIG4817	3940712_c2_12	10895	24998	225	75
CONTIG4817	3990632_c3_13	10896	24999	609	203
CONTIG4818	33282162_f1_1	10897	25000	240	80
CONTIG4819	412525_c3_15	10898	25001	300	100
CONTIG482	7087943_f3_1	10899	25002	270	90
CONTIG4821	33329652_f2_4	10900	25003	267	89
CONTIG4821	10365786_f2_5	10901	25004	195	65
CONTIG4821	25673177_f2_6	10902	25005	312	104
CONTIG4821	29343807_f2_7	10903	25006	207	69
CONTIG4821	5906575_c2_12	10904	25007	198	66
CONTIG4822	6540_f2_7	10905	25008	393	131
CONTIG4827	23704387_f2_3	10906	25009	255	85
CONTIG4827	23604700_f2_5	10907	25010	183	61
CONTIG4827	390637_f3_6	10908	25011	183	61
CONTIG4827	15703575_c2_10	10909	25012	231	77
CONTIG4828	22673337_f1_3	10910	25013	201	67
CONTIG4829	1953135_f2_5	10911	25014	192	64
CONTIG4829	29318805_c1_12	10912	25015	651	217
CONTIG483	822175_f1_1	10913	25016	630	210
CONTIG4830	22070325_f1_1	10914	25017	1419	473
CONTIG4830	10722325_f1_2	10915	25018	207.	69
CONTIG4830	1348900_f2_4	10916	25019	438	146

CONTIG4830	5859375_c2_8	10917	25020	186	62
CONTIG4831	444627_c3_3	10918	25021	252	84
CONTIG4831	14254035_c3_4	10919	25022	183	61
CONTIG4834	203127_f1_1	10920	25023	246	82
CONTIG4834	3910650_f2_2	10921	25024	516	172
CONTIG4835	14704500_f3_4	10922	25025	195	65
CONTIG4835	21696931_c2_8	10923	25026	1203	401
CONTIG4836	4765887_c1_4	10924	25027	195	65
CONTIG4838	3368937_f3_5	10925	25028	201	67
CONTIG4838	1954438_c2_8	10926	25029	267	89
CONTIG4839	4462568_f2_3	10927	25030	303	101
CONTIG4839	47311_f3_5	10928	25031	207	69
CONTIG4839	23438900_c1_9	10929	25032	255	85
CONTIG4839	23694656_c2_11	10930	25033	207	69
CONTIG4839	175625_f3_13	10931	25034	252	84
CONTIG484	29298775_f3_1	10932	25035	216	72
CONTIG4840	25899926_f2_3	10933	25036	195	65
CONTIG4840	3221012_f2_4	10934	25037	438	146
CONTIG4840	5094013_f3_6	10935	25038	186	62
CONTIG4840	7064201_c1_8	10936	25039	363	121
CONTIG4841	35740628_f2_2	10937	25040	195	65
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CONTIG4842	33399137_c1_6	10941	25044	264	88
CONTIG4843	4709686_f2_3	10942	25045	1239	413
CONTIG4844	805175_c1_5	10943	25046	222	74
CONTIG4844	29313432_c2_9	10944	25047	213	71
CONTIG4847	2166663_f2_1	10945	25048	1077	359
CONTIG4847	960003_c1_8	10946	25049	213	71
CONTIG4848	25409817_f1_2	10947	25050	195	65
CONTIG4849	24429802_f1_1	10948	25051	216	72
CONTIG4849	4727141_c3_8	10949	25052	231	77

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CONTIG4850	24400702_f1_1	10950	25053	189	63
CONTIG4850	4547192_c2_12	10951	25054	195	65
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CONTIG4852	14646937_f3_5	10953	25056	228	76
CONTIG4852	13703211_c1_9	10954	25057	1626	542
CONTIG4853	14534377_f1_1	10955	25058	213	71
CONTIG4853	6906277_f2_2	10956	25059	867	289
CONTIG4854	3142301_f3_3	10957	25060	228	76
CONTIG4854	6906687_c1_4	10958	25061	237	79
CONTIG4854	798511_c3_7	10959	25062	258	86
CONTIG4855	21723792_f3_4	10960	25063	222	74
CONTIG4856	24851082_f2_3	10961	25064	183	61
CONTIG4856	23626306_c2_12	10962	25065	216	72
CONTIG4857	24818753_f1_1	10963	25066	249	83
CONTIG4857	22069752_f3_6	10964	25067	234	78
CONTIG4858	9790650_c1_5	10965	25068	198	66
CONTIG4858	6035661_c2_6	10966	25069	204	68
CONTIG4858	782886_c3_7	10967	25070	186	62
CONTIG4859	579812_c1_8	10968	25071	267	89
CONTIG4859	23946075_c2_11	10969	25072	1116	372
CONTIG4860	5506556_f1_1	10970	25073	297	99
CONTIG4860	24649092_f1_3	10971	25074	231	77
CONTIG4860	36601712_c2_8	10972	25075	270	90
CONTIG4861	4797160_f3_6	10973	25076	651	217
CONTIG4862	175312_f1_1	10974	25077	240	80
CONTIG4862	16520943_f2_4	10975	25078	1542	514
CONTIG4863	20734427_c2_4	10976	25079	348	116
CONTIG4864	4725282_f2_6	10977	25080	360	120
CONTIG4864	975055_c2_9	10978	25081	222	74
CONTIG4865	35745808_f2_3	10979	25082	189	63
CONTIG4865	3183177_f2_4	10980	25083	267	89
CONTIG4865	4727051_c3_11	10981	25084	576	192
CONTIG4866	10663376_f1_1	10982	25085	192	64

CONTIG4866	26375888_f2_2	10983	25086	1281	427
CONTIG4866	42517_c1_7	10984	25087	198	66
CONTIG4866	24219680_c1_8	10985	25088	339	113
CONTIG4867	799057_c3_9	10986	25089	279	93
CONTIG4868	24414033_f2_2	10987	25090	207	69
CONTIG4869	34570292_f1_2	10988	25091	111	
CONTIG4872	490890_f1_1	10989	25092	771	257
CONTIG4872	2078286_c1_5	10990	25093	195	65
CONTIG4872	20117251_c1_6	10991	25094	189	63
CONTIG4873	4978126_f3_3	10992	25095	321	107
CONTIG4873	34383392_f3_4	10993	25096	213	71
CONTIG4874	20516627_f3_3	10994	25097	219	73
CONTIG4876	6719135_f2_3	10995	25098	216	72
CONTIG4876	24470202_f3_6	10996	25099	222	74
CONTIG4876	6552_f3_7	10997	25100	249	83
CONTIG4876	1462503_c3_11	10998	25101	198	66
CONTIG4877	1210005_c2_6	10999	25102	183	61
CONTIG4878	36568755_f3_4	11000	25103	207	69
CONTIG4878	24392181_c3_8	11001	25104	216	72
CONTIG4879	14242686_f2_6	11002	25105	273	91
CONTIG4879	5907678_f3_12	11003	25106	192	64
CONTIG4879	6647805_c1_14	11004	25107	192	64
CONTIG488	2932787_c1_4	11005	25108	351	117
CONTIG4880	900_f1_1	11006	25109	255	85
CONTIG4880	2765660_c1_7	11007	25110	291	97
CONTIG4881	35947177_c1_6	11008	25111	1296	432
CONTIG4881	21881711_c2_11	11009	25112	225	75
CONTIG4882	14339062_c1_8	11010	25113	219	73
CONTIG4882	6025186_c3_10	11011	25114	246	82
CONTIG4883	410040_c1_8	11012	25115	186	62
CONTIG4883	9958528_c2_9	11013	25116	276	92
CONTIG4883	23612936_c2_10	11014	25117	186	62
CONTIG4885	11180157_f3_6	11015	25118	1743	581

CONTIG	Identifier				
CONTIG4885	4694003_f3_7	11016	25119	228	76
CONTIG4887	9776015_f3_2	11017	25120	282	94
CONTIG4887	24391068_c2_4	11018	25121	192	64
CONTIG4887	430375_c2_5	11019	25122	192	64
CONTIG4888	14197175_f2_2	11020	25123	192	64
CONTIG4890	35890_c1_6	11021	25124	225	75
CONTIG4891	22945260_f1_1	11022	25125	333	111
CONTIG4891	2745927_f2_3	11023	25126	207	69
CONTIG4891	31662753_f2_4	11024	25127	192	64
CONTIG4891	10164181_f3_6	11025	25128	243	81
CONTIG4897	24610777_c2_4	11026	25129	390	130
CONTIG4898	4354543_f2_2	11027	25130	183	61
CONTIG4898	24025012_c2_5	11028	25131	249	83
CONTIG49	4179708_f1_1	11029	25132	183	61
CONTIG4900	10738777_f2_5	11030	25133	642	214
CONTIG4900	29845302_c2_9	11031	25134	240	80
CONTIG4901	25444067_c2_7	11032	25135	207	69
CONTIG4903	20115885_f2_2	11033	25136	189	63
CONTIG4903	31284425_f3_4	11034	25137	807	269
CONTIG4906	35207811_f2_2	11035	25138	186	62
CONTIG4906	35205406_f2_3	11036	25139	189	63
CONTIG4906	21520125_c1_7	11037	25140	837	279
CONTIG4908	36148255_c2_7	11038	25141	249	83
CONTIG4908	9876290_c2_8	11039	25142	300	100
CONTIG4908	251260_c2_9	11040	25143	291	97
CONTIG4908	10721901_c3_10	11041	25144	195	65
CONTIG4909	25990699_c1_5	11042	25145	189	63
CONTIG4910	20501562_c2_3	11043	25146	696	232
CONTIG4910	5913913_c2_4	11044	25147	237	79
CONTIG4911	275458_f2_1	11045	25148	207	69
CONTIG4911	2929003_c1_10	11046	25149	198	66
CONTIG4911	24410808_c3_15	11047	25150	474	158
CONTIG4912	9865757_c1_4	11048	25151	354	118

CONTIG4913	25508427_c1_8	11049	25152	279	93
CONTIG4914	23953400_f1_2	11050	25153	210	70
CONTIG4915	25943811_f2_4	11051	25154	219	73
CONTIG4915	22734385_c3_10	11052	25155	186	62
CONTIG4919	3000207_f2_3	11053	25156	468	156
CONTIG4920	585942_f1_1	11054	25157	192	64
CONTIG4920	9954160_f3_4	11055	25158	183	61
CONTIG4920	24609450_c1_8	11056	25159	225	75
CONTIG4921	12003837_f2_2	11057	25160	195	65
CONTIG4922	33392155_f2_2	11058	25161	201	67
CONTIG4923	20523515_f3_5	11059	25162	327	109
CONTIG4926	285753_f2_4	11060	25163	435	145
CONTIG4927	10317301_f3_6	11061	25164	321	107
CONTIG4927	20312877_c1_10	11062	25165	186	62
CONTIG4928	24798282_c1_5	11063	25166	207	69
CONTIG4928	15761308_c3_10	11064	25167	195	65
CONTIG4928	23914043_c3_12	11065	25168	294	98
CONTIG4929	10314037_f1_1	11066	25169	231	77
CONTIG4929	25944137_f2_2	11067	25170	252	84
CONTIG4929	24000662_f2_5	11068	25171	252	84
CONTIG4929	785890_f3_6	11069	25172	279	93
CONTIG4929	22461637_c1_7	11070	25173	267	89
CONTIG4930	156552_c2_4	11071	25174	183	61
CONTIG4931	10573330_f1_1	11072	25175	327	109
CONTIG4931	25660285_c2_13	11073	25176	264	88
CONTIG4931	20522181_c3_17	11074	25177	189	63
CONTIG4931	1350811_c3_19	11075	25178	255	85
CONTIG4932	9948412_f2_5	11076	25179	195	65
CONTIG4932	19728407_f3_8	11077	25180	360	120
CONTIG4932	4109700_c2_13	11078	25181	279	93
CONTIG4932	23484563_c2_14	11079	25182	441	147
CONTIG4932	93781_c2_15	11080	25183	240	80
CONTIG4934	21516301_f2_2	11081	25184	825	275

CONTIG4936	5097175_f2_3	11082	25185	201	67
CONTIG4937	4797212_f1_1	11083	25186	1227	409
CONTIG4938	24619662_f1_2	11084	25187	216	72
CONTIG4939	1384825_f2_3	11085	25188	615	205
CONTIG4939	34176303_f3_8	11086	25189	1038	346
CONTIG4939	6517082_c2_13	11087	25190	531	177
CONTIG494	35836587_f1_1	11088	25191	186	62
CONTIG494	11727341_f2_2	11089	25192	183	61
CONTIG494	2867175_c3_4	11090	25193	189	63
CONTIG4941	16492158_c1_5	11091	25194	186	62
CONTIG4941	472953_c3_8	11092	25195	249	83
CONTIG4942	4147252_c2_21	11093	25196	213	71
CONTIG4944	1961580_f1_2	11094	25197	336	112
CONTIG4944	3008780_f2_4	11095	25198	210	70
CONTIG4944	23648512_c1_12	11096	25199	183	61
CONTIG4944	24417933_c2_13	11097	25200	252	84
CONTIG4945	21650128_c2_10	11098	25201	231	77
CONTIG4947	35390658_f3_6	11099	25202	237	79
CONTIG4947	24819541_c1_7	11100	25203	225	75
CONTIG4948	5117181_f1_2	11101	25204	204	68
CONTIG4948	12676052_c1_10	11102	25205	195	65
CONTIG4949	1963285_f1_1	11103	25206	219	73
CONTIG4949	2787827_c2_7	11104	25207	192	64
CONTIG4951	10727302_f1_2	11105	25208	195	65
CONTIG4951	6845265_f2_5	11106	25209	273	91
CONTIG4953	22459686_f1_1	11107	25210	192	64
CONTIG4953	22694627_f1_2	11108	25211	522	174
CONTIG4953	10171957_f2_3	11109	25212	231	77
CONTIG4953	5891250_f3_6	11110	25213	186	62
CONTIG4955	2147825_f1_1	11111	25214	222	74
CONTIG4955	3908588_c3_8	11112	25215	1686	562
CONTIG4956	21484511_f1_1	11113	25216	825	275
CONTIG4956	36335785_c3_6	11114	25217	183	61

CONTIG4957	29492012_c3_12	11115	25218	585	195
CONTIG4958	4475277_c1_8	11116	25219	330	110
CONTIG4958	20328927_c2_11	11117	25220	456	152
CONTIG4959	4766458_f3_5	11118	25221	186	62
CONTIG4959	34160305_c2_7	11119	25222	351	117
CONTIG4960	234382_f2_2	11120	25223	186	62
CONTIG4961	12687762_f3_4	11121	25224	276	92
CONTIG4962	173212_f1_3	11122	25225	204	68
CONTIG4962	21724030_f3_5	11123	25226	540	180
CONTIG4963	4723501_f1_1	11124	25227	246	82
CONTIG4964	6698753_f3_7	11125	25228	267	89
CONTIG4965	21673167_c1_3	11126	25229	201	67
CONTIG4965	23476075_c2_5	11127	25230	225	75
CONTIG4967	7048505_f3_7	11128	25231	240	80
CONTIG4967	34072178_c3_10	11129	25232	585	195
CONTIG4968	34383327_f3_2	11130	25233	240	80
CONTIG4969	25442155_f2_2	11131	25234	231	77
CONTIG4971	9819050_c1_6	11132	25235	525	175
CONTIG4972	24417201_f3_7	11133	25236	204	68
CONTIG4974	14109750_f2_7	11134	25237	249	83
CONTIG4975	23911055_f2_6	11135	25238	204	68
CONTIG4975	24023512_c1_10	11136	25239	237	79
CONTIG4975	4073500_c2_14	11137	25240	267	89
CONTIG4976	2910902_f3_7	11138	25241	501	167
CONTIG4976	35314752_c2_16	11139	25242	189	63
CONTIG4977	21507827_f1_3	11140	25243	303	101
CONTIG4977	4083502_c1_7	11141	25244	600	200
CONTIG4977	23832501_c1_8	11142	25245	207	69
CONTIG4977	23444713_f3_5	11143	25246	1392	464
CONTIG4978	29488825_c1_8	11144	25247	201	67
CONTIG4978	24414092_c3_13	11145	25248	372	124
CONTIG4979	10745760_f3_9	11146	25249	228	76
CONTIG4979	13851586_c1_13	11147	25250	192	64

CONTIG4979	5276587_c2_15	11148	25251	312	104
CONTIG4980	22381952_c1_6	11149	25252	231	77
CONTIG4981	34085160_f2_1	11150	25253	210	70
CONTIG4981	24417313_f3_2	11151	25254	321	107
CONTIG4981	23626302_f3_5	11152	25255	195	65
CONTIG4981	14301280_c1_7	11153	25256	219	73
CONTIG4981	19789036_c2_8	11154	25257	255	85
CONTIG4982	24414062_c1_12	11155	25258	222	74
CONTIG4982	34272145_c2_13	11156	25259	558	186
CONTIG4983	1073317_f2_5	11157	25260	228	76
CONTIG4984	36366307_c3_11	11158	25261	423	141
CONTIG4985	14860718_f1_1	11159	25262	276	92
CONTIG4985	30119627_f3_4	11160	25263	1566	522
CONTIG4986	24422762_f1_1	11161	25264	453	151
CONTIG4986	11912502_f2_3	11162	25265	195	65
CONTIG4987	26252187_c1_5	11163	25266	195	65
CONTIG4988	25447182_f3_3	11164	25267	186	62
CONTIG4988	4147343_c1_5	11165	25268	297	99
CONTIG4989	20501302_f2_2	11166	25269	198	66
CONTIG4989	2047528_c2_5	11167	25270	909	303
CONTIG4990	23601535_f2_5	11168	25271	876	292
CONTIG4990	34251636_f3_6	11169	25272	183	61
CONTIG4991	22301250_f2_2	11170	25273	204	68
CONTIG4993	9929563_f3_4	11171	25274	198	66
CONTIG4993	33398427_c1_6	11172	25275	342	114
CONTIG4994	21898450_c2_7	11173	25276	648	216
CONTIG4995	4156331_f2_1	11174	25277	189	63
CONTIG4995	19585265_f2_2	11175	25278	429	143
CONTIG4995	12895128_c1_4	11176	25279	252	84
CONTIG4995	4937801_c2_6	11177	25280	240	80
CONTIG4996	14660261_c2_8	11178	25281	198	66
CONTIG4996	26369053_f2_2	11179	25282	186	62
CONTIG4996	5313388_c3_12	11180	25283	186	62

CONTIG4998	6837875_f1_4	11181	25284	261	87
CONTIG4998	22343937_c3_14	11182	25285	186	62
CONTIG4999	3915630_c2_9	11183	25286	234	78
CONTIG5	1173006_f1_1	11184	25287	324	108
CONTIG50	10831286_f1_1	11185	25288	261	87
CONTIG500	4412750_f3_3	11186	25289	225	75
CONTIG5000	14969593_f1_1	11187	25290	609	203
CONTIG5000	29298200_c1_7	11188	25291	198	66
CONTIG5001	24632882_f1_2	11189	25292	186	62
CONTIG5001	33604503_c1_4	11190	25293	192	64
CONTIG5001	4725625_c1_5	11191	25294	609	203
CONTIG5002	3465_f2_5	11192	25295	198	66
CONTIG5002	33672136_c1_9	11193	25296	186	62
CONTIG5005	3579216_f1_1	11194	25297	252	84
CONTIG5006	4035963_f1_1	11195	25298	213	71
CONTIG5007	14540930_c1_8	11196	25299	234	78
CONTIG5008	4773285_f1_1	11197	25300	423	141
CONTIG5008	25442515_f3_4	11198	25301	198	66
CONTIG5008	6756301_c1_5	11199	25302	192	64
CONTIG501	43006925_c1_1	11200	25303	207	69
CONTIG5010	25555507_c1_4	11201	25304	216	72
CONTIG5012	22343750_f1_1	11202	25305	651	217
CONTIG5012	2069058_f3_4	11203	25306	276	92
CONTIG5013	14064757_f1_1	11204	25307	273	91
CONTIG5013	23438400_f3_3	11205	25308	249	83
CONTIG5013	34096092_c1_4	11206	25309	198	66
CONTIG5014	29493785_c1_1	11207	25310	201	67
CONTIG5014	24410956_c3_2	11208	25311	216	72
CONTIG5016	22070177_f1_1	11209	25312	186	62
CONTIG5017	24689067_f3_2	11210	25313	216	72
CONTIG5018	10431301_f3_7	11211	25314	258	86
CONTIG5018	14535010_f3_10	11212	25315	189	63
CONTIG5018	5100016_c2_16	11213	25316	279	93

CONTIG5019	26611263_f2_3	11214	25317	228	76	
CONTIG5019	2110885_f2_4	11215	25318	216	72	
CONTIG5019	5868768_c1_7	11216	25319	204	68	
CONTIG5019	2140818_c2_9	11217	25320	198	66	
CONTIG502	21613910_f1_1	11218	25321	204	68	
CONTIG502	24667066_f3_2	11219	25322	315	105	
CONTIG5021	4339180_f2_4	11220	25323	390	130	
CONTIG5021	25679763_f3_6	11221	25324	252	84	
CONTIG5021	24410325_c1_8	11222	25325	288	96	
CONTIG5023	24798577_f2_2	11223	25326	198	66	
CONTIG5024	801562_f2_2	11224	25327	234	78	
CONTIG5024	15894410_f3_5	11225	25328	792	264	
CONTIG5024	797130_c1_7	11226	25329	300	100	
CONTIG5025	2739056_c1_8	11227	25330	204	68	
CONTIG5025	236250_c2_7	11228	25331	204	68	
CONTIG5026	25641327_f2_4	11229	25332	477	159	
CONTIG5027	2350126_f2_2	11230	25333	363	121	
CONTIG5028	23629700_c3_14	11231	25334	291	97	
CONTIG5028	30287687_c3_15	11232	25335	264	88	
CONTIG5029	14642177_c2_9	11233	25336	270	90	
CONTIG5029	20735451_c2_10	11234	25337	1659	553	
CONTIG5029	78928_c3_14	11235	25338	228	76	
CONTIG5030	818760_f1_1	11236	25339	930	310	
CONTIG5030	1987812_f1_3	11237	25340	1167	389	
CONTIG5030	204750_c3_10	11238	25341	207	69	
CONTIG5031	4177277_f3_3	11239	25342	228	76	
CONTIG5032	26617302_c1_8	11240	25343	228	76	
CONTIG5032	26211562_c3_11	11241	25344	333	111	
CONTIG5032	10634682_c3_12	11242	25345	1311	437	
CONTIG5033	4875325_f1_1	11243	25346	252	84	
CONTIG5033	2145307_f1_2	11244	25347	213	71	
CONTIG5033	24428377_c1_5	11245	25348	252	84	
CONTIG5033	23458527_c1_6	11246	25349	216	72	

CONTIG5034	13759413_f1_1	11247	25350	891	297
CONTIG5034	22690937_c1_10	11248	25351	267	89
CONTIG5035	30182642_f2_7	11249	25352	207	69
CONTIG5035	4377313_c2_12	11250	25353	216	72
CONTIG5035	3989012_c2_13	11251	25354	708	236
CONTIG5036	14098402_f3_6	11252	25355	231	77
CONTIG5036	36360938_c1_7	11253	25356	228	76
CONTIG5036	21507678_c2_9	11254	25357	354	118
CONTIG5037	23649063_c2_6	11255	25358	246	82
CONTIG5039	14254667_c1_4	11256	25359	366	122
CONTIG504	29339805_c1_4	11257	25360	195	65
CONTIG504	29493785_c2_5	11258	25361	270	90
CONTIG5040	191566_f1_1	11259	25362	258	86
CONTIG5040	431557_f3_5	11260	25363	345	115
CONTIG5041	26772325_f2_2	11261	25364	894	298
CONTIG5041	36132217_c3_15	11262	25365	651	217
CONTIG5042	20320311_f3_4	11263	25366	201	67
CONTIG5042	402257_c3_10	11264	25367	2025	675
CONTIG5043	34156500_c1_8	11265	25368	243	81
CONTIG5044	23875627_f1_1	11266	25369	1329	443
CONTIG5044	20354510_c2_5	11267	25370	216	72
CONTIG5047	6095640_f3_5	11268	25371	234	78
CONTIG5049	23478181_f3_7	11269	25372	243	81
CONTIG505	35425831_f3_1	11270	25373	876	292
CONTIG5050	6267_c1_4	11271	25374	279	93
CONTIG5050	20876512_c3_7	11272	25375	294	98
CONTIG5050	10970287_c3_8	11273	25376	201	67
CONTIG5051	22863265_c3_10	11274	25377	267	89
CONTIG5052	30079093_f1_1	11275	25378	807	269
CONTIG5052	23626265_c3_6	11276	25379	192	64
CONTIG5053	23907900_f3_5	11277	25380	204	68
CONTIG5054	431275_f2_3	11278	25381	210	70
CONTIG5054	25397687_c2_9	11279	25382	837	279

CONTIG5054	15642186_c2_10	11280	25383	321	107
CONTIG5055	23615882_f3_9	11281	25384	210	70
CONTIG5056	10739027_f1_2	11282	25385	222	74
CONTIG5057	1250_f3_3	11283	25386	309	103
CONTIG5057	21600626_c1_5	11284	25387	186	62
CONTIG5057	33282510_c1_6	11285	25388	210	70
CONTIG5057	10547012_c2_8	11286	25389	213	71
CONTIG5057	26281625_c3_10	11287	25390	186	62
CONTIG506	4335275_c1_3	11288	25391	687	229
CONTIG5058	33406577_c3_8	11289	25392	231	77
CONTIG5058	1406587_c3_9	11290	25393	228	76
CONTIG5059	35284392_c1_7	11291	25394	387	129
CONTIG5060	156377_f2_3	11292	25395	270	90
CONTIG5060	24850205_f2_3	11293	25396	372	124
CONTIG5060	29314525_c2_6	11294	25397	294	98
CONTIG5062	1367212_c3_10	11295	25398	216	72
CONTIG5062	234403_c3_11	11296	25399	201	67
CONTIG5063	3907218_f1_1	11297	25400	915	305
CONTIG5063	14220718_f3_5	11298	25401	186	62
CONTIG5063	26370312_c2_12	11299	25402	240	80
CONTIG5064	32965_f2_1	11300	25403	294	98
CONTIG5064	267_f2_2	11301	25404	438	146
CONTIG5065	11723160_f2_2	11302	25405	420	140
CONTIG5065	20319650_c2_10	11303	25406	288	96
CONTIG5066	11056586_c1_10	11304	25407	192	64
CONTIG5066	35448938_c1_11	11305	25408	201	67
CONTIG5067	11739436_c2_7	11306	25409	243	81
CONTIG5067	24412578_c3_8	11307	25410	201	67
CONTIG5067	20406537_c3_9	11308	25411	183	61
CONTIG5068	23641080_f3_6	11309	25412	192	64
CONTIG5068	885936_c2_9	11310	25413	1686	562
CONTIG5069	34175376_f1_1	11311	25414	189	63
CONTIG5069	4741061_c2_8	11312	25415	243	81

CONTIG507	14063177_c1_2	11313	25416	195	65
CONTIG5070	4765876_c1_5	11314	25417	204	68
CONTIG5070	30089376_c1_5	11315	25418	288	96
CONTIG5070	35943812_c2_8	11316	25419	213	71
CONTIG5071	4157777_c2_10	11317	25420	1056	352
CONTIG5072	198403_f1_2	11318	25421	270	90
CONTIG5073	2914762_f2_1	11319	25422	198	66
CONTIG5073	4506876_f3_3	11320	25423	852	284
CONTIG5073	5890640_c1_4	11321	25424	294	98
CONTIG5073	24485688_c1_5	11322	25425	267	89
CONTIG5073	20703160_c1_6	11323	25426	1368	456
CONTIG5073	164061_c1_7	11324	25427	1107	369
CONTIG5074	26305442_c2_8	11325	25428	192	64
CONTIG5075	24428212_c1_5	11326	25429	201	67
CONTIG5077	4117752_f2_1	11327	25430	183	61
CONTIG5077	32206260_f3_4	11328	25431	192	64
CONTIG5077	14140966_c3_8	11329	25432	270	90
CONTIG5078	7032942_c2_10	11330	25433	201	67
CONTIG5080	1367202_f3_8	11331	25434	276	92
CONTIG5080	119017_c1_11	11332	25435	432	144
CONTIG5080	34008282_c3_15	11333	25436	219	73
CONTIG5081	24016517_f3_3	11334	25437	213	71
CONTIG5081	16204531_c2_8	11335	25438	237	79
CONTIG5082	4454651_f2_5	11336	25439	237	79
CONTIG5083	550627_f1_1	11337	25440	312	104
CONTIG5083	4898250_f3_5	11338	25441	1932	644
CONTIG5083	35163150_c1_6	11339	25442	195	65
CONTIG5083	1046900_c2_7	11340	25443	219	73
CONTIG5083	4485950_c3_10	11341	25444	480	160
CONTIG5084	15740888_f1_3	11342	25445	465	155
CONTIG5085	24657875_c3_11	11343	25446	213	71
CONTIG5086	4187626_c3_6	11344	25447	261	87
CONTIG5087	23906256_c1_6	11345	25448	219	73

CONTIG5089	34181541_f2_3	11346	25449	216	72
CONTIG509	87550_f1_1	11347	25450	288	96
CONTIG5090	34101000_f1_1	11348	25451	885	295
CONTIG5090	35156307_f2_2	11349	25452	252	84
CONTIG5090	24062775_c1_6	11350	25453	276	92
CONTIG5091	35948377_c1_10	11351	25454	1134	378
CONTIG5091	22394443_c2_12	11352	25455	1149	383
CONTIG5092	21679687_f1_1	11353	25456	267	89
CONTIG5092	20100660_f3_6	11354	25457	336	112
CONTIG5092	30703520_c1_7	11355	25458	201	67
CONTIG5092	23555153_c1_9	11356	25459	258	86
CONTIG5092	24000157_c2_12	11357	25460	192	64
CONTIG5093	1956575_f1_1	11358	25461	885	295
CONTIG5093	33286567_c3_8	11359	25462	609	203
CONTIG5094	33626637_f3_9	11360	25463	195	65
CONTIG5095	976576_f2_4	11361	25464	207	69
CONTIG5095	15046875_f3_6	11362	25465	198	66
CONTIG5095	34006885_c1_7	11363	25466	249	83
CONTIG5095	4711516_c1_8	11364	25467	183	61
CONTIG5096	23600252_c1_8	11365	25468	270	90
CONTIG5096	4883436_c2_11	11366	25469	186	62
CONTIG5096	4298125_c3_13	11367	25470	249	83
CONTIG5096	4354500_c3_14	11368	25471	198	66
CONTIG5097	25554688_f1_1	11369	25472	234	78
CONTIG5097	781650_c3_6	11370	25473	198	66
CONTIG5098	14253350_f1_1	11371	25474	192	64
CONTIG5098	33242050_f1_2	11372	25475	213	71
CONTIG5098	14745175_f2_4	11373	25476	183	61
CONTIG5099	24494416_f2_3	11374	25477	210	70
CONTIG5099	13829950_c3_8	11375	25478	189	63
CONTIG51	14650635_c2_2	11376	25479	201	67
CONTIG5100	29547302_c2_5	11377	25480	213	71
CONTIG5100	4960893_c3_9	11378	25481	195	65

CONTIG5101	24642007_c1_10	11379	25482	228	76
CONTIG5102	12693375_c1_3	11380	25483	294	98
CONTIG5103	35203450_f3_4	11381	25484	195	65
CONTIG5104	24492693_f2_2	11382	25485	699	233
CONTIG5105	31288402_f1_2	11383	25486	195	65
CONTIG5105	2739761_f3_5	11384	25487	258	86
CONTIG5105	10720287_c3_14	11385	25488	228	76
CONTIG5106	1063132_f1_1	11386	25489	234	78
CONTIG5106	29923387_c2_7	11387	25490	225	75
CONTIG5106	5083466_c2_8	11388	25491	198	66
CONTIG5106	14144525_c3_10	11389	25492	195	65
CONTIG5107	34652217_f1_4	11390	25493	402	134
CONTIG5107	5134437_c2_8	11391	25494	183	61
CONTIG5108	14649000_f2_3	11392	25495	234	78
CONTIG5108	2928903_c1_5	11393	25496	1137	379
CONTIG5109	26210878_f1_4	11394	25497	282	94
CONTIG5109	24412638_c2_12	11395	25498	375	125
CONTIG511	24735627_f1_1	11396	25499	975	325
CONTIG5110	22296930_f1_2	11397	25500	249	83
CONTIG5110	26600908_f2_4	11398	25501	720	240
CONTIG5110	15829628_c1_6	11399	25502	297	99
CONTIG5110	786692_c1_7	11400	25503	279	93
CONTIG5112	35157800_f3_4	11401	25504	210	70
CONTIG5112	4488877_f3_5	11402	25505	294	98
CONTIG5113	15907168_f1_1	11403	25506	630	210
CONTIG5113	14569077_c2_4	11404	25507	1503	501
CONTIG5115	22276382_f1_7	11405	25508	234	78
CONTIG5115	29937526_c3_16	11406	25509	186	62
CONTIG5115	26348253_c3_19	11407	25510	345	115
CONTIG5117	783510_f3_6	11408	25511	234	78
CONTIG5118	25647302_f1_1	11409	25512	1893	631
CONTIG5118	5977012_c2_6	11410	25513	192	64
CONTIG512	19537577_f1_1	11411	25514	222	74

CONTIG512	24730326_f1_2	11412	25515	402	134
CONTIG5121	20407750_c1_7	11413	25516	210	70
CONTIG5124	10166387_f1_1	11414	25517	1497	499
CONTIG5124	35198276_f1_3	11415	25518	264	88
CONTIG5124	30274025_f3_8	11416	25519	426	142
CONTIG5124	11210931_c3_16	11417	25520	816	272
CONTIG5125	10364138_f1_1	11418	25521	360	120
CONTIG5125	417337_f1_2	11419	25522	234	78
CONTIG5125	10631885_c2_16	11420	25523	645	215
CONTIG5126	3612S808_f1_2	11421	25524	1425	475
CONTIG5126	2845036_f3_4	11422	25525	246	82
CONTIG5126	22713275_f3_5	11423	25526	438	146
CONTIG5126	14158410_f3_6	11424	25527	936	312
CONTIG5126	34251718_c1_8	11425	25528	225	75
CONTIG5128	817567_f1_1	11426	25529	183	61
CONTIG5128	4026025_c1_9	11427	25530	183	61
CONTIG5128	25_c3_12	11428	25531	243	81
CONTIG513	23864412_f1_1	11429	25532	360	120
CONTIG5130	22551016_f1_2	11430	25533	207	69
CONTIG5130	6741050_f3_6	11431	25534	207	69
CONTIG5132	24417213_c1_10	11432	25535	204	68
CONTIG5133	24804635_f2_2	11433	25536	237	79
CONTIG5133	22303431_c3_12	11434	25537	189	63
CONTIG5133	15647962_c3_14	11435	25538	192	64
CONTIG5134	23844036_c3_11	11436	25539	183	61
CONTIG5135	4825_c3_19	11437	25540	447	149
CONTIG5137	29500375_f2_5	11438	25541	630	210
CONTIG5137	21988265_c1_10	11439	25542	207	69
CONTIG5137	24007165_c2_13	11440	25543	192	64
CONTIG5138	4144441_c1_5	11441	25544	222	74
CONTIG5138	35804150_c2_10	11442	25545	222	74
CONTIG5138	4773262_c2_11	11443	25546	207	69
CONTIG5138	24395162_c3_17	11444	25547	1206	402

CONTIG5139	20078761_f2_3	11445	25548	360	120
CONTIG5139	13830063_c1_6	11446	25549	183	61
CONTIG514	12593890_f2_2	11447	25550	279	93
CONTIG5141	2815642_f3_4	11448	25551	237	79
CONTIG5141	23448458_c1_5	11449	25552	264	88
CONTIG5141	4781561_c2_8	11450	25553	366	122
CONTIG5142	10942162_c2_7	11451	25554	207	69
CONTIG5143	19734675_f2_4	11452	25555	216	72
CONTIG5143	22303752_f3_11	11453	25556	228	76
CONTIG5145	23947652_f1_1	11454	25557	216	72
CONTIG5146	25407792_f3_9	11455	25558	216	72
CONTIG5146	7241306_c1_11	11456	25559	438	146
CONTIG5146	21540876_c2_13	11457	25560	324	108
CONTIG5147	242000_f1_1	11458	25561	207	69
CONTIG5147	6328177_f3_5	11459	25562	834	278
CONTIG5147	24421968_c1_8	11460	25563	204	68
CONTIG5147	973428_c3_13	11461	25564	243	81
CONTIG5149	3229682_f1_2	11462	25565	189	63
CONTIG5149	43001930_c1_7	11463	25566	189	63
CONTIG5149	26054567_c2_8	11464	25567	1197	399
CONTIG5149	22667182_c2_10	11465	25568	267	89
CONTIG5149	32220285_c3_12	11466	25569	246	82
CONTIG5150	19573537_f1_1	11467	25570	231	77
CONTIG5150	30109812_f2_7	11468	25571	285	95
CONTIG5151	1053140_f1_1	11469	25572	228	76
CONTIG5151	23625442_c2_6	11470	25573	207	69
CONTIG5152	26677_c1_5	11471	25574	186	62
CONTIG5153	953762_c1_7	11472	25575	261	87
CONTIG5154	25397180_c2_15	11473	25576	225	75
CONTIG5154	33297175_c3_17	11474	25577	186	62
CONTIG5155	985175_f1_2	11475	25578	237	79
CONTIG5155	24348277_f3_6	11476	25579	453	151
CONTIG5155	39128_c1_8	11477	25580	186	62

CONTIG5155	4069761_c1_10	11478	25581	183	61
CONTIG5155	30110812_c2_15	11479	25582	183	61
CONTIG5155	21525062_c2_16	11480	25583	207	69
CONTIG5155	23602002_c3_19	11481	25584	306	102
CONTIG5157	21729061_c3_11	11485	25588	222	74
CONTIG5157	22382755_c2_7	11484	25587	306	102
CONTIG5157	30267632_f3_3	11483	25586	183	61
CONTIG5155	600880_f1_1	11482	25585	291	97
CONTIG5158	25991031_f3_5	11486	25589	195	65
CONTIG5158	22477187_f3_6	11487	25590	183	61
CONTIG5159	24805261_f1_1	11488	25591	204	68
CONTIG516	19563908_c2_1	11489	25592	198	66
CONTIG5160	7080077_f3_7	11490	25593	204	68
CONTIG5163	3907512_c2_6	11491	25594	207	69
CONTIG5164	14495325_c1_8	11492	25595	195	65
CONTIG5164	21722002_c2_11	11493	25596	201	67
CONTIG5165	26253375_f1_1	11494	25597	186	62
CONTIG5166	3930_f1_1	11495	25598	303	101
CONTIG5168	22464057_f2_6	11496	25599	255	85
CONTIG5169	196926_f3_6	11497	25600	978	326
CONTIG517	30350276_f2_2	11498	25601	216	72
CONTIG5171	20323306_f3_6	11499	25602	405	135
CONTIG5171	26207682_c1_8	11500	25603	240	80
CONTIG5171	2922505_c2_10	11501	25604	207	69
CONTIG5172	4881300_f3_4	11502	25605	270	90
CONTIG5173	164018_c1_3	11503	25606	201	67
CONTIG5176	16415952_c1_5	11504	25607	192	64
CONTIG5178	6662691_f1_1	11505	25608	195	65
CONTIG5178	390950_f1_3	11506	25609	363	121
CONTIG5179	12207757_f1_4	11507	25610	210	70
CONTIG5179	987625_f1_5	11508	25611	240	80
CONTIG5179	29923502_f2_7	11509	25612	243	81
CONTIG5179	5866382_c2_17	11510	25613	348	116

CONTIG5179	23641002_c3_18	11511	25614	396	132
CONTIG5179	13771927_c3_20	11512	25615	207	69
CONTIG518	35351538_f3_1	11513	25616	213	71
CONTIG5180	12698387_f1_2	11514	25617	213	71
CONTIG5180	23675652_c2_11	11515	25618	189	63
CONTIG5181	20916277_c3_8	11516	25619	192	64
CONTIG5182	35707813_c2_6	11517	25620	315	105
CONTIG5182	14244126_c3_10	11518	25621	657	219
CONTIG5182	29381902_c3_11	11519	25622	558	186
CONTIG5183	19720087_f1_1	11520	25623	261	87
CONTIG5183	23485290_c1_9	11521	25624	267	89
CONTIG5183	42875_c3_18	11522	25625	243	81
CONTIG5184	24892162_c3_14	11523	25626	198	66
CONTIG5185	480202_f3_3	11524	25627	240	80
CONTIG5185	968902_c2_8	11525	25628	252	84
CONTIG5185	2539127_c2_9	11526	25629	522	174
CONTIG5185	15040902_c3_11	11527	25630	399	133
CONTIG5185	1968777_c3_12	11528	25631	246	82
CONTIG5186	9768776_c2_14	11529	25632	234	78
CONTIG5186	22064510_c3_19	11530	25633	342	114
CONTIG5188	14237508_f3_3	11531	25634	231	77
CONTIG5188	35323467_c1_4	11532	25635	603	201
CONTIG5188	19767125_c1_5	11533	25636	222	74
CONTIG5188	24495286_c2_6	11534	25637	297	99
CONTIG5188	20365825_c2_7	11535	25638	597	199
CONTIG5189	9774166_c1_13	11536	25639	891	297
CONTIG5191	24423756_f1_1	11537	25640	219	73
CONTIG5191	9941630_f1_4	11538	25641	189	63
CONTIG5191	20501933_c1_8	11539	25642	261	87
CONTIG5192	26182181_f1_1	11540	25643	2097	699
CONTIG5192	10634661_c1_10	11541	25644	519	173
CONTIG5193	4101510_f2_2	11542	25645	204	68
CONTIG5193	32600327_f3_4	11543	25646	231	77

CONTIG5193	5087678_c1_6	11544	25647	183	61
CONTIG5194	5109456_f2_3	11545	25648	204	68
CONTIG5197	13694035_c2_6	11546	25649	189	63
CONTIG5197	10724142_c3_10	11547	25650	195	65
CONTIG5198	859656_c1_6	11548	25651	297	99
CONTIG5198	23865936_c1_7	11549	25652	189	63
CONTIG52	2770930_f2_3	11550	25653	207	69
CONTIG520	192325_c2_3	11551	25654	186	62
CONTIG5200	34250082_c3_13	11552	25655	252	84
CONTIG5201	6832842_f2_4	11553	25656	186	62
CONTIG5201	11735911_f2_5	11554	25657	198	66
CONTIG5201	789125_f3_7	11555	25658	216	72
CONTIG5201	128180_f3_8	11556	25659	264	88
CONTIG5201	35937_c1_9	11557	25660	183	61
CONTIG5201	4767150_c2_12	11558	25661	213	71
CONTIG5202	1204452_f1_2	11559	25662	192	64
CONTIG5204	24492178_c2_5	11560	25663	258	86
CONTIG5204	35157955_c3_7	11561	25664	204	68
CONTIG5206	6062628_f1_1	11562	25665	222	74
CONTIG5206	4726407_f1_2	11563	25666	1542	514
CONTIG5206	870450_f3_8	11564	25667	231	77
CONTIG5208	33397128_f3_7	11565	25668	192	64
CONTIG5208	7069011_c2_11	11566	25669	657	219
CONTIG5209	21489032_c1_10	11567	25670	399	133
CONTIG5209	554660_c2_12	11568	25671	204	68
CONTIG5209	13852005_c3_14	11569	25672	339	113
CONTIG521	101503_f1_2	11570	25673	309	103
CONTIG521	26369053_f3_4	11571	25674	201	67
CONTIG5210	32165825_f3_6	11572	25675	234	78
CONTIG5210	24801532_f3_7	11573	25676	720	240
CONTIG5210	24804635_c1_11	11574	25677	237	79
CONTIG5210	36620931_c2_13	11575	25678	183	61
CONTIG5212	34553176_c3_17	11576	25679	273	91

CONTIG5213	24883590_f2_4	11577	25680	471	157
CONTIG5213	14571041_f2_5	11578	25681	201	67
CONTIG5213	2929675_f2_7	11579	25682	249	83
CONTIG5213	23673386_c1_10	11580	25683	192	64
CONTIG5213	14474016_c1_11	11581	25684	225	75
CONTIG5213	36572512_c2_13	11582	25685	198	66
CONTIG5214	6064842_c2_19	11583	25686	195	65
CONTIG5215	978377_f1_2	11584	25687	525	175
CONTIG5215	23859683_c2_9	11585	25688	468	156
CONTIG522	157087_c2_10	11586	25689	210	70
CONTIG5215	3313825_c3_15	11587	25690	231	77
CONTIG5216	4895687_f3_11	11588	25691	252	84
CONTIG5218	23632787_f3_8	11589	25692	186	62
CONTIG5219	22463457_f2_1	11590	25693	192	64
CONTIG5219	10642635_f2_2	11591	25694	228	76
CONTIG5219	2788128_c3_7	11592	25695	183	61
CONTIG522	6853313_c2_2	11593	25696	951	317
CONTIG5220	25500636_f2_3	11594	25697	339	113
CONTIG5220	819000_c2_9	11595	25698	414	138
CONTIG5220	19703267_c3_10	11596	25699	222	74
CONTIG5221	33208150_c3_21	11597	25700	294	98
CONTIG5222	20754415_c1_6	11598	25701	183	61
CONTIG5224	594025_c1_3	11599	25702	252	84
CONTIG5224	4335750_c3_5	11600	25703	1188	396
CONTIG5225	19564010_c1_4	11601	25704	312	104
CONTIG5225	22116451_c2_8	11602	25705	198	66
CONTIG5225	4166568_c3_10	11603	25706	393	131
CONTIG5226	24414086_f1_1	11604	25707	306	102
CONTIG5226	4172128_f2_3	11605	25708	183	61
CONTIG5227	4876557_f1_1	11606	25709	225	75
CONTIG5227	4031942_f2_2	11607	25710	189	63
CONTIG5227	14238905_f3_6	11608	25711	192	64
CONTIG5227	5126885_f3_7	11609	25712	201	67

CONTIG5227	13829015_f3_8	11610	25713	312	104
CONTIG5227	22658136_c1_9	11611	25714	249	83
CONTIG5229	36366561_f1_4	11612	25715	885	295
CONTIG5229	1037761_f2_5	11613	25716	225	75
CONTIG5229	35203942_f3_10	11614	25717	267	89
CONTIG5229	4687650_c3_18	11615	25718	441	147
CONTIG523	12548512_c3_3	11616	25719	261	87
CONTIG5231	36345933_f2_3	11617	25720	255	85
CONTIG5231	6025387_c2_6	11618	25721	990	330
CONTIG5232	33687926_f1_2	11619	25722	276	92
CONTIG5232	2000943_c1_9	11620	25723	198	66
CONTIG5234	34100932_f2_5	11621	25724	1272	424
CONTIG5234	428432_f3_6	11622	25725	192	64
CONTIG5235	5161432_f3_5	11623	25726	240	80
CONTIG5235	26600911_f3_7	11624	25727	447	149
CONTIG5235	4119707_f3_8	11625	25728	189	63
CONTIG5235	26368801_c2_14	11626	25729	186	62
CONTIG5236	26344443_f1_1	11627	25730	348	116
CONTIG5237	23830063_f1_1	11628	25731	219	73
CONTIG5237	36135927_c1_5	11629	25732	195	65
CONTIG5238	5866425_c2_6	11630	25733	393	131
CONTIG5238	24423501_c3_7	11631	25734	339	113
CONTIG5238	1984557_c3_8	11632	25735	198	66
CONTIG5238	2813180_c3_9	11633	25736	243	81
CONTIG5238	30744080_c3_10	11634	25737	195	65
CONTIG524	1302180_f2_2	11635	25738	189	63
CONTIG5240	20709436_f2_1	11636	25739	267	89
CONTIG5240	34079686_f2_2	11637	25740	276	92
CONTIG5240	656378_c1_6	11638	25741	225	75
CONTIG5240	25585151_c2_8	11639	25742	195	65
CONTIG5240	11900015_c3_12	11640	25743	201	67
CONTIG5241	1181515_f3_6	11641	25744	225	75
CONTIG5241	24645325_c1_8	11642	25745	1512	504

CONTIG5241	23650277_c1_9	11643	25746	378	126
CONTIG5242	15891875_c2_10	11644	25747	189	63
CONTIG5243	2645464_c2_8	11645	25748	393	131
CONTIG5246	21973437_f2_2	11646	25749	300	100
CONTIG5246	35162552_c3_14	11647	25750	183	61
CONTIG5247	24414087_f1_5	11648	25751	195	65
CONTIG5247	445212_f2_7	11649	25752	192	64
CONTIG5247	6333163_f3_12	11650	25753	186	62
CONTIG5247	12314702_f3_13	11651	25754	444	148
CONTIG5248	2596041_c1_8	11652	25755	234	78
CONTIG5249	21726510_c1_6	11653	25756	1080	360
CONTIG5249	24413187_c3_21	11654	25757	2751	917
CONTIG5249	2441037_c2_10	11655	25758	201	67
CONTIG5250	550002_f1_1	11656	25759	219	73
CONTIG5250	3986375_c1_5	11657	25760	216	72
CONTIG5250	31525311_c1_6	11658	25761	186	62
CONTIG5250	3370942_c3_9	11659	25762	222	74
CONTIG5251	1771910_c1_16	11660	25763	204	68
CONTIG5251	23948327_c2_18	11661	25764	204	68
CONTIG5252	4023438_f2_2	11662	25765	207	69
CONTIG5252	11026507_c1_4	11663	25766	204	68
CONTIG5252	32228437_c3_8	11664	25767	297	99
CONTIG5253	26448551_c1_9	11665	25768	216	72
CONTIG5253	2064032_c1_10	11666	25769	300	100
CONTIG5253	24901518_c2_11	11667	25770	228	76
CONTIG5254	2128508_f1_3	11668	25771	213	71
CONTIG5254	21504428_f2_8	11669	25772	342	114
CONTIG5255	23437875_f2_2	11670	25773	777	259
CONTIG5255	32552202_f3_2	11671	25774	789	263
CONTIG5256	26209677_c1_4	11672	25775	378	126
CONTIG5256	1173915_f1_2	11673	25776	216	72
CONTIG5257	34180317_f3_4	11674	25777	204	68
CONTIG5257	36144812_c3_8	11675	25778	246	82

CONTIG5258	78286_f1_5	11676	25779	246	82
CONTIG5258	788461_c2_11	11677	25780	549	183
CONTIG5262	14115625_f1_1	11678	25781	1038	346
CONTIG5262	398562_f2_5	11679	25782	204	68
CONTIG5262	30273337_c3_10	11680	25783	189	63
CONTIG5263	6672187_f1_1	11681	25784	183	61
CONTIG5263	1364010_f3_8	11682	25785	201	67
CONTIG5263	15078876_c3_14	11683	25786	396	132
CONTIG5264	4297802_f3_4	11684	25787	714	238
CONTIG5264	1254715_c1_8	11685	25788	216	72
CONTIG5265	9961682_f1_1	11686	25789	1149	383
CONTIG5265	12523257_f2_4	11687	25790	189	63
CONTIG5265	24665712_f3_5	11688	25791	183	61
CONTIG5266	22268787_f1_1	11689	25792	213	71
CONTIG5266	33633375_f2_5	11690	25793	261	87
CONTIG5266	4460903_c2_14	11691	25794	231	77
CONTIG5266	16406518_c3_16	11692	25795	186	62
CONTIG5267	194687_f3_4	11693	25796	306	102
CONTIG5267	20112505_f3_5	11694	25797	243	81
CONTIG5267	9960887_c2_7	11695	25798	231	77
CONTIG5267	24648431_c3_10	11696	25799	417	139
CONTIG5268	9797502_f1_2	11697	25800	216	72
CONTIG5268	12269018_f2_6	11698	25801	210	70
CONTIG5268	4034430_f3_10	11699	25802	951	317
CONTIG5268	1261170_f3_11	11700	25803	366	122
CONTIG5269	21912681_f2_4	11701	25804	309	103
CONTIG5269	2343750_f3_6	11702	25805	198	66
CONTIG5269	23437675_c1_9	11703	25806	405	135
CONTIG5269	23907681_c3_11	11704	25807	198	66
CONTIG527	24880375_f3_3	11705	25808	228	76
CONTIG527	11110816_c2_5	11706	25809	570	190
CONTIG5270	20508436_f2_4	11707	25810	219	73
CONTIG5270	35351550_f2_5	11708	25811	237	79

CONTIG5270	14225893_f3_7	11709	25812	282	94
CONTIG5270	212665_f3_8	11710	25813	237	79
CONTIG5270	20917001_c2_9	11711	25814	204	68
CONTIG5272	4534550_f2_3	11712	25815	777	259
CONTIG5272	10726062_f2_4	11713	25816	192	64
CONTIG5272	3136267_f3_7	11714	25817	204	68
CONTIG5272	24417557_c1_10	11715	25818	270	90
CONTIG5273	991450_f1_2	11716	25819	459	153
CONTIG5273	19532136_f3_4	11717	25820	183	61
CONTIG5274	3167875_c1_12	11718	25821	189	63
CONTIG5274	25518768_c1_13	11719	25822	1041	347
CONTIG5275	4380_f1_3	11720	25823	213	71
CONTIG5275	19730336_f1_4	11721	25824	876	292
CONTIG5275	23859691_c1_15	11722	25825	189	63
CONTIG5275	250711_c1_18	11723	25826	1470	490
CONTIG5276	36136380_f1_1	11724	25827	204	68
CONTIG5276	19735925_f1_3	11725	25828	279	93
CONTIG5276	35203151_f2_6	11726	25829	186	62
CONTIG5276	24351557_f3_8	11727	25830	186	62
CONTIG5278	4097160_f1_2	11728	25831	882	294
CONTIG5278	204387_c1_8	11729	25832	225	75
CONTIG5278	33289002_c1_9	11730	25833	261	87
CONTIG5279	1054000_f1_1	11731	25834	531	177
CONTIG5279	4880311_f2_4	11732	25835	633	211
CONTIG5279	6834688_c1_12	11733	25836	258	86
CONTIG5279	22032803_c2_15	11734	25837	210	70
CONTIG5280	1048437_f3_7	11735	25838	246	82
CONTIG5280	21491431_c2_13	11736	25839	372	124
CONTIG5281	4699093_f1_1	11737	25840	243	81
CONTIG5281	2475326_f3_4	11738	25841	318	106
CONTIG5281	26367187_f3_7	11739	25842	183	61
CONTIG5282	4798200_c2_9	11740	25843	282	94
CONTIG5283	4117807_f1_1	11741	25844	654	218

CONTIG5283	24015925_f2_3	11742	25845	192	64
CONTIG5283	23468932_f3_6	11743	25846	204	68
CONTIG5284	29531500_c1_3	11744	25847	1002	334
CONTIG5287	26382192_f2_2	11745	25848	198	66
CONTIG5287	972125_f3_3	11746	25849	936	312
CONTIG5287	24225681_c3_10	11747	25850	234	78
CONTIG5288	23643761_c3_18	11748	25851	183	61
CONTIG5289	26564750_f3_5	11749	25852	204	68
CONTIG5289	24306588_c2_11	11750	25853	264	88
CONTIG5290	6438457_f1_2	11751	25854	186	62
CONTIG5291	4886253_c1_11	11752	25855	192	64
CONTIG5291	2350427_c3_18	11753	25856	438	146
CONTIG5292	21485762_f3_9	11754	25857	255	85
CONTIG5292	24233882_c3_15	11755	25858	573	191
CONTIG5293	32688500_f3_3	11756	25859	807	269
CONTIG5294	6690951_f2_4	11757	25860	183	61
CONTIG5296	22145075_c2_11	11758	25861	225	75
CONTIG5297	240692_f1_1	11759	25862	228	76
CONTIG5297	33799026_f3_8	11760	25863	183	61
CONTIG5297	14223392_c1_13	11761	25864	273	91
CONTIG5298	24257175_f2_3	11762	25865	201	67
CONTIG5298	15671950_c2_7	11763	25866	507	169
CONTIG5299	5156312_f2_3	11764	25867	273	91
CONTIG5299	4782952_f3_7	11765	25868	567	189
CONTIG5299	34181563_c1_8	11766	25869	216	72
CONTIG5299	23632067_c1_14	11767	25870	192	64
CONTIG5299	36366061_c1_15	11768	25871	294	98
CONTIG5299	32422012_c2_22	11769	25872	192	64
CONTIG530	15663303_f1_1	11770	25873	600	200
CONTIG5300	10975837_f2_2	11771	25874	1590	530
CONTIG5301	392302_f2_3	11772	25875	186	62
CONTIG5301	35157955_c3_18	11773	25876	225	75
CONTIG5303	14492128_f2_5	11774	25877	186	62

CONTIG5303	33225010_c3_16	11775	25878	192	64
CONTIG5304	23625312_f1_1	11776	25879	726	242
CONTIG5304	20320186_f1_2	11777	25880	192	64
CONTIG5305	6901637_f1_1	11778	25881	186	62
CONTIG5306	32229552_c2_13	11779	25882	231	77
CONTIG5306	21617200_c3_18	11780	25883	192	64
CONTIG5307	429561_c3_12	11781	25884	204	68
CONTIG5309	4378313_f1_1	11782	25885	657	219
CONTIG5309	4100425_f1_2	11783	25886	183	61
CONTIG5310	24398462_f3_6	11784	25887	339	113
CONTIG5310	24648415_f2_5	11785	25888	219	73
CONTIG5311	12165962_c1_8	11786	25889	198	66
CONTIG5311	24726625_c3_14	11787	25890	183	61
CONTIG5312	20330007_f2_5	11788	25891	459	153
CONTIG5312	9846942_f3_6	11789	25892	186	62
CONTIG5312	7078575_c3_11	11790	25893	201	67
CONTIG5312	30328788_c3_12	11791	25894	195	65
CONTIG5313	436_c1_8	11792	25895	213	71
CONTIG5313	21515791_c3_11	11793	25896	198	66
CONTIG5314	16413936_f3_9	11794	25897	189	63
CONTIG5315	1988875_c3_14	11795	25898	258	86
CONTIG5316	11141892_f2_4	11796	25899	195	65
CONTIG5316	31413_c2_16	11797	25900	195	65
CONTIG5316	798127_c3_18	11798	25901	285	95
CONTIG5316	23534385_c3_19	11799	25902	468	156
CONTIG5318	23673291_f2_3	11800	25903	225	75
CONTIG5318	21662762_c2_7	11801	25904	252	84
CONTIG5319	10837558_f1_1	11802	25905	243	81
CONTIG5319	24801436_f2_2	11803	25906	213	71
CONTIG5319	4735676_c1_4	11804	25907	183	61
CONTIG5320	22117278_f2_3	11805	25908	210	70
CONTIG5321	20503142_f1_4	11806	25909	1323	441
CONTIG5323	5871078_f2_4	11807	25910	204	68

CONTIG5323	29533375_c3_12	11808	25911	2118	706
CONTIG5324	6433177_f1_3	11809	25912	186	62
CONTIG5324	7039075_c2_14	11810	25913	201	67
CONTIG5325	23479805_f1_2	11811	25914	255	85
CONTIG5327	33398258_c1_6	11812	25915	204	68
CONTIG5329	9850182_f3_4	11813	25916	201	67
CONTIG5329	22037675_c1_9	11814	25917	576	192
CONTIG5330	24335910_f3_2	11815	25918	267	89
CONTIG533	16209687_f1_1	11816	25919	198	66
CONTIG5330	16853135_f3_5	11817	25920	198	66
CONTIG5330	24234753_c1_9	11818	25921	264	88
CONTIG5330	14584763_c1_11	11819	25922	237	79
CONTIG5330	683215_c2_12	11820	25923	192	64
CONTIG5330	5261580_c3_14	11821	25924	222	74
CONTIG5331	21878465_f1_1	11822	25925	381	127
CONTIG5331	24251900_c1_6	11823	25926	195	65
CONTIG5334	198813_c2_8	11824	25927	849	283
CONTIG5334	429561_c2_9	11825	25928	204	68
CONTIG5335	3937510_f2_2	11826	25929	1095	365
CONTIG5335	31250052_c3_11	11827	25930	225	75
CONTIG5336	1174007_f2_5	11828	25931	192	64
CONTIG5336	26213413_f3_8	11829	25932	228	76
CONTIG5338	20428386_c1_11	11830	25933	483	161
CONTIG5338	24414062_f1_1	11831	25934	267	89
CONTIG5338	24417630_f3_6	11832	25935	189	63
CONTIG5338	14485250_c1_8	11833	25936	183	61
CONTIG5339	6024051_c3_11	11834	25937	186	62
CONTIG5339	907201_f2_3	11835	25938	183	61
CONTIG5339	1984577_f2_5	11836	25939	210	70
CONTIG534	515777_c3_10	11837	25940	339	113
CONTIG534	33365876_f2_1	11838	25941	306	102
CONTIG534	9820132_c2_5	11839	25942	270	90
CONTIG5340	12523392_f2_2	11840	25943	546	182

CONTIG5341	33781505_f2_8	11841	25944	261	87
CONTIG5342	1391263_f1_2	11842	25945	246	82
CONTIG5343	14548186_c2_18	11843	25946	216	72
CONTIG5343	5125007_c3_26	11844	25947	531	177
CONTIG5344	56313_f1_3	11845	25948	192	64
CONTIG5344	34117307_f1_5	11846	25949	267	89
CONTIG5345	1028626_f2_6	11847	25950	192	64
CONTIG5345	5115642_c1_18	11848	25951	465	155
CONTIG5346	2970462S_c1_8	11849	25952	249	83
CONTIG5347	33619527_c2_10	11850	25953	2040	680
CONTIG5348	3126963_f3_8	11851	25954	216	72
CONTIG5349	13783200_f1_1	11852	25955	249	83
CONTIG5349	16797050_c1_8	11853	25956	198	66
CONTIG5349	1705627_c1_9	11854	25957	225	75
CONTIG5349	426402_c3_11	11855	25958	195	65
CONTIG535	20894667_f2_1	11856	25959	270	90
CONTIG5350	10162937_f1_4	11857	25960	183	61
CONTIG5350	1172175_f2_8	11858	25961	528	176
CONTIG5351	10938836_f1_1	11859	25962	240	80
CONTIG5352	6757750_f2_1	11860	25963	240	80
CONTIG5352	6820182_c1_6	11861	25964	255	85
CONTIG5352	26192052_c3_11	11862	25965	258	86
CONTIG5353	2741638_c1_12	11863	25966	183	61
CONTIG5353	24015902_c3_16	11864	25967	606	202
CONTIG5356	33788386_f1_1	11865	25968	519	173
CONTIG5356	13682930_f3_3	11866	25969	201	67
CONTIG5356	4172755_c2_8	11867	25970	186	62
CONTIG5357	4820392_f1_4	11868	25971	243	81
CONTIG5357	125300_f2_5	11869	25972	201	67
CONTIG5357	5116557_c1_16	11870	25973	1119	373
CONTIG5358	4117313_c2_11	11871	25974	189	63
CONTIG5359	11756937_c3_16	11872	25975	819	273
CONTIG536	33619125_c2_4	11873	25976	273	91

CONTIG5360	4037512_f2_4	11874	25977	258	86
CONTIG5360	29301028_c2_11	11875	25978	276	92
CONTIG5360	13798305_c3_13	11876	25979	279	93
CONTIG5361	6439076_f2_2	11877	25980	255	85
CONTIG5361	29486285_c3_10	11878	25981	201	67
CONTIG5361	4886292_c3_12	11879	25982	423	141
CONTIG5361	23687507_c3_14	11880	25983	204	68
CONTIG5362	21892038_f2_6	11881	25984	300	100
CONTIG5363	29463528_f2_5	11882	25985	267	89
CONTIG5363	23629158_f2_11	11883	25986	201	67
CONTIG5363	20345053_c1_20	11884	25987	183	61
CONTIG5363	22556636_c2_23	11885	25988	267	89
CONTIG5364	21929082_f2_6	11886	25989	240	80
CONTIG5365	24485937_f1_2	11887	25990	285	95
CONTIG5365	158125_f2_9	11888	25991	183	61
CONTIG5366	30268887_c3_8	11889	25992	201	67
CONTIG5367	24410890_f3_8	11890	25993	243	81
CONTIG5368	1050638_f2_3	11891	25994	270	90
CONTIG5368	6726411_c1_9	11892	25995	351	117
CONTIG5368	30516952_c2_12	11893	25996	192	64
CONTIG5368	523276_c3_18	11894	25997	273	91
CONTIG5369	6015682_c3_9	11895	25998	552	184
CONTIG537	290627_c2_1	11896	25999	189	63
CONTIG5370	30157932_f1_1	11897	26000	357	119
CONTIG5370	14142586_f2_3	11898	26001	213	71
CONTIG5370	4730267_c1_10	11899	26002	432	144
CONTIG5371	13870187_c3_21	11900	26003	222	74
CONTIG5371	4417152_c1_14	11901	26004	309	103
CONTIG5372	109400_f2_7	11902	26005	363	121
CONTIG5372	1985312_f3_11	11903	26006	195	65
CONTIG5372	20115892_c3_18	11904	26007	291	97
CONTIG5373	6567_c2_7	11905	26008	588	196
CONTIG5373	13789062_c2_8	11906	26009	231	77

CONTIG5374	16454077_f1_2	11907	26010	228	76
CONTIG5374	3408380_c2_9	11908	26011	255	85
CONTIG5374	12507258_c2_10	11909	26012	189	63
CONTIG5376	35350333_c2_16	11910	26013	252	84
CONTIG5377	6844057_f1_2	11911	26014	201	67
CONTIG5377	392312_f1_3	11912	26015	198	66
CONTIG5377	24390675_c3_11	11913	26016	186	62
CONTIG538	33208215_c3_12	11914	26017	561	187
CONTIG5379	23867177_f1_4	11915	26018	213	71
CONTIG5379	22151556_f3_9	11916	26019	1137	379
CONTIG5378	26367312_f3_10	11917	26020	315	105
CONTIG5379	23474152_f3_1	11918	26021	726	242
CONTIG5380	14658305_f2_5	11919	26022	246	82
CONTIG5380	2241625_f3_9	11920	26023	216	72
CONTIG5380	19688760_c1_10	11921	26024	195	65
CONTIG5380	4720035_c3_17	11922	26025	531	177
CONTIG5382	26288187_f2_6	11923	26026	279	93
CONTIG5383	6131927_c1_5	11924	26027	231	77
CONTIG5383	29303760_c3_12	11925	26028	225	75
CONTIG5383	4082658_c3_13	11926	26029	261	87
CONTIG5384	24869724_c1_12	11927	26030	363	121
CONTIG5384	5101500_c1_14	11928	26031	309	103
CONTIG5384	6284465_c2_17	11929	26032	183	61
CONTIG5384	4067511_c2_18	11930	26033	408	136
CONTIG5384	994788_c3_19	11931	26034	1089	363
CONTIG5386	5267187_f1_1	11932	26035	210	70
CONTIG5387	24879836_f2_5	11933	26036	219	73
CONTIG5387	19585800_f2_6	11934	26037	198	66
CONTIG5387	4422125_f2_10	11935	26038	219	73
CONTIG5388	881578_c2_9	11936	26039	417	139
CONTIG5388	23868752_c3_12	11937	26040	720	240
CONTIG5389	34095075_f1_3	11938	26041	231	77
CONTIG5389	23442132_f1_4	11939	26042	183	61

CONTIG5389	5861500_f2_6	11940	26043	207	69
CONTIG5389	29344562_c1_10	11941	26044	189	63
CONTIG5389	13867907_c1_11	11942	26045	216	72
CONTIG5389	25396962_c2_15	11943	26046	186	62
CONTIG5389	24414062_c3_18	11944	26047	282	94
CONTIG5390	19719377_c1_9	11945	26048	195	65
CONTIG5390	20421930_c3_19	11946	26049	441	147
CONTIG5391	23984382_f3_15	11947	26050	312	104
CONTIG5391	32078877_c1_17	11948	26051	1434	478
CONTIG5391	24470258_c2_20	11949	26052	261	87
CONTIG5392	1362512_c1_3	11950	26053	183	61
CONTIG5392	9813760_c2_8	11951	26054	270	90
CONTIG5392	19768751_c3_11	11952	26055	183	61
CONTIG5394	20360467_f2_3	11953	26056	216	72
CONTIG5394	10195317_f2_4	11954	26057	240	80
CONTIG5394	24617250_f3_7	11955	26058	282	94
CONTIG5394	22445188_c1_9	11956	26059	189	63
CONTIG5394	19691430_c2_14	11957	26060	432	144
CONTIG5395	10969066_f2_1	11958	26061	189	63
CONTIG5395	4804053_f2_2	11959	26062	246	82
CONTIG5395	835885_c2_5	11960	26063	339	113
CONTIG5395	16837665_c3_7	11961	26064	225	75
CONTIG5395	4487500_c3_9	11962	26065	222	74
CONTIG5395	1207682_c3_10	11963	26066	246	82
CONTIG5397	19766250_f3_10	11964	26067	195	65
CONTIG5397	13720278_c2_21	11965	26068	222	74
CONTIG5397	976562_c2_22	11966	26069	210	70
CONTIG5397	29948386_c3_23	11967	26070	312	104
CONTIG5397	0_c3_27	11968	26071	183	61
CONTIG5398	20964067_c1_10	11969	26072	207	69
CONTIG5398	6039517_c3_17	11970	26073	183	61
CONTIG5399	46942_f1_1	11971	26074	207	69
CONTIG5399	30517567_c1_13	11972	26075	201	67

CONTIG5399	235005_c1_15	11973	26076	204	68
CONTIG54	2039793_f2_1	11974	26077	336	112
CONTIG54	2620967_c2_3	11975	26078	330	110
CONTIG5400	5977202_f1_1	11976	26079	207	69
CONTIG5400	6850953_f2_4	11977	26080	213	71
CONTIG5400	876425_c1_9	11978	26081	183	61
CONTIG5400	1228432_c2_10	11979	26082	267	89
CONTIG5401	1257183_f3_5	11980	26083	357	119
CONTIG5401	24492191_c1_9	11981	26084	246	82
CONTIG5402	23850018_c3_15	11982	26085	252	84
CONTIG5402	1210825_f3_5	11983	26086	1326	442
CONTIG5403	25578126_c2_13	11984	26087	243	81
CONTIG5403	4962715_f1_1	11985	26088	249	83
CONTIG5404	11178175_c1_6	11986	26089	225	75
CONTIG5405	4698275_c1_6	11987	26090	231	77
CONTIG5405	35583505_f3_3	11988	26091	258	86
CONTIG5406	4734382_f3_4	11989	26092	561	187
CONTIG5406	6119012_c3_13	11990	26093	195	65
CONTIG5407	787502_c3_14	11991	26094	225	75
CONTIG5407	1227212_f1_1	11992	26095	183	61
CONTIG5407	4956877_f1_3	11993	26096	321	107
CONTIG5407	5343803_f2_5	11994	26097	264	88
CONTIG5407	6416406_f3_6	11995	26098	258	86
CONTIG5407	14735927_f3_7	11996	26099	243	81
CONTIG5408	22531688_c2_13	11997	26100	183	61
CONTIG5408	34564025_f1_3	11998	26101	297	99
CONTIG5408	2383442_f3_6	11999	26102	183	61
CONTIG5408	5196890_f3_7	12000	26103	213	71
CONTIG5408	24390881_c2_10	12001	26104	270	90
CONTIG5409	257750_f1_2	12002	26105	186	62
CONTIG5409	1960762_f2_5	12003	26106	240	80
CONTIG5409	25392038_f3_10	12004	26107	279	93
CONTIG5409	5899063_f3_11	12005	26108	192	64

CONTIG5409	16798452_f3_13	12006	26109	183	61
CONTIG5409	23961013_c1_14	12007	26110	414	138
CONTIG5409	25397137_c1_16	12008	26111	252	84
CONTIG5409	1054781_c1_17	12009	26112	189	63
CONTIG5409	48782_c3_22	12010	26113	312	104
CONTIG541	35805160_f2_1	12011	26114	222	74
CONTIG5410	24116427_c2_14	12012	26115	207	69
CONTIG5411	22437717_f2_2	12013	26116	306	102
CONTIG5411	22533426_f2_3	12014	26117	717	239
CONTIG5412	24804635_f1_3	12015	26118	339	113
CONTIG5412	1992631_f2_4	12016	26119	1626	542
CONTIG5412	5370260_f3_9	12017	26120	204	68
CONTIG5412	26265680_c1_13	12018	26121	246	82
CONTIG5412	24801532_c3_19	12019	26122	795	265
CONTIG5413	24486281_f1_1	12020	26123	186	62
CONTIG5413	5173588_c2_17	12021	26124	186	62
CONTIG5415	22047343_c3_16	12022	26125	936	312
CONTIG5415	4100328_f2_3	12023	26126	267	89
CONTIG5415	31265887_f3_8	12024	26127	225	75
CONTIG5417	15110953_c1_11	12025	26128	231	77
CONTIG5418	33754437_f1_3	12026	26129	255	85
CONTIG5418	1178125_f1_4	12027	26130	207	69
CONTIG5418	24227127_f1_5	12028	26131	321	107
CONTIG5418	21485968_f3_9	12029	26132	192	64
CONTIG5418	12613937_c2_13	12030	26133	207	69
CONTIG5418	13875188_c3_18	12031	26134	195	65
CONTIG5419	24423126_f1_1	12032	26135	195	65
CONTIG5419	6129816_f2_2	12033	26136	222	74
CONTIG5419	23634513_f2_4	12034	26137	183	61
CONTIG5419	2384375_f3_6	12035	26138	183	61
CONTIG5419	23613761_f3_9	12036	26139	285	95
CONTIG542	244818_f1_1	12037	26140	906	302
CONTIG5420	6893752_c3_14	12038	26141	234	78

CONTIG5422	11718750_c1_14	12039	26142	204	68
CONTIG5422	22538175_c3_22	12040	26143	315	105
CONTIG5423	14876550_f1_1	12041	26144	2082	694
CONTIG5423	13781556_f3_2	12042	26145	621	207
CONTIG5424	125701_c3_13	12043	26146	186	62
CONTIG5424	16803817_c3_14	12044	26147	219	73
CONTIG5425	19776928_f1_2	12045	26148	207	69
CONTIG5426	5256587_f2_3	12046	26149	285	95
CONTIG5426	31365640_f3_5	12047	26150	300	100
CONTIG5426	12895275_c2_11	12048	26151	210	70
CONTIG5427	24392052_f1_2	12049	26152	192	64
CONTIG5427	5984437_f3_4	12050	26153	234	78
CONTIG5427	3392056_f3_12	12051	26154	195	65
CONTIG5429	22275128_f1_1	12052	26155	1329	443
CONTIG5429	25426680_c1_7	12053	26156	297	99
CONTIG5429	21881886_c1_8	12054	26157	183	61
CONTIG5429	24220286_c3_10	12055	26158	195	65
CONTIG5429	20757886_c3_11	12056	26159	234	78
CONTIG543	12312692_f2_1	12057	26160	645	215
CONTIG543	21759677_f3_2	12058	26161	258	86
CONTIG5430	14102176_c1_14	12059	26162	900	300
CONTIG5430	23704776_c1_15	12060	26163	300	100
CONTIG5431	5914078_f2_5	12061	26164	222	74
CONTIG5431	2734755_c2_11	12062	26165	195	65
CONTIG5432	24789826_f2_9	12063	26166	273	91
CONTIG5432	22460937_c1_16	12064	26167	366	122
CONTIG5433	32120177_f3_5	12065	26168	255	85
CONTIG5433	1179165_c3_13	12066	26169	207	69
CONTIG5434	23475782_f1_2	12067	26170	237	79
CONTIG5434	48402_c3_8	12068	26171	246	82
CONTIG5434	14636505_c3_9	12069	26172	201	67
CONTIG5434	26345277_c3_10	12070	26173	642	214
CONTIG5435	33440715_f3_5	12071	26174	192	64

CONTIG5435	14194066_c2_12	12072	26175	216	72
CONTIG5435	20751953_c3_15	12073	26176	198	66
CONTIG5435	36025676_c3_17	12074	26177	195	65
CONTIG5436	14569375_f1_3	12075	26178	441	147
CONTIG5436	195375_f2_4	12076	26179	270	90
CONTIG5436	34179502_f2_6	12077	26180	270	90
CONTIG5436	12222530_f3_10	12078	26181	249	83
CONTIG5437	21984702_f3_11	12079	26182	669	223
CONTIG5437	3314437_f1_2	12080	26183	930	310
CONTIG5438	10660905_f3_12	12081	26184	342	114
CONTIG5438	4084387_c1_15	12082	26185	186	62
CONTIG5438	24080308_c3_19	12083	26186	492	164
CONTIG5438	158_c3_21	12084	26187	270	90
CONTIG5439	26257817_f1_2	12085	26188	321	107
CONTIG5439	10834828_f2_5	12086	26189	207	69
CONTIG5439	35429578_f3_6	12087	26190	348	116
CONTIG5439	24398402_c2_11	12088	26191	192	64
CONTIG5439	25426702_c3_14	12089	26192	204	68
CONTIG544	1183450_c2_3	12090	26193	189	63
CONTIG5440	5909642_f1_3	12091	26194	198	66
CONTIG5440	12675285_f2_4	12092	26195	219	73
CONTIG5440	30205018_f2_5	12093	26196	303	101
CONTIG5441	4511015_f1_5	12094	26197	234	78
CONTIG5442	19564627_f1_3	12095	26198	258	86
CONTIG5442	22462563_c1_12	12096	26199	420	140
CONTIG5442	16406681_c1_13	12097	26200	462	154
CONTIG5443	22382132_f1_1	12098	26201	1419	473
CONTIG5444	10739437_f1_1	12099	26202	1392	464
CONTIG5444	10937_f2_3	12100	26203	969	323
CONTIG5444	2815875_f3_6	12101	26204	195	65
CONTIG5445	4146950_f3_4	12102	26205	219	73
CONTIG5446	5894833_c1_9	12103	26206	231	77
CONTIG5447	6931311_c1_16	12104	26207	195	65

CONTIG5447	34573325_c2_19	12105	26208	219	73
CONTIG5448	20504076_f2_5	12106	26209	216	72
CONTIG5448	24785937_c3_19	12107	26210	192	64
CONTIG5449	35361013_c2_7	12108	26211	228	76
CONTIG5449	31253_c3_10	12109	26212	183	61
CONTIG545	4703201_f2_1	12110	26213	210	70
CONTIG545	782261_c2_5	12111	26214	183	61
CONTIG5451	24033305_f2_4	12112	26215	225	75
CONTIG5451	34079055_c2_11	12113	26216	315	105
CONTIG5451	788316_c3_16	12114	26217	234	78
CONTIG5452	24507637_f1_2	12115	26218	225	75
CONTIG5452	23860252_f1_3	12116	26219	297	99
CONTIG5452	34079686_f3_6	12117	26220	276	92
CONTIG5452	22146012_c1_7	12118	26221	219	73
CONTIG5452	2868825_c2_8	12119	26222	321	107
CONTIG5452	656378_c3_9	12120	26223	225	75
CONTIG5453	781287_f2_10	12121	26224	741	247
CONTIG5453	24730326_f2_11	12122	26225	540	180
CONTIG5455	5117175_f1_1	12123	26226	222	74
CONTIG5455	15036551_c3_9	12124	26227	192	64
CONTIG5456	12304687_f3_2	12125	26228	219	73
CONTIG5456	13082682_c2_7	12126	26229	237	79
CONTIG5456	22063426_c2_8	12127	26230	294	98
CONTIG5456	12125000_c2_9	12128	26231	666	222
CONTIG5457	12609511_f2_3	12129	26232	213	71
CONTIG5458	5289688_c2_12	12130	26233	237	79
CONTIG5458	19712640_c3_15	12131	26234	219	73
CONTIG5458	400910_c3_17	12132	26235	222	74
CONTIG5459	33992215_f2_7	12133	26236	186	62
CONTIG5459	10550312_c1_12	12134	26237	954	318
CONTIG5459	9765942_c2_13	12135	26238	279	93
CONTIG5459	29480381_c2_14	12136	26239	456	152
CONTIG5459	21972013_c3_16	12137	26240	210	70

CONTIG5460	4774062_f1_5	12138	26241	612	204
CONTIG5460	24801532_f3_13	12139	26242	552	184
CONTIG5460	24789037_f3_14	12140	26243	309	103
CONTIG5460	30275307_f3_15	12141	26244	801	267
CONTIG5460	1208288_c3_28	12142	26245	201	67
CONTIG5461	2239463_f1_1	12143	26246	201	67
CONTIG5461	14881640_f1_3	12144	26247	189	63
CONTIG5461	24395832_c2_14	12145	26248	198	66
CONTIG5462	4097540_c1_8	12146	26249	189	63
CONTIG5463	9767000_f1_2	12147	26250	237	79
CONTIG5463	35270842_f1_3	12148	26251	210	70
CONTIG5463	875317_f1_4	12149	26252	249	83
CONTIG5463	167182_f1_5	12150	26253	237	79
CONTIG5463	12532675_f2_10	12151	26254	198	66
CONTIG5463	13712640_f3_11	12152	26255	210	70
CONTIG5463	24612755_c2_13	12153	26256	330	110
CONTIG5464	35254090_c1_9	12156	26259	288	96
CONTIG5464	31429537_f1_2	12155	26258	390	130
CONTIG5464	24648382_f1_1	12154	26257	207	69
CONTIG5464	4865967_c1_10	12157	26260	189	63
CONTIG5464	579388_c1_12	12158	26261	186	62
CONTIG5465	33203125_f3_3	12159	26262	183	61
CONTIG5466	550192_f1_1	12160	26263	252	84
CONTIG5467	4110878_f3_12	12161	26264	204	68
CONTIG5467	20515637_c1_13	12162	26265	330	110
CONTIG5467	2818752_c2_18	12163	26266	282	94
CONTIG5469	23548533_c1_10	12164	26267	999	333
CONTIG5469	29500125_c3_17	12165	26268	198	66
CONTIG547	6767637_c1_4	12166	26269	201	67
CONTIG547	29848136_c2_5	12167	26270	279	93
CONTIG547	24226633_c2_6	12168	26271	201	67
CONTIG5470	22539063_c1_7	12169	26272	240	80
CONTIG5474	34156512_f2_1	12170	26273	210	70

CONTIG5474	6693828_c1_12	12171	26274	198	66
CONTIG5475	23835040_f1_3	12172	26275	189	63
CONTIG5475	22454055_f2_5	12173	26276	279	93
CONTIG5475	1375275_f3_7	12174	26277	189	63
CONTIG5475	25429512_c2_12	12175	26278	333	111
CONTIG5476	14742162_c2_10	12176	26279	219	73
CONTIG5477	6681326_f3_11	12177	26280	339	113
CONTIG5477	9954757_f1_2	12178	26281	219	73
CONTIG5477	6656526_c1_12	12179	26282	906	302
CONTIG5478	30478200_c1_13	12180	26283	1041	347
CONTIG5478	36609427_f1_1	12181	26284	426	142
CONTIG5478	25429665_c2_11	12182	26285	678	226
CONTIG5478	20600325_f2_3	12183	26286	210	70
CONTIG5479	15657757_f2_5	12184	26287	771	257
CONTIG5479	30644155_f1_1	12185	26288	216	72
CONTIG548	3360580_f1_1	12186	26289	327	109
CONTIG548	35351562_f1_2	12187	26290	210	70
CONTIG5480	33397151_c1_5	12188	26291	216	72
CONTIG5480	19938161_c3_9	12189	26292	834	278
CONTIG5481	26204450_f3_7	12190	26293	183	61
CONTIG5482	25820432_f1_2	12191	26294	207	69
CONTIG5482	7229677_f1_6	12192	26295	270	90
CONTIG5482	24487717_f2_7	12193	26296	240	80
CONTIG5482	3329587_f2_10	12194	26297	225	75
CONTIG5482	244712_c1_15	12195	26298	234	78
CONTIG5483	9860000_f1_1	12196	26299	228	76
CONTIG5483	21537802_f1_2	12197	26300	345	115
CONTIG5483	24296882_f2_3	12198	26301	249	83
CONTIG5483	26595126_f3_6	12199	26302	336	112
CONTIG5484	20105375_c1_18	12200	26303	201	67
CONTIG5485	978438_f1_2	12201	26304	594	198
CONTIG5485	4151063_f2_3	12202	26305	183	61
CONTIG5485	31250061_c1_8	12203	26306	189	63

CONTIG5485	24413562_c2_9	12204	26307	309	103
CONTIG5486	6024140_f2_4	12205	26308	294	98
CONTIG5487	23648513_f1_1	12206	26309	435	145
CONTIG5487	22306312_f1_3	12207	26310	183	61
CONTIG5487	7214808_f3_7	12208	26311	204	68
CONTIG5487	3320163_c1_13	12209	26312	198	66
CONTIG5488	211068_c3_13	12210	26313	1335	445
CONTIG5489	391250_c3_7	12211	26314	216	72
CONTIG5489	4876586_c3_8	12212	26315	231	77
CONTIG5490	3025126_f1_1	12213	26316	279	93
CONTIG5490	16453131_f3_7	12214	26317	378	126
CONTIG5492	26754657_f2_1	12215	26318	213	71
CONTIG5493	23648252_f2_4	12216	26319	648	216
CONTIG5493	32552177_c2_9	12217	26320	189	63
CONTIG5493	4694801_c3_15	12218	26321	216	72
CONTIG5494	812927_f1_3	12219	26322	282	94
CONTIG5494	33319057_f2_4	12220	26323	213	71
CONTIG5494	23916062_f3_11	12221	26324	234	78
CONTIG5494	23850635_c3_19	12222	26325	186	62
CONTIG5495	12901955_f1_3	12223	26326	249	83
CONTIG5495	31437752_f2_9	12224	26327	192	64
CONTIG5495	24094627_c1_12	12225	26328	216	72
CONTIG5496	29532590_f2_7	12226	26329	186	62
CONTIG5497	4104653_f3_4	12227	26330	216	72
CONTIG5498	36112750_f2_2	12228	26331	213	71
CONTIG5498	159626_c2_9	12229	26332	441	147
CONTIG5498	24064067_c2_10	12230	26333	225	75
CONTIG5498	33203382_c3_11	12231	26334	222	74
CONTIG550	27377555_c2_2	12232	26335	666	222
CONTIG5500	36519017_c3_17	12233	26336	204	68
CONTIG5501	34580002_f2_7	12234	26337	225	75
CONTIG5501	35681325_c1_17	12235	26338	192	64
CONTIG5501	22767131_c1_21	12236	26339	255	85

CONTIG5501	21567912_c2_29	12237	26340	210	70
CONTIG5502	3954050_f2_3	12238	26341	189	63
CONTIG5503	253_f1_3	12239	26342	678	226
CONTIG5504	20508287_f3_6	12240	26343	396	132
CONTIG5504	7203187_c1_12	12241	26344	213	71
CONTIG5504	3320306_c3_18	12242	26345	1239	413
CONTIG5504	20881252_c3_19	12243	26346	219	73
CONTIG5505	23913202_c2_12	12244	26347	267	89
CONTIG5505	25535307_f1_3	12245	26348	264	88
CONTIG5505	2535686_f2_5	12246	26349	420	140
CONTIG5506	11110911_c2_11	12247	26350	678	226
CONTIG5506	4162503_c1_11	12248	26351	261	87
CONTIG5506	781287_f2_4	12249	26352	318	106
CONTIG5507	34078537_f1_3	12250	26353	204	68
CONTIG5507	15656250_f1_3	12251	26354	201	67
CONTIG5507	781302_f1_4	12252	26355	183	61
CONTIG5508	2226577_c2_14	12253	26356	408	136
CONTIG5508	32693806_f1_1	12254	26357	654	218
CONTIG5509	14456325_c1_21	12255	26358	255	85
CONTIG5509	4960932_f1_1	12256	26359	306	102
CONTIG5509	32037837_f2_4	12257	26360	330	110
CONTIG5509	26214161_f3_5	12258	26361	201	67
CONTIG5509	22709818_c1_7	12259	26362	231	77
CONTIG5509	13860887_c2_11	12260	26363	204	68
CONTIG551	4805438_c2_12	12261	26364	204	68
CONTIG5510	25437800_c3_3	12262	26365	198	66
CONTIG5510	4766927_f1_6	12263	26366	207	69
CONTIG5510	2458437_f3_11	12264	26367	252	84
CONTIG5510	4790903_f3_13	12265	26368	753	251
CONTIG5510	6362505_c2_18	12266	26369	201	67
CONTIG5511	25449187_f1_1	12267	26370	297	99
CONTIG5511	20317_f1_2	12268	26371	186	62

CONTIG5511	30273282_f2_7	12270	26373	210	70
CONTIG5511	26851705_f3_9	12271	26374	207	69
CONTIG5511	22755_f3_10	12272	26375	270	90
CONTIG5511	10956401_f3_11	12273	26376	240	80
CONTIG5513	29329437_f1_5	12274	26377	213	71
CONTIG5514	1284692_f1_2	12275	26378	213	71
CONTIG5514	19742706_f1_3	12276	26379	207	69
CONTIG5514	24253410_f2_4	12277	26380	198	66
CONTIG5514	6829688_f3_5	12278	26381	249	83
CONTIG5515	23631561_f1_4	12279	26382	336	112
CONTIG5517	24494061_c1_5	12280	26383	228	76
CONTIG5517	6643750_c3_12	12281	26384	183	61
CONTIG5518	36360433_f2_5	12282	26385	2940	980
CONTIG5518	29453131_c2_17	12283	26386	312	104
CONTIG5520	23650308_f3_10	12284	26387	198	66
CONTIG5520	13676555_f3_11	12285	26388	417	139
CONTIG5520	782553_c1_13	12286	26389	183	61
CONTIG5520	24392137_c1_16	12287	26390	300	100
CONTIG5520	10835756_c3_19	12288	26391	219	73
CONTIG5521	4385953_f3_17	12289	26392	267	89
CONTIG5522	20589388_f1_4	12290	26393	195	65
CONTIG5522	15_f2_6	12291	26394	192	64
CONTIG5522	24650928_f2_10	12292	26395	645	215
CONTIG5523	24814843_f1_2	12293	26396	225	75
CONTIG5523	9800012_f3_14	12294	26397	936	312
CONTIG5523	12697031_c3_21	12295	26398	291	97
CONTIG5524	3141301_f3_9	12296	26399	204	68
CONTIG5524	2164812_c3_18	12297	26400	186	62
CONTIG5524	26461693_c3_21	12298	26401	375	125
CONTIG5525	14453182_f1_1	12299	26402	186	62
CONTIG5525	1312_c3_12	12300	26403	231	77
CONTIG5525	2851402_c3_13	12301	26404	210	70
CONTIG5526	33287677_f2_4	12302	26405	225	75

CONTIG5526	6845625_c1_9	12303	26406	333	111
CONTIG5527	30469081_f2_2	12304	26407	213	71
CONTIG5527	30282825_c1_7	12305	26408	318	106
CONTIG5527	24225380_c2_8	12306	26409	297	99
CONTIG5527	26776715_c2_10	12307	26410	315	105
CONTIG5527	23675250_c2_11	12308	26411	231	77
CONTIG5527	5973302_c3_14	12309	26412	627	209
CONTIG5528	4547780_f1_1	12310	26413	189	63
CONTIG5528	4901502_f2_4	12311	26414	753	251
CONTIG5528	4882785_f3_5	12312	26415	201	67
CONTIG5528	24885967_c3_14	12313	26416	594	198
CONTIG5529	4095327_f3_9	12314	26417	213	71
CONTIG553	7062552_c3_4	12315	26418	183	61
CONTIG5530	1413180_c1_9	12316	26419	348	116
CONTIG5530	26888_c2_10	12317	26420	186	62
CONTIG5530	4082327_c2_11	12318	26421	189	63
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CONTIG5531	21604067_f1_8	12320	26423	195	65
CONTIG5531	14298462_f1_9	12321	26424	309	103
CONTIG5531	30500001_f3_19	12322	26425	225	75
CONTIG5531	34261326_f3_21	12323	26426	258	86
CONTIG5531	4689650_c1_24	12324	26427	219	73
CONTIG5532	1995952_f1_2	12325	26428	216	72
CONTIG5532	13850906_c3_14	12326	26429	282	94
CONTIG5533	9923375_f3_3	12327	26430	201	67
CONTIG5533	26267165_c1_4	12328	26431	198	66
CONTIG5533	4729007_c1_6	12329	26432	192	64
CONTIG5533	25953462_c2_8	12330	26433	216	72
CONTIG5533	30275067_c3_10	12331	26434	186	62
CONTIG5533	13788876_c3_11	12332	26435	192	64
CONTIG5533	804056_c3_12	12333	26436	201	67
CONTIG5534	163186_f2_4	12334	26437	192	64
CONTIG5534	423442_f2_7	12335	26438	189	63

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CONTIG5534	12207760_c3_20	12338	26441	423	141
CONTIG5535	24423577_f2_4	12339	26442	222	74
CONTIG5535	26853262_c1_14	12340	26443	252	84
CONTIG5536	25671882_f1_1	12341	26444	192	64
CONTIG5536	34578137_f3_6	12342	26445	204	68
CONTIG5536	33625275_c1_10	12343	26446	861	287
CONTIG5536	34175900_c1_13	12344	26447	195	65
CONTIG5536	19628405_c2_14	12345	26448	246	82
CONTIG5537	31683333_c1_11	12346	26449	186	62
CONTIG5537	24015637_c3_28	12347	26450	225	75
CONTIG5538	6836540_f3_10	12348	26451	231	77
CONTIG5538	19961402_f3_11	12349	26452	192	64
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CONTIG5540	34100905_c1_15	12351	26454	660	220
CONTIG5541	26742001_f1_4	12352	26455	951	317
CONTIG5541	5100801_f2_10	12353	26456	291	97
CONTIG5541	1978188_f3_13	12354	26457	1329	443
CONTIG5541	3986276_c2_16	12355	26458	240	80
CONTIG5541	179816_c2_19	12356	26459	231	77
CONTIG5542	22145711_f2_9	12357	26460	186	62
CONTIG5542	21744387_f3_11	12358	26461	276	92
CONTIG5542	12626912_c2_17	12359	26462	210	70
CONTIG5542	10318901_c3_19	12360	26463	198	66
CONTIG5542	2948292_c3_20	12361	26464	270	90
CONTIG5543	22062803_f3_9	12362	26465	909	303
CONTIG5543	21689802_c1_13	12363	26466	201	67
CONTIG5543	6662660_c3_17	12364	26467	552	184
CONTIG5545	9772000_c2_14	12365	26468	204	68
CONTIG5546	1197928_f1_1	12366	26469	234	78
CONTIG5546	14709807_c2_18	12367	26470	390	130
CONTIG5546	5079515_c2_20	12368	26471	189	63

CONTIG5546	24000131_c3_21	12369	26472	267	89
CONTIG5547	34620313_f3_7	12370	26473	189	63
CONTIG5547	35548250_c1_11	12371	26474	1575	525
CONTIG5548	24394053_f3_8	12372	26475	186	62
CONTIG5548	390630_c1_9	12373	26476	318	106
CONTIG5548	22125056_c1_12	12374	26477	243	81
CONTIG5548	4569627_c1_13	12375	26478	213	71
CONTIG5549	25601640_c2_9	12376	26479	210	70
CONTIG5550	11796937_f1_2	12377	26480	246	82
CONTIG5550	2071001_c1_11	12378	26481	204	68
CONTIG5550	24667066_c3_16	12379	26482	303	101
CONTIG5551	4424027_f1_1	12380	26483	240	80
CONTIG5551	4719012_f1_2	12381	26484	210	70
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CONTIG5551	986013_f3_7	12383	26486	354	118
CONTIG5551	31734500_c3_18	12384	26487	219	73
CONTIG5552	16065657_f3_8	12385	26488	756	252
CONTIG5552	22839765_c1_11	12386	26489	216	72
CONTIG5553	12614027_f1_1	12387	26490	1158	386
CONTIG5553	61r1257_f2_6	12388	26491	213	71
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CONTIG5554	4704387_f2_5	12391	26494	261	87
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CONTIG5555	32222000_c3_18	12394	26497	210	70
CONTIG5556	10640805_f1_2	12395	26498	237	79
CONTIG5557	26203142_f1_2	12396	26499	645	215
CONTIG5558	21757068_f2_5	12397	26500	243	81
CONTIG5558	20337552_c1_13	12398	26501	228	76
CONTIG5558	31454802_c3_24	12399	26502	249	83
CONTIG5559	22110968_c3_21	12400	26503	261	87
CONTIG556	23984680_f1_1	12401	26504	459	153

CONTIG5560	2142575_c3_20	12402	26505	285	95
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CONTIG5561	23537526_f3_9	12404	26507	192	64
CONTIG5561	494077_c1_13	12405	26508	213	71
CONTIG5561	11223888_c2_14	12406	26509	693	231
CONTIG5562	6126500_c2_10	12407	26510	234	78
CONTIG5562	15022505_c3_12	12408	26511	567	189
CONTIG5563	837925_f1_1	12409	26512	195	65
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CONTIG5563	14739010_c1_17	12411	26514	237	79
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CONTIG5565	36136436_f1_1	12415	26518	339	113
CONTIG5565	1953412_f2_12	12416	26519	207	69
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CONTIG5566	19801533_f2_7	12419	26522	483	161
CONTIG5567	15704531_f1_1	12420	26523	228	76
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CONTIG5568	29328378_f1_4	12422	26525	321	107
CONTIG5568	23476627_c1_11	12423	26526	303	101
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CONTIG5568	24300888_c1_14	12425	26528	309	103
CONTIG5568	7142265_c2_18	12426	26529	237	79
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CONTIG5569	1956325_c1_7	12428	26531	1239	413
CONTIG5569	33203250_c2_10	12429	26532	282	94
CONTIG5570	14259506_f2_4	12430	26533	360	120
CONTIG5570	36221941_f3_6	12431	26534	279	93
CONTIG5570	35807756_c1_11	12432	26535	195	65
CONTIG5571	31439002_f1_2	12433	26536	189	63
CONTIG5571	16485638_f2_8	12434	26537	297	99

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CONTIG5572	12692876_f1_2	12438	26541	222	74
CONTIG5572	4034431_f3_11	12439	26542	996	332
CONTIG5572	20330001_c3_18	12440	26543	414	138
CONTIG5573	24492192_f3_5	12441	26544	186	62
CONTIG5573	56587_c1_9	12442	26545	210	70
CONTIG5573	22756651_c2_10	12443	26546	1227	409
CONTIG5573	29456251_c2_12	12444	26547	1662	554
CONTIG5574	79388_f2_8	12445	26548	639	213
CONTIG5574	29298900_c1_15	12446	26549	936	312
CONTIG5574	4804563_c3_18	12447	26550	237	79
CONTIG5575	20367067_f1_1	12448	26551	645	215
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CONTIG5575	10038127_f2_5	12450	26553	279	93
CONTIG5575	24476403_c2_16	12451	26554	222	74
CONTIG5575	4884375_c3_17	12452	26555	234	78
CONTIG5575	24102177_c3_20	12453	26556	183	61
CONTIG5576	30553265_f1_3	12454	26557	237	79
CONTIG5576	35804715_f1_5	12455	26558	249	83
CONTIG5576	21502330_f2_7	12456	26559	291	97
CONTIG5576	34088906_f2_10	12457	26560	201	67
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CONTIG5576	24801532_c3_24	12459	26562	360	120
CONTIG5579	34073800_f2_5	12460	26563	201	67
CONTIG5579	6056675_f2_10	12461	26564	189	63
CONTIG5579	10548130_f3_12	12462	26565	222	74
CONTIG5579	23828325_f3_13	12463	26566	222	74
CONTIG5579	24798500_c1_17	12464	26567	222	74
CONTIG5579	14656385_c3_22	12465	26568	189	63
CONTIG5579	9803438_c3_23	12466	26569	234	78
CONTIG5579	3126912_c3_24	12467	26570	225	75

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CONTIG5581	23728407_c1_12	12471	26574	1944	648
CONTIG5581	11991075_c1_13	12472	26575	1023	341
CONTIG5582	22769640_f1_1	12473	26576	204	68
CONTIG5582	23828125_c1_14	12474	26577	261	87
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CONTIG5582	89001_c3_23	12476	26579	1059	353
CONTIG5583	816256_f2_7	12477	26580	237	79
CONTIG5583	6648387_f3_9	12478	26581	258	86
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CONTIG5584	26207531_f1_2	12480	26583	228	76
CONTIG5584	9775287_c3_12	12481	26584	186	62
CONTIG5584	4147276_f2_4	12482	26585	192	64
CONTIG5585	33828452_f1_2	12483	26586	201	67
CONTIG5585	4063937_f2_4	12484	26587	306	102
CONTIG5585	14306551_f3_11	12485	26588	228	76
CONTIG5586	23681462_c3_22	12486	26589	207	69
CONTIG5587	24251075_f2_6	12487	26590	195	65
CONTIG5587	23617787_f2_8	12488	26591	195	65
CONTIG5587	19695262_c3_23	12489	26592	1788	596
CONTIG5588	23477276_c1_10	12490	26593	318	106
CONTIG5589	9866401_f3_11	12491	26594	471	157
CONTIG5589	13860025_c3_25	12492	26595	198	66
CONTIG559	21695325_c2_1	12493	26596	219	73
CONTIG559	14554087_c3_2	12494	26597	363	121
CONTIG5590	24406318_f2_5	12495	26598	207	69
CONTIG5590	6019140_f2_6	12496	26599	234	78
CONTIG5590	117825_f3_14	12497	26600	186	62
CONTIG5590	12792937_c1_15	12498	26601	210	70
CONTIG5590	23913212_c2_19	12499	26602	222	74
CONTIG5590	35345302_c3_22	12500	26603	210	70

CONTIG5591	24414052_c2_11	12501	26604	228	76
CONTIG5592	10585378_c2_5	12502	26605	609	203
CONTIG5592	20086015_c3_7	12503	26606	213	71
CONTIG5592	33985002_c3_9	12504	26607	678	226
CONTIG5593	4885841_f1_1	12505	26608	327	109
CONTIG5593	23629403_f3_6	12506	26609	189	63
CONTIG5593	4818931_f3_10	12507	26610	183	61
CONTIG5593	629682_c2_16	12508	26611	285	95
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CONTIG5594	21759702_c1_13	12511	26614	195	65
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CONTIG5595	986025_c3_13	12514	26617	1101	367
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CONTIG5596	23410_f3_13	12516	26619	249	83
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CONTIG5598	589717_f1_1	12519	26622	231	77
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CONTIG5598	24511068_f2_10	12521	26624	540	180
CONTIG5598	15085765_f3_11	12522	26625	207	69
CONTIG5598	16144783_f3_14	12523	26626	213	71
CONTIG5598	11757300_c3_25	12524	26627	195	65
CONTIG5599	29945875_f1_2	12525	26628	204	68
CONTIG5599	20709436_f2_6	12526	26629	267	89
CONTIG5599	23925017_c1_13	12527	26630	1179	393
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CONTIG5600	7031938_f1_3	12530	26633	225	75
CONTIG5600	24414212_c1_18	12531	26634	270	90
CONTIG5600	34430252_c2_20	12532	26635	210	70
CONTIG5600	111588_c3_24	12533	26636	381	127

CONTIG5600	3984762_c3_25	12534	26637	240	80
CONTIG5602	25581627_f1_4	12535	26638	267	89
CONTIG5602	24397660_c2_14	12536	26639	1743	581
CONTIG5602	24039057_c2_17	12537	26640	462	154
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CONTIG5603	4773262_f3_7	12540	26643	417	139
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CONTIG5604	34619036_f3_7	12542	26645	204	68
CONTIG5604	969002_c1_9	12543	26646	243	81
CONTIG5604	859430_c2_10	12544	26647	195	65
CONTIG5604	21675280_c3_12	12545	26648	573	191
CONTIG5605	4957510_f2_5	12546	26649	267	89
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CONTIG5605	9804687_c2_16	12549	26652	186	62
CONTIG5606	22289650_f2_14	12550	26653	264	88
CONTIG5606	10562913_c2_42	12551	26654	279	93
CONTIG5606	16516706_c2_45	12552	26655	204	68
CONTIG5607	14652010_f2_5	12553	26656	813	271
CONTIG5607	5267501_c1_7	12554	26657	195	65
CONTIG5607	1214126_c3_15	12555	26658	270	90
CONTIG5608	5316550_f2_6	12556	26659	1374	458
CONTIG5608	30120441_c3_19	12557	26660	282	94
CONTIG5608	34640925_c3_20	12558	26661	195	65
CONTIG5609	4454125_f1_2	12559	26662	264	88
CONTIG5609	5861260_f2_4	12560	26663	2094	698
CONTIG561	1050937_f3_1	12561	26664	198	66
CONTIG5610	14847842_f3_5	12562	26665	204	68
CONTIG5611	14540802_f1_1	12563	26666	240	80
CONTIG5611	2551018_f3_4	12564	26667	234	78
CONTIG5611	273453_f3_6	12565	26668	222	74
CONTIG5611	21695305_c1_8	12566	26669	306	102

CONTIG5612	10048780_c2_14	12567	26670	345	115
CONTIG5613	34569675_f1_2	12568	26671	183	61
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CONTIG5614	33399087_f2_6	12572	26675	189	63
CONTIG5614	1497283_f2_9	12573	26676	339	113
CONTIG5614	815667_c2_19	12574	26677	264	88
CONTIG5615	2144752_f1_3	12575	26678	198	66
CONTIG5615	6909383_f2_7	12576	26679	204	68
CONTIG5615	36617136_f2_11	12577	26680	183	61
CONTIG5615	6640686_f3_15	12578	26681	1497	499
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CONTIG5615	29320206_f2_8	12580	26683	405	135
CONTIG5616	22283128_c1_19	12581	26684	201	67
CONTIG5616	15902206_c1_21	12582	26685	255	85
CONTIG5616	13785055_c2_28	12583	26686	294	98
CONTIG5616	34553582_c2_30	12584	26687	258	86
CONTIG5616	16600282_c2_31	12585	26688	507	169
CONTIG5616	4709507_c3_34	12586	26689	765	255
CONTIG5616	2750391_c3_35	12587	26690	336	112
CONTIG5617	25626890_f2_3	12588	26691	339	113
CONTIG5617	4704652_f3_5	12589	26692	1854	618
CONTIG5618	23632877_f1_1	12590	26693	333	111
CONTIG5618	23600042_c2_22	12591	26694	192	64
CONTIG5618	25478377_c3_29	12592	26695	366	122
CONTIG5619	7832_f1_4	12593	26696	195	65
CONTIG5620	156461_f3_7	12594	26697	345	115
CONTIG5620	24304587_c1_11	12595	26698	231	77
CONTIG5620	23835902_c2_16	12596	26699	1182	394
CONTIG5621	2756510_f1_1	12597	26700	249	83
CONTIG5622	814152_c1_12	12598	26701	237	79
CONTIG5623	20484630_c3_11	12599	26702	207	69

CONTIG5624	12990638_f2_5	12600	26703	198	66
CONTIG5625	34470775_f1_5	12601	26704	186	62
CONTIG5625	23648312_f2_12	12602	26705	192	64
CONTIG5625	4100641_c2_22	12603	26706	189	63
CONTIG5625	2869193_c2_24	12604	26707	1995	665
CONTIG5625	4970337_c2_25	12605	26708	204	68
CONTIG5625	10682625_c3_27	12606	26709	237	79
CONTIG5626	21506962_f3_5	12607	26710	222	74
CONTIG5627	20709436_f2_4	12608	26711	267	89
CONTIG5627	20507752_c1_10	12609	26712	213	71
CONTIG5627	4798135_c3_11	12610	26713	1548	516
CONTIG5628	3160142_c3_13	12611	26714	276	92
CONTIG5628	34104687_f2_6	12612	26715	183	61
CONTIG5628	24074140_f3_9	12613	26716	216	72
CONTIG5628	395280_c2_13	12614	26717	393	131
CONTIG563	11179637_c3_23	12615	26718	252	84
CONTIG5629	10752136_f2_6	12616	26719	363	121
CONTIG5629	161267_c3_20	12617	26720	240	80
CONTIG563	3945377_f1_1	12618	26721	219	73
CONTIG563	24398425_c2_4	12619	26722	447	149
CONTIG5630	13673200_f1_1	12620	26723	201	67
CONTIG5630	35323378_f3_7	12621	26724	204	68
CONTIG5630	14500138_c3_21	12622	26725	786	262
CONTIG5630	664507_c3_22	12623	26726	543	181
CONTIG5631	24414707_f1_1	12624	26727	303	101
CONTIG5631	30712642_f2_4	12625	26728	1953	651
CONTIG5631	21692300_c1_9	12626	26729	210	70
CONTIG5631	2050062_c2_10	12627	26730	528	176
CONTIG5631	21878540_c3_13	12628	26731	1224	408
CONTIG5631	13859517_c1_12	12629	26732	420	140
CONTIG5633	14353562_c2_15	12630	26733	1476	492
CONTIG5633	37503_c3_18	12631	26734	246	82
CONTIG5634	164678_c3_28	12632	26735	255	85

CONTIG5635	11737887_c3_19	12633	26736	405	135
CONTIG5636	24407802_f3_5	12634	26737	315	105
CONTIG5637	472S892_f2_5	12635	26738	186	62
CONTIG5637	2421943_c1_13	12636	26739	252	84
CONTIG5637	22360675_c1_18	12637	26740	294	98
CONTIG5638	15024215_c2_20	12638	26741	222	74
CONTIG5638	437913_f1_1	12639	26742	186	62
CONTIG5638	12511300_f2_8	12640	26743	510	170
CONTIG5638	23992630_f2_9	12641	26744	219	73
CONTIG5638	236260_f2_10	12642	26745	207	69
CONTIG5639	9945303_c1_13	12643	26746	186	62
CONTIG5639	31836090_c2_17	12644	26747	324	108
CONTIG5639	10269660_c3_20	12645	26748	1017	339
CONTIG5639	25815637_c3_22	12646	26749	957	319
CONTIG5639	23439393_c3_23	12647	26750	246	82
CONTIG564	24626562_c3_3	12648	26751	183	61
CONTIG5640	421903_c3_13	12649	26752	183	61
CONTIG5641	14656516_c1_11	12650	26753	831	277
CONTIG5641	10975386_c3_16	12651	26754	186	62
CONTIG5642	110136_f1_1	12652	26755	279	93
CONTIG5642	4303425_f3_6	12653	26756	252	84
CONTIG5642	22519063_c3_23	12654	26757	201	67
CONTIG5643	35401660_f1_2	12655	26758	204	68
CONTIG5643	20095015_f1_3	12656	26759	1206	402
CONTIG5643	981837_f2_5	12657	26760	273	91
CONTIG5643	288128_f2_6	12658	26761	183	61
CONTIG5643	1369062_f2_7	12659	26762	897	299
CONTIG5643	12890675_f2_11	12660	26763	279	93
CONTIG5643	23909627_c1_20	12661	26764	225	75
CONTIG5643	34259632_c2_26	12662	26765	471	157
CONTIG5643	25390052_c3_31	12663	26766	204	68
CONTIG5643	15835882_c3_32	12664	26767	297	99
CONTIG5644	13757906_f3_10	12665	26768	258	86

CONTIG5644	14885900_f3_11	12666	26769	279	93
CONTIG5644	16522588_f3_12	12667	26770	186	62
CONTIG5645	2929687_f2_6	12668	26771	207	69
CONTIG5646	24254451_f2_13	12669	26772	207	69
CONTIG5646	22376400_c2_15	12670	26773	216	72
CONTIG5647	4069068_f1_5	12671	26774	264	88
CONTIG5647	1975050_f1_7	12672	26775	195	65
CONTIG5648	29879385_f1_3	12673	26776	333	111
CONTIG5648	14851632_f2_5	12674	26777	1140	380
CONTIG5648	4741292_f3_11	12675	26778	231	77
CONTIG5648	3131937_c1_14	12676	26779	318	106
CONTIG5648	29533140_c2_20	12677	26780	204	68
CONTIG5648	31369057_c3_21	12678	26781	318	106
CONTIG5648	16587807_c3_23	12679	26782	201	67
CONTIG5649	1381582_f1_5	12680	26783	183	61
CONTIG5649	2072018_f3_10	12681	26784	207	69
CONTIG5649	628438_f3_12	12682	26785	540	180
CONTIG5649	21523912_c2_17	12683	26786	183	61
CONTIG5650	14274132_f3_12	12684	26787	273	91
CONTIG5651	33369063_f1_3	12685	26788	228	76
CONTIG5651	26855302_c1_17	12686	26789	600	200
CONTIG5651	4892325_c1_18	12687	26790	1149	383
CONTIG5651	10401950_c3_30	12688	26791	357	119
CONTIG5652	13069211_f1_4	12689	26792	228	76
CONTIG5652	4095887_f3_14	12690	26793	510	170
CONTIG5652	19691086_c1_16	12691	26794	189	63
CONTIG5652	14538307_c1_18	12692	26795	189	63
CONTIG5652	4687555_c2_23	12693	26796	261	87
CONTIG5653	4805252_c1_15	12694	26797	747	249
CONTIG5653	14964427_c2_18	12695	26798	594	198
CONTIG5654	13850317_f1_1	12696	26799	231	77
CONTIG5654	14708135_f3_7	12697	26800	216	72
CONTIG5654	25984660_c1_9	12698	26801	285	95

CONTIG5655	6737890_c2_14	12699	26802	261	87
CONTIG5655	10651077_c2_15	12700	26803	189	63
CONTIG5655	21723792_c3_19	12701	26804	261	87
CONTIG5655	35429578_c3_20	12702	26805	330	110
CONTIG5655	22925152_c3_24	12703	26806	363	121
CONTIG5656	9768811_f1_1	12704	26807	336	112
CONTIG5656	25674002_f1_3	12705	26808	339	113
CONTIG5656	21516687_f2_4	12706	26809	711	237
CONTIG5656	4804142_f2_7	12707	26810	276	92
CONTIG5656	16443767_f3_11	12708	26811	303	101
CONTIG5657	36621088_f3_11	12709	26812	201	67
CONTIG5657	10726025_f3_13	12710	26813	1272	424
CONTIG5657	3131930_c1_14	12711	26814	195	65
CONTIG5657	24413902_c3_21	12712	26815	624	208
CONTIG5658	292842_f1_3	12713	26816	204	68
CONTIG5658	24304552_f1_5	12714	26817	204	68
CONTIG5658	30501261_c1_16	12715	26818	183	61
CONTIG5659	21537500_f1_4	12716	26819	189	63
CONTIG5659	6723407_f2_7	12717	26820	711	237
CONTIG5659	22656930_f3_15	12718	26821	186	62
CONTIG5659	16973300_c1_16	12719	26822	255	85
CONTIG5659	5361312_c2_24	12720	26823	186	62
CONTIG5659	12709502_c3_27	12721	26824	192	64
CONTIG5659	16444682_c3_28	12722	26825	684	228
CONTIG566	47187775_f1_1	12723	26826	252	84
CONTIG566	23861643_f2_2	12724	26827	183	61
CONTIG5660	1407762_f1_5	12725	26828	201	67
CONTIG5660	30741436_f3_10	12726	26829	243	81
CONTIG5660	10238408_c1_18	12727	26830	201	67
CONTIG5660	22304842_c2_20	12728	26831	201	67
CONTIG5661	167018_c1_8	12729	26832	240	80
CONTIG5661	12990638_c2_11	12730	26833	198	66
CONTIG5661	1953125_c2_13	12731	26834	183	61

CONTIG5662	2199015_f2_7	12732	26835	396	132
CONTIG5662	23907755_c3_12	12733	26836	573	191
CONTIG5663	22712625_f2_6	12734	26837	447	149
CONTIG5663	24415812_f2_8	12735	26838	183	61
CONTIG5663	37878_f3_10	12736	26839	579	193
CONTIG5663	1562_f3_11	12737	26840	201	67
CONTIG5664	4494027_f3_8	12738	26841	264	88
CONTIG5665	24414188_f3_5	12739	26842	198	66
CONTIG5665	36131437_f3_6	12740	26843	195	65
CONTIG5665	178877_c3_24	12741	26844	375	125
CONTIG5667	21659762_f3_6	12742	26845	306	102
CONTIG5667	12626502_f3_7	12743	26846	318	106
CONTIG5667	10241328_f3_8	12744	26847	264	88
CONTIG5667	16600806_c2_14	12745	26848	201	67
CONTIG5667	11819125_c2_15	12746	26849	267	89
CONTIG5667	2143755_c2_16	12747	26850	366	122
CONTIG5667	26457806_c2_17	12748	26851	330	110
CONTIG5668	34101687_f2_2	12749	26852	342	114
CONTIG5668	29489177_f2_4	12750	26853	384	128
CONTIG5668	3148317_f3_5	12751	26854	333	111
CONTIG5668	10750188_f3_6	12752	26855	378	126
CONTIG5668	10563175_c2_13	12753	26856	216	72
CONTIG5668	23444527_c3_14	12754	26857	336	112
CONTIG5668	1253160_c3_16	12755	26858	243	81
CONTIG5669	33757837_f1_1	12756	26859	264	88
CONTIG5669	11148308_f1_2	12757	26860	1323	441
CONTIG5669	23992051_f1_4	12758	26861	198	66
CONTIG5669	21522692_c3_29	12759	26862	204	68
CONTIG5669	9766541_c3_30	12760	26863	234	78
CONTIG567	23961542_f3_2	12761	26864	396	132
CONTIG5670	19537932_f1_1	12762	26865	312	104
CONTIG5670	35431925_f1_2	12763	26866	453	151
CONTIG5670	6140761_f2_7	12764	26867	453	151

CONTIG5670	24039062_f2_8	12765	26868	273	91
CONTIG5670	34261068_c2_29	12766	26869	258	86
CONTIG5670	958465_c3_35	12767	26870	195	65
CONTIG5671	23944003_f1_1	12768	26871	423	141
CONTIG5671	6095260_f1_2	12769	26872	312	104
CONTIG5671	14223251_f1_4	12770	26873	198	66
CONTIG5671	6363267_f1_5	12771	26874	1773	591
CONTIG5672	19569203_f2_6	12772	26875	216	72
CONTIG5672	24223408_f3_11	12773	26876	228	76
CONTIG5672	9800012_f3_14	12774	26877	234	78
CONTIG5672	21884467_c1_15	12775	26878	231	77
CONTIG5672	29725812_c2_20	12776	26879	333	111
CONTIG5672	11929011_c3_21	12777	26880	354	118
CONTIG5673	3923250_f1_2	12778	26881	183	61
CONTIG5673	24314037_f3_18	12779	26882	201	67
CONTIG5673	20203527_c1_26	12780	26883	225	75
CONTIG5673	32071965_c3_33	12781	26884	207	69
CONTIG5673	15736261_c3_45	12782	26885	183	61
CONTIG5674	29297000_f1_2	12783	26886	195	65
CONTIG5674	23860951_f1_3	12784	26887	219	73
CONTIG5674	21537682_f2_4	12785	26888	240	80
CONTIG5674	10970437_f2_5	12786	26889	1026	342
CONTIG5674	24642300_c1_11	12787	26890	2082	694
CONTIG5675	32141900_f2_6	12788	26891	636	212
CONTIG5675	21898261_f3_10	12789	26892	1674	558
CONTIG5675	20426553_f3_11	12790	26893	210	70
CONTIG5676	6683567_f2_9	12791	26894	336	112
CONTIG5676	9895413_f3_13	12792	26895	375	125
CONTIG5677	13854005_f1_6	12793	26896	186	62
CONTIG5677	31379050_f3_11	12794	26897	201	67
CONTIG5677	39062_c1_18	12795	26898	639	213
CONTIG5677	23834635_c1_22	12796	26899	279	93
CONTIG5678	23672202_f2_1	12797	26900	213	71

CONTIG5678	41062_f2_4	12798	26901	216	72
CONTIG5678	14550008_f3_7	12799	26902	249	83
CONTIG5678	10744676_c3_18	12800	26903	501	167
CONTIG5680	115950_f3_19	12801	26904	252	84
CONTIG5681	625_c1_9	12802	26905	471	157
CONTIG5682	4400426_f2_11	12803	26906	474	158
CONTIG5682	9954682_c1_19	12804	26907	378	126
CONTIG5683	25635075_f3_10	12805	26908	186	62
CONTIG5683	11985002_c1_13	12806	26909	183	61
CONTIG5684	5880261_c2_15	12807	26910	183	61
CONTIG5685	20421875_c2_9	12808	26911	1275	425
CONTIG5686	13790912_c1_18	12809	26912	288	96
CONTIG5686	20742010_c2_22	12810	26913	1428	476
CONTIG5687	878752_f3_14	12811	26914	264	88
CONTIG5687	2441557_c1_17	12812	26915	210	70
CONTIG5687	19803590_c2_19	12813	26916	219	73
CONTIG5687	34088906_c3_21	12814	26917	198	66
CONTIG5687	35804715_c3_22	12815	26918	249	83
CONTIG5687	11142517_c3_24	12816	26919	219	73
CONTIG5688	4487667_f2_7	12817	26920	423	141
CONTIG5688	24394677_c1_14	12818	26921	624	208
CONTIG5688	24259687_c2_19	12819	26922	270	90
CONTIG5688	10603468_c3_24	12820	26923	318	106
CONTIG5689	62_f1_1	12821	26924	483	161
CONTIG5690	2539525_f3_11	12822	26925	207	69
CONTIG5690	93763_f3_12	12823	26926	210	70
CONTIG5690	19539075_c1_15	12824	26927	222	74
CONTIG5690	36329412_c1_16	12825	26928	297	99
CONTIG5690	4726416_c1_17	12826	26929	294	98
CONTIG5690	26351535_c3_29	12827	26930	426	142
CONTIG5690	19697765_c3_30	12828	26931	195	65
CONTIG5691	34085907_c2_25	12829	26932	414	138
CONTIG5691	15739027_c2_26	12830	26933	312	104

CONTIG5691	13016450_c3_31	12831	26934	261	87
CONTIG5693	2317_f1_3	12832	26935	195	65
CONTIG5693	10548275_c1_14	12833	26936	68	
CONTIG5693	23594680_c2_17	12834	26937	759	253
CONTIG5693	34179000_c3_20	12835	26938	264	88
CONTIG5694	11114200_c1_14	12836	26939	249	83
CONTIG5694	22460938_c1_15	12837	26940	204	68
CONTIG5694	24645300_c1_16	12838	26941	528	176
CONTIG5694	33834677_c3_24	12839	26942	216	72
CONTIG5695	33319425_f1_1	12840	26943	237	79
CONTIG5695	4332180_f2_6	12841	26944	330	110
CONTIG5695	975027_f3_9	12842	26945	240	80
CONTIG5695	6542575_c2_12	12843	26946	216	72
CONTIG5695	6054687_c2_14	12844	26947	198	66
CONTIG5695	3301512_c3_16	12845	26948	192	64
CONTIG5696	2626925_f2_4	12846	26949	198	66
CONTIG5696	9788300_f3_7	12847	26950	210	70
CONTIG5696	9788312_c1_13	12848	26951	1038	346
CONTIG5697	11725056_f1_1	12849	26952	1179	393
CONTIG5697	10735301_f2_6	12850	26953	402	134
CONTIG5697	23632937_f3_8	12851	26954	279	93
CONTIG5697	31526957_f3_9	12852	26955	264	88
CONTIG5697	1986550_c1_15	12853	26956	198	66
CONTIG5697	6931677_c2_18	12854	26957	432	144
CONTIG5697	21737755_c2_20	12855	26958	369	123
CONTIG5697	26596928_c3_29	12856	26959	213	71
CONTIG5697	4018882_c3_30	12857	26960	186	62
CONTIG5698	14557812_f1_4	12858	26961	195	65
CONTIG5698	4022126_f1_5	12859	26962	225	75
CONTIG5698	6269068_f1_6	12860	26963	192	64
CONTIG5698	25656312_c1_17	12861	26964	381	127
CONTIG5698	6020801_c2_24	12862	26965	303	101
CONTIG5699	207943_c1_22	12863	26966	240	80

CONTIG5699	25425317_c1_24	12864	26967	258	86
CONTIG5700	11881253_f1_2	12865	26968	216	72
CONTIG5700	2080463_f1_3	12866	26969	483	161
CONTIG5700	23836002_f2_4	12867	26970	198	66
CONTIG5700	115687_f3_9	12868	26971	195	65
CONTIG5700	11015876_c1_18	12869	26972	234	78
CONTIG5700	3210933_c2_24	12870	26973	261	87
CONTIG5701	23632026_f2_4	12871	26974	195	65
CONTIG5701	34079686_c1_8	12872	26975	273	91
CONTIG5701	20583182_c1_9	12873	26976	270	90
CONTIG5701	4117837_c2_11	12874	26977	276	92
CONTIG5701	6023577_c3_14	12875	26978	204	68
CONTIG5701	6813900_c3_15	12876	26979	219	73
CONTIG5701	687_c3_17	12877	26980	252	84
CONTIG5703	21964141_f1_5	12878	26981	330	110
CONTIG5703	12301575_f1_6	12879	26982	270	90
CONTIG5703	20491627_f2_13	12880	26983	219	73
CONTIG5703	31751293_f2_14	12881	26984	192	64
CONTIG5703	15917932_f3_17	12882	26985	459	153
CONTIG5703	24667066_f3_22	12883	26986	303	101
CONTIG5703	957061_f3_23	12884	26987	225	75
CONTIG5703	33527_c2_33	12885	26988	225	75
CONTIG5703	26385962_c2_35	12886	26989	447	149
CONTIG5704	26382937_f1_1	12887	26990	294	98
CONTIG5704	14564408_f2_5	12888	26991	195	65
CONTIG5704	35167502_f2_6	12889	26992	198	66
CONTIG5704	13691965_f3_7	12890	26993	183	61
CONTIG5704	29477068_c2_16	12891	26994	219	73
CONTIG5704	2469006_c3_18	12892	26995	2019	673
CONTIG5705	26692758_f1_1	12893	26996	1251	417
CONTIG5705	35976703_c1_16	12894	26997	189	63
CONTIG5706	4688561_f1_5	12895	26998	231	77
CONTIG5706	26189801_f2_7	12896	26999	195	65

CONTIG5706	22457507_f2_8	12897	27000	201	67
CONTIG5706	24095313_c2_20	12898	27001	555	185
CONTIG5706	20704750_c2_22	12899	27002	219	73
CONTIG5706	33204806_c3_24	12900	27003	222	74
CONTIG5706	33439392_c3_26	12901	27004	204	68
CONTIG5707	22303381_f3_9	12902	27005	198	66
CONTIG5707	24878437_c1_15	12903	27006	198	66
CONTIG5708	14729642_f3_15	12904	27007	192	64
CONTIG5708	24641937_c2_23	12905	27008	303	101
CONTIG5708	969075_c3_25	12906	27009	192	64
CONTIG5708	16850433_c3_26	12907	27010	267	89
CONTIG5709	14234385_f1_1	12908	27011	204	68
CONTIG5710	600187_f1_1	12909	27012	351	117
CONTIG5710	56566_f3_7	12910	27013	189	63
CONTIG5710	12271886_c1_13	12911	27014	189	63
CONTIG5710	6062507_c3_22	12912	27015	234	78
CONTIG5711	14571011_c2_9	12913	27016	255	85
CONTIG5711	4006326_c3_15	12914	27017	702	234
CONTIG5712	19411_f1_3	12915	27018	255	85
CONTIG5712	6038317_f3_11	12916	27019	288	96
CONTIG5712	35788_f3_12	12917	27020	267	89
CONTIG5712	29695781_c2_20	12918	27021	267	89
CONTIG5712	1296926_c3_23	12919	27022	300	100
CONTIG5712	1173436_c3_25	12920	27023	1881	627
CONTIG5714	21770837_f1_1	12921	27024	231	77
CONTIG5714	24657927_c1_15	12922	27025	219	73
CONTIG5714	35781251_c3_22	12923	27026	192	64
CONTIG5714	863750_c3_24	12924	27027	231	77
CONTIG5715	33236256_f1_2	12925	27028	303	101
CONTIG5715	23524132_f3_6	12926	27029	207	69
CONTIG5715	204337_f3_7	12927	27030	237	79
CONTIG5715	26750952_c1_8	12928	27031	198	66
CONTIG5715	24273325_c2_17	12929	27032	246	82

CONTIG5716	25447183_c1_19	12930	27033	189	63
CONTIG5716	1962916_c2_24	12931	27034	294	98
CONTIG5716	23829125_c2_25	12932	27035	228	76
CONTIG5717	34182813_c3_19	12933	27036	564	188
CONTIG5718	3132636_f2_5	12934	27037	189	63
CONTIG5718	30084840_f2_7	12935	27038	210	70
CONTIG5719	19720150_f3_7	12936	27039	1635	545
CONTIG5719	19628956_f3_8	12937	27040	189	63
CONTIG5719	3931325_c1_9	12938	27041	195	65
CONTIG5719	20830378_c2_12	12939	27042	243	81
CONTIG5719	34163952_c3_18	12940	27043	210	70
CONTIG5719	24398411_c3_17	12941	27044	249	83
CONTIG572	13160953_f1_1	12942	27045	225	75
CONTIG5720	20986535_f1_1	12943	27046	207	69
CONTIG5720	26697180_f1_2	12944	27047	633	211
CONTIG5720	22851415_f3_11	12945	27048	693	231
CONTIG5720	16015625_c3_28	12946	27049	258	86
CONTIG5721	7039692_f2_3	12947	27050	255	85
CONTIG5721	24860007_f2_8	12948	27051	306	102
CONTIG5721	2790780_f3_11	12949	27052	219	73
CONTIG5721	2909430_f3_12	12950	27053	741	247
CONTIG5721	11807875_f3_15	12951	27054	555	185
CONTIG5721	42152_c1_19	12952	27055	213	71
CONTIG5721	24259506_c3_27	12953	27056	216	72
CONTIG5722	24022818_c1_11	12954	27057	189	63
CONTIG5722	29303425_c2_19	12955	27058	555	185
CONTIG5723	24241437_c1_20	12956	27059	183	61
CONTIG5723	24647875_c2_22	12957	27060	264	88
CONTIG5723	25396887_c3_33	12958	27061	198	66
CONTIG5723	35970636_c3_34	12959	27062	327	109
CONTIG5724	22292137_f3_11	12960	27063	201	67
CONTIG5724	9929652_c1_15	12961	27064	213	71
CONTIG5724	5972127_c1_19	12962	27065	228	76

CONTIG5724	11900015_c2_21	12963	27066	195	65
CONTIG5724	23612782_c2_22	12964	27067	1062	354
CONTIG5724	5267962_c2_23	12965	27068	552	184
CONTIG5724	35429578_c2_25	12966	27069	414	138
CONTIG5724	26756500_c3_28	12967	27070	198	66
CONTIG5725	20079517_f1_2	12968	27071	186	62
CONTIG5725	22444752_f1_3	12969	27072	195	65
CONTIG5725	21964140_f1_4	12970	27073	330	110
CONTIG5725	16820318_f2_5	12971	27074	282	94
CONTIG5725	24667066_f2_9	12972	27075	189	63
CONTIG5725	14259506_f3_12	12973	27076	360	120
CONTIG5725	23835781_f3_13	12974	27077	222	74
CONTIG5725	10570432_c2_23	12975	27078	183	61
CONTIG5725	24242177_f1_2	12976	27079	189	63
CONTIG5726	1406551_f3_14	12977	27080	216	72
CONTIG5726	24031336_c1_20	12978	27081	216	72
CONTIG5726	2757910_c2_26	12979	27082	183	61
CONTIG5727	2475277_f2_7	12980	27083	225	75
CONTIG5727	29718936_f2_8	12981	27084	222	74
CONTIG5727	4417640_f3_14	12982	27085	210	70
CONTIG5727	35156877_c3_31	12983	27086	213	71
CONTIG5728	14062760_f1_1	12984	27087	234	78
CONTIG5728	9773288_f1_2	12985	27088	327	109
CONTIG5728	14579375_f3_11	12986	27089	219	73
CONTIG5728	35359425_f3_12	12987	27090	237	79
CONTIG5728	10564031_c1_16	12988	27091	195	65
CONTIG5728	6145910_c2_19	12989	27092	222	74
CONTIG5729	878752_f2_5	12990	27093	282	94
CONTIG5729	10980181_f2_6	12991	27094	198	66
CONTIG5729	197652_f3_14	12992	27095	192	64
CONTIG5729	14297187_c1_18	12993	27096	237	79
CONTIG5729	30078411_c2_24	12994	27097	213	71
CONTIG5729	16191885_c3_32	12995	27098	189	63

CONTIG5729	24667066_c3_33	12996	27099	240	80
CONTIG5731	36610912_f1_2	12997	27100	198	66
CONTIG5731	24798432_f2_6	12998	27101	603	201
CONTIG5731	10553327_f2_8	12999	27102	321	107
CONTIG5731	11751251_f2_9	13000	27103	534	178
CONTIG5731	31489638_c3_28	13001	27104	273	91
CONTIG5732	24410927_f1_1	13002	27105	198	66
CONTIG5732	4111013_c2_28	13003	27106	372	124
CONTIG5732	4719011_c3_34	13004	27107	669	223
CONTIG5733	4103152_c2_21	13005	27108	330	110
CONTIG5733	172812_c3_28	13006	27109	201	67
CONTIG5733	23711001_c3_30	13007	27110	204	68
CONTIG5733	4104700_c3_34	13008	27111	318	106
CONTIG5734	14851527_f2_4	13009	27112	186	62
CONTIG5734	12500336_c1_8	13010	27113	378	126
CONTIG5734	29470157_c2_15	13011	27114	765	255
CONTIG5734	13679037_c3_18	13012	27115	186	62
CONTIG5735	22469582_f1_2	13013	27116	606	202
CONTIG5735	24422182_c1_12	13014	27117	303	101
CONTIG5735	2_c2_23	13015	27118	201	67
CONTIG5737	110125_f1_2	13016	27119	183	61
CONTIG5737	21641075_f2_6	13017	27120	273	91
CONTIG5737	35273411_c3_18	13018	27121	192	64
CONTIG5739	4898563_c2_24	13019	27122	276	92
CONTIG5740	24727187_f1_4	13020	27123	348	116
CONTIG5741	4720816_f2_7	13021	27124	267	89
CONTIG5741	548127_c1_14	13022	27125	204	68
CONTIG5741	6304713_c2_15	13023	27126	1422	474
CONTIG5741	21991563_c2_17	13024	27127	198	66
CONTIG5741	5285805_c3_18	13025	27128	750	250
CONTIG5742	31330025_c3_27	13026	27129	558	186
CONTIG5742	2531012_c3_30	13027	27130	210	70
CONTIG5743	3932775_f1_4	13028	27131	189	63

CONTIG5743	20431562_f2_7	13029	27132	61
CONTIG5743	22150075_f2_10	13030	27133	91
CONTIG5743	12375631_f3_13	13031	27134	143
CONTIG5743	10562761_c1_14	13032	27135	72
CONTIG5743	34157637_c2_22	13033	27136	198
CONTIG5743	35209700_c2_23	13034	27137	63
CONTIG5743	12925302_c2_24	13035	27138	66
CONTIG5743	4879025_c3_26	13036	27139	77
CONTIG5744	10947537_f1_7	13037	27140	99
CONTIG5744	26194000_f2_8	13038	27141	96
CONTIG5745	24613155_f1_2	13039	27142	64
CONTIG5745	26855326_c2_18	13040	27143	65
CONTIG5746	878752_f1_2	13041	27144	104
CONTIG5746	989162_f2_5	13042	27145	113
CONTIG5746	35804715_c1_13	13043	27146	83
CONTIG5746	21932625_c2_15	13044	27147	121
CONTIG5746	29493785_c2_18	13045	27148	67
CONTIG5747	26683428_f1_1	13046	27149	94
CONTIG5747	12584427_f2_22	13047	27150	64
CONTIG5748	30085913_f2_8	13048	27151	95
CONTIG5749	24414063_f2_6	13049	27152	96
CONTIG5749	9932311_c2_19	13050	27153	65
CONTIG5749	4978202_c3_27	13051	27154	74
CONTIG575	24688830_c3_1	13052	27155	85
CONTIG5750	40_f1_4	13053	27156	68
CONTIG5750	4151052_c1_14	13054	27157	78
CONTIG5751	11900015_f2_4	13055	27158	65
CONTIG5751	11900015_f3_6	13056	27159	65
CONTIG5751	3167325_f3_7	13057	27160	62
CONTIG5752	12538307_f1_3	13058	27161	65
CONTIG5752	2757930_c1_15	13059	27162	64
CONTIG5752	3157877_c2_21	13060	27163	543
CONTIG5753	22289036_f1_1	13061	27164	255

CONTIG5753	13706557_f2_5	13062	27165	273	91
CONTIG5753	24035912_f2_6	13063	27166	315	105
CONTIG5753	24023326_f2_7	13064	27167	186	62
CONTIG5753	891937_f3_10	13065	27168	606	202
CONTIG5753	14882882_c3_24	13066	27169	183	61
CONTIG5754	14651430_f1_1	13067	27170	288	96
CONTIG5754	10964057_c1_22	13068	27171	561	187
CONTIG5754	29296875_c1_27	13069	27172	240	80
CONTIG5754	7035006_c2_31	13070	27173	207	69
CONTIG5755	24219082_f1_1	13071	27174	273	91
CONTIG5755	1181300_c3_17	13072	27175	204	68
CONTIG5755	9859393_c3_18	13073	27176	189	63
CONTIG5756	10548180_f1_6	13074	27177	732	244
CONTIG5756	5973453_c2_19	13075	27178	222	74
CONTIG5757	953936_f2_4	13076	27179	327	109
CONTIG5757	24007050_f3_6	13077	27180	204	68
CONTIG5758	14538927_f3_12	13078	27181	210	70
CONTIG5759	978128_f3_12	13079	27182	228	76
CONTIG5760	22689127_f3_18	13080	27183	273	91
CONTIG5760	2225925_c1_20	13081	27184	204	68
CONTIG5761	4152187_f3_11	13082	27185	222	74
CONTIG5761	4085931_c1_22	13083	27186	402	134
CONTIG5762	33137_f1_3	13084	27187	393	131
CONTIG5762	10594127_f3_18	13085	27188	198	66
CONTIG5762	11914078_c1_20	13086	27189	309	103
CONTIG5762	24408502_c1_25	13087	27190	204	68
CONTIG5762	26367837_c2_29	13088	27191	222	74
CONTIG5762	29489025_c2_31	13089	27192	243	81
CONTIG5763	26803436_f1_5	13090	27193	243	81
CONTIG5763	14851562_f2_8	13091	27194	231	77
CONTIG5763	3908313_c1_12	13092	27195	189	63
CONTIG5763	5268827_c1_18	13093	27196	198	66
CONTIG5764	35350088_f1_4	13094	27197	309	103

CONTIG5764	24297655_f2_7	13095	27198	234	78
CONTIG5764	11913875_f3_13	13096	27199	222	74
CONTIG5764	33289176_c1_20	13097	27200	186	62
CONTIG5764	4506910_c1_21	13098	27201	204	68
CONTIG5764	32089462_c2_29	13099	27202	192	64
CONTIG5764	12688886_c3_33	13100	27203	933	311
CONTIG5765	10579802_f1_3	13101	27204	315	105
CONTIG5765	4703587_f2_5	13102	27205	309	103
CONTIG5765	6642215_f2_10	13103	27206	192	64
CONTIG5765	3205006_f3_14	13104	27207	213	71
CONTIG5765	20191251_c1_23	13105	27208	213	71
CONTIG5765	24429642_c2_25	13106	27209	189	63
CONTIG5765	26620453_c3_29	13107	27210	1974	658
CONTIG5766	24081262_f1_3	13108	27211	213	71
CONTIG5766	978881_f2_15	13109	27212	207	69
CONTIG5766	158162_c2_27	13110	27213	228	76
CONTIG5766	6140751_c2_32	13111	27214	186	62
CONTIG5766	34157277_c3_34	13112	27215	240	80
CONTIG5766	4805340_c3_39	13113	27216	261	87
CONTIG5767	22054512_f1_3	13114	27217	840	280
CONTIG5767	24473390_c1_31	13115	27218	198	66
CONTIG5767	16051952_c1_38	13116	27219	330	110
CONTIG5767	2789765_c2_43	13117	27220	192	64
CONTIG5768	4034455_c1_18	13118	27221	282	94
CONTIG5768	1973875_c3_24	13119	27222	186	62
CONTIG5769	24256637_f1_2	13120	27223	309	103
CONTIG5769	156302_f3_9	13121	27224	192	64
CONTIG5769	1054687_c1_12	13122	27225	213	71
CONTIG5769	30353555_c2_15	13123	27226	228	76
CONTIG5769	24390887_c3_19	13124	27227	195	65
CONTIG5770	24257127_f1_4	13125	27228	210	70
CONTIG5770	30485250_f1_6	13126	27229	207	69
CONTIG5770	23635962_f3_19	13127	27230	315	105

CONTIG5770	35282932_c2_27	13128	27231	189	63
CONTIG5771	4062763_f1_2	13129	27232	276	92
CONTIG5771	14648252_f2_5	13130	27233	225	75
CONTIG5771	961567_f3_19	13131	27234	312	104
CONTIG5771	1990913_c2_39	13132	27235	195	65
CONTIG5772	32165825_f1_1	13133	27236	234	78
CONTIG5772	22316942_f2_11	13134	27237	255	85
CONTIG5772	24789037_f3_20	13135	27238	312	104
CONTIG5773	14297187_c2_38	13136	27239	240	80
CONTIG5773	13133575_c1_22	13137	27240	195	65
CONTIG5774	24735938_c1_23	13138	27241	303	101
CONTIG5774	10351588_f2_9	13139	27242	186	62
CONTIG5774	5978418_f3_12	13140	27243	225	75
CONTIG5774	24064512_c2_25	13141	27244	189	63
CONTIG5775	266330_f3_15	13142	27245	1518	506
CONTIG5775	14158436_c1_19	13143	27246	453	151
CONTIG5775	969063_f1_1	13144	27247	231	77
CONTIG5775	78138_f1_9	13145	27248	192	64
CONTIG5775	15787837_c1_22	13146	27249	243	81
CONTIG5775	25598762_c2_24	13147	27250	198	66
CONTIG5776	4101675_f1_2	13148	27251	276	92
CONTIG5776	34195437_f1_3	13149	27252	246	82
CONTIG5776	22900012_f2_8	13150	27253	411	137
CONTIG5776	13710751_f3_16	13151	27254	339	113
CONTIG5776	875251_c2_26	13152	27255	204	68
CONTIG5776	21878130_c3_31	13153	27256	186	62
CONTIG5777	787927_c3_35	13154	27257	210	70
CONTIG5777	22375807_f2_3	13155	27258	435	145
CONTIG5777	23471880_f3_10	13156	27259	264	88
CONTIG5777	81402_f3_15	13157	27260	222	74
CONTIG5777	29333512_c1_17	13158	27261	207	69
CONTIG5777	24322128_c2_24	13159	27262	183	61
CONTIG5778	31883388_f2_12	13160	27263	213	71

CONTIG5778	14866507_f2_17	13161	27264	252	84
CONTIG5778	7054677_f3_20	13162	27265	210	70
CONTIG5778	5329752_f3_21	13163	27266	402	134
CONTIG5778	31798388_c3_31	13164	27267	207	69
CONTIG5779	11909650_c1_16	13165	27268	279	93
CONTIG5779	34089026_c2_18	13166	27269	207	69
CONTIG5780	3945932_f1_4	13167	27270	1083	361
CONTIG5780	42305_c2_26	13168	27271	201	67
CONTIG5781	23594525_f2_12	13169	27272	285	95
CONTIG5781	4079661_f3_14	13170	27273	198	66
CONTIG5781	4489510_f3_16	13171	27274	237	79
CONTIG5782	24414142_f2_9	13172	27275	210	70
CONTIG5782	29881928_c1_16	13173	27276	249	83
CONTIG5782	20367250_c2_19	13174	27277	675	225
CONTIG5783	1991625_c3_26	13175	27278	198	66
CONTIG5783	26015953_f1_3	13176	27279	183	61
CONTIG5783	24492187_f2_11	13177	27280	225	75
CONTIG5783	34266952_c1_27	13178	27281	720	240
CONTIG5784	25401900_c2_29	13179	27282	201	67
CONTIG5784	23600678_f1_2	13180	27283	198	66
CONTIG5784	26609383_f2_4	13181	27284	240	80
CONTIG5784	10313125_f3_11	13182	27285	192	64
CONTIG5784	992187_c1_15	13183	27286	213	71
CONTIG5784	21672813_c1_16	13184	27287	279	93
CONTIG5784	14147838_c2_18	13185	27288	222	74
CONTIG5784	14256252_c2_19	13186	27289	192	64
CONTIG5784	29304635_c3_27	13187	27290	216	72
CONTIG5784	6835150_c3_28	13188	27291	207	69
CONTIG5784	24304682_c3_29	13189	27292	255	85
CONTIG5785	2445312_f1_2	13190	27293	192	64
CONTIG5785	19955386_f2_9	13191	27294	420	140
CONTIG5785	23516316_f3_18	13192	27295	192	64
CONTIG5785	11797161_f3_20	13193	27296	342	114

CONTIG5785	162575_c3_32	13194	27297	195	65
CONTIG5786	11767091_f3_15	13195	27298	213	71
CONTIG5786	35270037_f3_16	13196	27299	189	63
CONTIG5786	953375_f3_20	13197	27300	219	73
CONTIG5786	11725278_c1_22	13198	27301	210	70
CONTIG5786	13680262_c1_23	13199	27302	186	62
CONTIG5786	30272077_c2_32	13200	27303	228	76
CONTIG5786	4332887_c3_39	13201	27304	210	70
CONTIG5787	14277251_f2_6	13202	27305	183	61
CONTIG5787	35235880_f2_9	13203	27306	186	62
CONTIG5787	2848518_f3_17	13204	27307	258	86
CONTIG5787	24392158_c2_28	13205	27308	234	78
CONTIG5787	24235300_c2_31	13206	27309	231	77
CONTIG5788	20524036_c1_19	13207	27310	363	121
CONTIG5789	13829376_f1_5	13208	27311	552	184
CONTIG5789	5163377_f1_6	13209	27312	186	62
CONTIG5789	1953177_c1_20	13210	27313	393	131
CONTIG5789	977175_c2_29	13211	27314	1407	469
CONTIG5789	2814375_c3_31	13212	27315	513	171
CONTIG5789	2923463_c3_32	13213	27316	204	68
CONTIG5790	4881312_f2_12	13214	27317	405	135
CONTIG5790	160307_f2_14	13215	27318	495	165
CONTIG5790	23632286_c1_19	13216	27319	303	101
CONTIG5790	4901587_c3_27	13217	27320	306	102
CONTIG5790	327_c3_33	13218	27321	366	122
CONTIG5791	19734840_f2_6	13219	27322	375	125
CONTIG5791	22445186_f2_10	13220	27323	195	65
CONTIG5791	6664200_f2_11	13221	27324	363	121
CONTIG5791	2032786_f2_12	13222	27325	222	74
CONTIG5791	33298505_f3_13	13223	27326	891	297
CONTIG5791	20317053_c1_20	13224	27327	723	241
CONTIG5792	22271966_c1_27	13225	27328	183	61
CONTIG5792	1970130_c2_34	13226	27329	237	79

CONTIG5793	5273451_f3_14	13227	27330	225	75
CONTIG5794	10632056_f1_1	13228	27331	1002	334
CONTIG5794	11176876_c2_33	13229	27332	183	61
CONTIG5794	6641255_c3_40	13230	27333	273	91
CONTIG5795	24267893_f2_8	13231	27334	213	71
CONTIG5795	24026638_f3_17	13232	27335	192	64
CONTIG5795	4957682_c1_22	13233	27336	648	216
CONTIG5795	20897202_c3_37	13234	27337	348	116
CONTIG5795	23515688_c3_38	13235	27338	198	66
CONTIG5795	6691253_c3_43	13236	27339	243	81
CONTIG5796	24407640_f1_2	13237	27340	237	79
CONTIG5796	35647032_f1_3	13238	27341	201	67
CONTIG5796	11837715_f1_5	13239	27342	204	68
CONTIG5796	20520276_f2_9	13240	27343	195	65
CONTIG5796	24019002_f2_10	13241	27344	222	74
CONTIG5796	4902312_f3_13	13242	27345	234	78
CONTIG5796	891052_f1_15	13243	27346	183	61
CONTIG5797	19579637_c3_31	13244	27347	216	72
CONTIG5797	20501343_c3_32	13245	27348	198	66
CONTIG5797	204465_c3_35	13246	27349	315	105
CONTIG5798	24432181_c2_37	13247	27350	207	69
CONTIG5798	5078955_c2_38	13248	27351	336	112
CONTIG5799	878752_f2_7	13249	27352	282	94
CONTIG5799	10980181_f2_8	13250	27353	198	66
CONTIG5799	30553265_c1_18	13251	27354	237	79
CONTIG5799	34407180_c2_26	13252	27355	1968	656
CONTIG5799	19803590_c3_28	13253	27356	219	73
CONTIG5799	29493785_c3_29	13254	27357	201	67
CONTIG5799	10823811_c3_30	13255	27358	198	66
CONTIG5800	11900015_c1_6	13256	27359	195	65
CONTIG5800	24410666_c1_7	13257	27360	192	64
CONTIG5800	11900015_c1_8	13258	27361	195	65
CONTIG5800	35203432_c2_9	13259	27362	462	154

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CONTIG5800	9929652_c3_10	13260	27363	192	64
CONTIG5800	3167325_c3_12	13261	27364	240	80
CONTIG5801	13753135_f2_7	13262	27365	504	168
CONTIG5801	29542502_f2_11	13263	27366	198	66
CONTIG5801	19726437_f2_15	13264	27367	192	64
CONTIG5802	24414062_f1_4	13265	27368	195	65
CONTIG5802	26199205_f1_5	13266	27369	204	68
CONTIG5802	22464087_f1_6	13267	27370	186	62
CONTIG5802	6136527_f1_9	13268	27371	252	84
CONTIG5802	16538432_f2_15	13269	27372	288	96
CONTIG5802	15032918_f2_16	13270	27373	342	114
CONTIG5802	11055383_c2_30	13271	27374	219	73
CONTIG5802	23844625_c2_35	13272	27375	189	63
CONTIG5802	2578200_c3_40	13273	27376	222	74
CONTIG5803	24394402_f1_1	13274	27377	195	65
CONTIG5803	21675010_f1_4	13275	27378	1092	364
CONTIG5803	5253762_c1_19	13276	27379	258	86
CONTIG5804	24634660_f1_5	13277	27380	492	164
CONTIG5804	24854681_f1_6	13278	27381	318	106
CONTIG5804	14846900_f1_7	13279	27382	651	217
CONTIG5804	24117250_f1_9	13280	27383	201	67
CONTIG5804	972155_f2_24	13281	27384	375	125
CONTIG5804	5865642_f3_33	13282	27385	216	72
CONTIG5804	26287555_c1_42	13283	27386	201	67
CONTIG5805	33395961_f2_9	13284	27387	276	92
CONTIG5805	35267811_c2_32	13285	27388	723	241
CONTIG5806	4875055_f2_11	13286	27389	519	173
CONTIG5806	5094087_f3_22	13287	27390	213	71
CONTIG5806	400453_c1_30	13288	27391	816	272
CONTIG5806	9859377_c2_36	13289	27392	897	299
CONTIG5806	4800125_c3_37	13290	27393	186	62
CONTIG5806	14267776_c3_39	13291	27394	276	92
CONTIG5806	20738825_c3_40	13292	27395	234	78

CONTIG5807	172055_f3_9	13293	27396	1026	342
CONTIG5808	22375030_f1_6	13294	27397	189	63
CONTIG5808	2000017_f2_9	13295	27398	189	63
CONTIG5808	5896900_f2_14	13296	27399	1716	572
CONTIG5808	29975942_f3_15	13297	27400	195	65
CONTIG5809	1056528_f2_11	13298	27401	1173	391
CONTIG5809	11754591_f3_14	13299	27402	630	210
CONTIG5809	10331386_c3_26	13300	27403	267	89
CONTIG5810	23636502_f2_10	13301	27404	333	111
CONTIG5810	24644026_f2_12	13302	27405	804	268
CONTIG5810	32320933_f3_14	13303	27406	183	61
CONTIG5810	20117811_f3_17	13304	27407	183	61
CONTIG5810	167661_c2_28	13305	27408	189	63
CONTIG5811	26428463_c3_40	13306	27409	210	70
CONTIG5811	12548430_c3_41	13307	27410	309	103
CONTIG5812	4881518_c3_27	13308	27411	390	130
CONTIG5812	6697843_c3_30	13309	27412	207	69
CONTIG5812	781375_c3_31	13310	27413	219	73
CONTIG5812	19726562_c3_34	13311	27414	777	259
CONTIG5813	20900_f3_20	13312	27415	210	70
CONTIG5813	33297261_f3_27	13313	27416	195	65
CONTIG5813	7050026_c2_53	13314	27417	318	106
CONTIG5814	1995306_f1_3	13315	27418	615	205
CONTIG5814	34234660_f3_15	13316	27419	216	72
CONTIG5814	14197183_f3_20	13317	27420	267	89
CONTIG5814	21759502_c1_32	13318	27421	294	98
CONTIG5814	2770182_c3_56	13319	27422	234	78
CONTIG5814	24259681_f1_2	13320	27423	1041	347
CONTIG5815	9860082_f1_4	13321	27424	216	72
CONTIG5815	24414061_f1_5	13322	27425	282	94
CONTIG5815	22750306_f2_13	13323	27426	270	90
CONTIG5815	26259682_f3_26	13324	27427	192	64
CONTIG5815	10944680_f3_27	13325	27428	639	213

CONTIG5815	30475280_c1_28	13326	27429	204	68
CONTIG5815	23725090_c2_37	13327	27430	279	93
CONTIG5816	11755015_f1_1	13328	27431	195	65
CONTIG5816	11900015_f1_2	13329	27432	195	65
CONTIG5816	11900015_f1_3	13330	27433	195	65
CONTIG5816	20709436_c1_7	13331	27434	267	89
CONTIG5816	31444658_c3_16	13332	27435	234	78
CONTIG5817	6031451_f1_3	13333	27436	252	84
CONTIG5817	30662750_c1_41	13334	27437	213	71
CONTIG5817	4335187_c2_49	13335	27438	327	109
CONTIG5817	24504652_c2_53	13336	27439	240	80
CONTIG5818	26206511_f2_13	13337	27440	762	254
CONTIG5818	21663430_f2_21	13338	27441	261	87
CONTIG5818	20879515_f2_22	13339	27442	183	61
CONTIG5818	3183302_c2_38	13340	27443	267	89
CONTIG5818	24351528_c3_48	13341	27444	222	74
CONTIG5818	4566252_c3_52	13342	27445	444	148
CONTIG5819	33314625_f1_4	13343	27446	189	63
CONTIG5819	116325_f2_6	13344	27447	216	72
CONTIG5819	430465_f2_12	13345	27448	312	104
CONTIG5819	23990937_f3_27	13346	27449	222	74
CONTIG5819	24429712_c1_30	13347	27450	282	94
CONTIG5819	9850632_c1_31	13348	27451	207	69
CONTIG5819	21645302_c3_54	13349	27452	372	124
CONTIG5819	32536393_c3_60	13350	27453	294	98
CONTIG5820	29475782_f1_5	13351	27454	231	77
CONTIG5820	23459625_f1_7	13352	27455	186	62
CONTIG5820	14507128_f1_8	13353	27456	225	75
CONTIG5820	812752_f1_9	13354	27457	195	65
CONTIG5820	35550068_f1_10	13355	27458	303	101
CONTIG5820	6147128_f1_13	13356	27459	249	83
CONTIG5820	19589425_f1_15	13357	27460	252	84
CONTIG5820	12549087_f2_18	13358	27461	237	79

CONTIG5820	24797305_f2_25	13359	27462	186	62
CONTIG5820	19818802_f2_26	13360	27463	240	80
CONTIG5820	4068801_f2_27	13361	27464	189	63
CONTIG5820	23554806_f3_35	13362	27465	207	69
CONTIG5820	25395266_f3_37	13363	27466	249	83
CONTIG5820	2220061_f3_38	13364	27467	288	96
CONTIG5820	4720633_f3_45	13365	27468	198	66
CONTIG5820	785337_f3_47	13366	27469	201	67
CONTIG5820	31534782_f3_50	13367	27470	183	61
CONTIG5820	4335018_f3_51	13368	27471	222	74
CONTIG5820	642167_f3_52	13369	27472	276	92
CONTIG5820	4070956_f3_58	13370	27473	189	63
CONTIG5820	23597803_c1_65	13371	27474	261	87
CONTIG5820	2828933_c2_69	13372	27475	192	64
CONTIG5820	26615910_c2_71	13373	27476	216	72
CONTIG5820	21885_c2_72	13374	27477	210	70
CONTIG5820	32595760_c2_76	13375	27478	198	66
CONTIG5820	812752_c3_77	13376	27479	195	65
CONTIG5820	10751388_c3_78	13377	27480	189	63
CONTIG5820	4162893_c3_79	13378	27481	213	71
CONTIG5820	6147757_c3_80	13379	27482	249	83
CONTIG5820	20727036_c3_81	13380	27483	234	78
CONTIG5820	2845257_c3_82	13381	27484	183	61
CONTIG5820	25886515_c3_84	13382	27485	303	101
CONTIG5821	19921890_f1_2	13383	27486	240	80
CONTIG5821	14895202_f1_12	13384	27487	255	85
CONTIG5821	12109393_f1_14	13385	27488	360	120
CONTIG5821	29551458_f2_23	13386	27489	210	70
CONTIG5821	19921890_f2_31	13387	27490	276	92
CONTIG5821	19921890_f2_33	13388	27491	240	80
CONTIG5821	12237505_f3_42	13389	27492	183	61
CONTIG5821	25977218_f3_45	13390	27493	189	63
CONTIG5821	13847790_f3_49	13391	27494	288	96

CONTIG5821	24010290_f3_51	13392	27495	231	77
CONTIG5821	5331418_c1_60	13393	27496	261	87
CONTIG5821	679716_c1_63	13394	27497	192	64
CONTIG5821	25839417_c3_90	13395	27498	240	80
CONTIG5821	13799081_c3_91	13396	27499	264	88
CONTIG584	24022327_f3_2	13397	27500	192	64
CONTIG586	790700_f2_1	13398	27501	186	62
CONTIG587	25426626_f1_1	13399	27502	186	62
CONTIG587	2031950_f3_2	13400	27503	306	102
CONTIG590	878278_c2_2	13401	27504	225	75
CONTIG591	9802088_c2_1	13402	27505	822	274
CONTIG594	19725302_c3_3	13403	27506	210	70
CONTIG596	917192_c3_1	13404	27507	828	276
CONTIG597	2912636_f3_3	13405	27508	369	123
CONTIG599	20390713_f1_1	13406	27509	594	198
CONTIG60	24398512_c3_2	13407	27510	477	159
CONTIG600	26767788_c1_3	13408	27511	486	162
CONTIG601	13953301_f1_1	13409	27512	318	106
CONTIG604	4337838_f1_1	13410	27513	723	241
CONTIG605	24394500_c3_3	13411	27514	207	69
CONTIG610	16593790_c2_1	13412	27515	210	70
CONTIG613	36539193_c2_6	13413	27516	243	81
CONTIG618	14456500_c1_1	13414	27517	225	75
CONTIG619	9929787_c3_2	13415	27518	774	258
CONTIG62	6114387_f1_1	13416	27519	264	88
CONTIG620	9776885_f1_1	13417	27520	468	156
CONTIG625	21594051_f3_2	13418	27521	306	102
CONTIG626	4589833_f2_2	13419	27522	207	69
CONTIG627	23986387_f3_1	13420	27523	201	67
CONTIG63	25397187_f1_1	13421	27524	258	86
CONTIG630	2079125_c3_2	13422	27525	183	61
CONTIG632	21676692_c1_3	13423	27526	231	77
CONTIG633	4804056_f2_1	13424	27527	219	73

CONTIG634	10196957_f2_1	13425	27528	567	189
CONTIG636	24304661_c1_1	13426	27529	204	68
CONTIG637	12537506_c2_2	13427	27530	183	61
CONTIG638	2393967_f3_3	13428	27531	324	108
CONTIG641	24929650_f1_2	13429	27532	327	109
CONTIG642	15815653_f2_2	13430	27533	243	81
CONTIG642	4711677_c1_3	13431	27534	219	73
CONTIG643	14459437_f1_1	13432	27535	750	250
CONTIG644	15057966_c2_2	13433	27536	186	62
CONTIG646	4328755_f1_1	13434	27537	492	164
CONTIG646	31683142_f3_2	13435	27538	405	135
CONTIG649	13782267_f1_1	13436	27539	285	95
CONTIG649	1968750_c1_3	13437	27540	210	70
CONTIG65	9957768_c3_2	13438	27541	402	134
CONTIG654	35633543_f2_1	13439	27542	753	251
CONTIG656	35792165_c2_5	13440	27543	198	66
CONTIG657	13096905_f1_1	13441	27544	942	314
CONTIG664	14562515_f1_1	13442	27545	777	259
CONTIG665	984439_c2_3	13443	27546	204	68
CONTIG666	25817187_f1_1	13444	27547	231	77
CONTIG667	85180_c2_3	13445	27548	387	129
CONTIG671	4181502_f1_1	13446	27549	384	128
CONTIG671	13859385_c2_2	13447	27550	252	84
CONTIG673	22457806_f2_1	13448	27551	339	113
CONTIG673	4765693_c1_2	13449	27552	192	64
CONTIG673	26359552_c3_3	13450	27553	240	80
CONTIG678	24666031_f2_2	13451	27554	474	158
CONTIG68	20392877_c3_2	13452	27555	249	83
CONTIG680	117825_f2_1	13453	27556	186	62
CONTIG681	24568811_f2_1	13454	27557	234	78
CONTIG682	5157515_c1_1	13455	27558	354	118
CONTIG682	23610062_c1_2	13456	27559	363	121
CONTIG684	5282878_f3_1	13457	27560	195	65

CONTIG684	24805442_c3_2	13458	27561	747	249
CONTIG686	9861317_f2_2	13459	27562	519	173
CONTIG692	25443842_c2_2	13460	27563	207	69
CONTIG693	26254813_c3_2	13461	27564	672	224
CONTIG694	31542708_f2_2	13462	27565	309	103
CONTIG694	240803_c3_3	13463	27566	459	153
CONTIG695	33714632_f2_2	13464	27567	204	68
CONTIG695	4068952_c2_3	13465	27568	258	86
CONTIG696	23910911_f3_3	13466	27569	192	64
CONTIG697	30469637_c1_3	13467	27570	246	82
CONTIG698	31683333_c1_2	13468	27571	360	120
CONTIG702	32041015_f1_1	13469	27572	210	70
CONTIG706	29690708_c3_4	13470	27573	201	67
CONTIG715	21907838_c1_2	13471	27574	348	116
CONTIG716	6019765_c3_5	13472	27575	576	192
CONTIG717	15675925_f3_1	13473	27576	369	123
CONTIG719	35189186_c3_3	13474	27577	189	63
CONTIG721	26257936_c1_2	13475	27578	195	65
CONTIG721	161267_c3_4	13476	27579	240	80
CONTIG725	24414555_c2_2	13477	27580	234	78
CONTIG727	24398463_c3_3	13478	27581	198	66
CONTIG729	36111012_c1_1	13479	27582	426	142
CONTIG732	6046883_c3_4	13480	27583	183	61
CONTIG733	34187765_f1_2	13481	27584	279	93
CONTIG733	16410912_c2_3	13482	27585	381	127
CONTIG736	965_f3_1	13483	27586	696	232
CONTIG739	24313191_c3_1	13484	27587	420	140
CONTIG74	22304787_c2_2	13485	27588	213	71
CONTIG740	35719443_f1_1	13486	27589	633	211
CONTIG741	14625311_f2_2	13487	27590	333	111
CONTIG741	29339662_f3_3	13488	27591	510	170
CONTIG742	25595183_f1_1	13489	27592	489	163
CONTIG743	26204625_f1_1	13490	27593	192	64

CONTIG743	12676567_c1_3	13491	27594	261	87
CONTIG744	35188387_c2_2	13492	27595	690	230
CONTIG745	15897912_f1_1	13493	27596	195	65
CONTIG746	2037907_c3_1	13494	27597	441	147
CONTIG747	25556942_f3_3	13495	27598	183	61
CONTIG747	26304017_f3_5	13496	27599	204	68
CONTIG748	24428268_c3_1	13497	27600	195	65
CONTIG748	9926525_f3_3	13498	27601	237	79
CONTIG750	24803406_c1_4	13499	27602	603	201
CONTIG750	21881400_c3_5	13500	27603	327	109
CONTIG750	15632192_c3_6	13501	27604	315	105
CONTIG752	4097052_c3_1	13502	27605	420	140
CONTIG754	2350135_c1_1	13503	27606	201	67
CONTIG758	3289176_c1_2	13504	27607	222	74
CONTIG76	21651950_f2_1	13505	27608	456	152
CONTIG760	33477150_c1_5	13506	27609	792	264
CONTIG771	24256686_f3_3	13507	27610	543	181
CONTIG773	15041040_f3_1	13508	27611	558	186
CONTIG774	398311_c3_2	13509	27612	204	68
CONTIG775	24648307_f1_1	13510	27613	306	102
CONTIG778	962963_c2_1	13511	27614	225	75
CONTIG779	290693_f1_1	13512	27615	666	222
CONTIG782	29578176_f2_1	13513	27616	198	66
CONTIG782	24022176_c3_2	13514	27617	423	141
CONTIG783	516580_f3_2	13515	27618	195	65
CONTIG784	2757013_c2_2	13516	27619	564	188
CONTIG786	24320275_c1_1	13517	27620	189	63
CONTIG788	4719450_c1_3	13518	27621	231	77
CONTIG789	2519627_c3_9	13519	27622	225	75
CONTIG790	14332786_f1_1	13520	27623	324	108
CONTIG790	22292061_f1_2	13521	27624	396	132
CONTIG791	9223253_f2_1	13522	27625	204	68
CONTIG795	4693803_f3_1	13523	27626	261	87

CONTIG796	24287525_f3_2	13524	27627	1068	356
CONTIG796	9772637_c3_5	13525	27628	222	74
CONTIG797	22127312_f1_1	13526	27629	201	67
CONTIG799	23713961_c2_4	13527	27630	279	93
CONTIG799	23912811_c3_7	13528	27631	201	67
CONTIG8	36542965_c2_2	13529	27632	258	86
CONTIG80	23831512_f2_1	13530	27633	186	62
CONTIG80	4350186_c1_3	13531	27634	201	67
CONTIG805	5079750_f2_1	13532	27635	489	163
CONTIG807	1359507_f2_1	13533	27636	183	61
CONTIG808	24698833_f1_1	13534	27637	759	253
CONTIG811	16822188_f2_2	13535	27638	204	68
CONTIG811	24406250_c1_4	13536	27639	390	130
CONTIG814	15744687_f3_3	13537	27640	249	83
CONTIG814	24416566_f2_1	13538	27641	465	155
CONTIG814	26464078_c2_4	13539	27642	192	64
CONTIG818	2048807_f2_2	13540	27643	186	62
CONTIG818	7886_f3_4	13541	27644	270	90
CONTIG821	2260077_c1_2	13542	27645	546	182
CONTIG826	24345252_f2_1	13543	27646	207	69
CONTIG826	171885_f3_2	13544	27647	720	240
CONTIG827	5157753_f2_1	13545	27648	336	112
CONTIG827	22364055_c3_2	13546	27649	207	69
CONTIG827	26369017_c3_3	13547	27650	216	72
CONTIG828	990937_c3_4	13548	27651	291	97
CONTIG829	31876526_f3_3	13549	27652	324	108
CONTIG829	4032590_c3_5	13550	27653	192	64
CONTIG832	22454813_f1_1	13551	27654	327	109
CONTIG834	34414152_f1_2	13552	27655	447	149
CONTIG837	4097200_c3_3	13553	27656	435	145
CONTIG839	30275630_c1_2	13554	27657	183	61
CONTIG84	20660053_f3_1	13555	27658	237	79
CONTIG842	6742887_f3_1	13556	27659	183	61

CONTIG842	24042561_c2_3	13557	27660	258	86
CONTIG845	4304652_f2_1	13558	27661	231	77
CONTIG846	25556587_c2_2	13559	27662	264	88
CONTIG848	16537757_f1_1	13560	27663	342	114
CONTIG848	34412811_f1_2	13561	27664	246	82
CONTIG851	24318953_f1_1	13562	27665	195	65
CONTIG851	4801468_c3_5	13563	27666	234	78
CONTIG852	4772177_f2_1	13564	27667	213	71
CONTIG855	3641438_c1_3	13565	27668	543	181
CONTIG856	21485927_c2_3	13566	27669	189	63
CONTIG857	11226588_c1_2	13567	27670	633	211
CONTIG858	878592_c3_2	13568	27671	864	288
CONTIG860	34629626_f1_1	13569	27672	294	98
CONTIG864	24480017_f1_1	13570	27673	348	116
CONTIG864	56338_c3_7	13571	27674	255	85
CONTIG866	991283_c1_2	13572	27675	183	61
CONTIG867	24892061_c2_2	13573	27676	204	68
CONTIG871	26562525_f3_1	13574	27677	276	92
CONTIG872	24806277_f3_2	13575	27678	186	62
CONTIG874	4331525_c3_3	13576	27679	186	62
CONTIG875	21912806_c1_6	13577	27680	234	78
CONTIG876	29375468_c1_2	13578	27681	291	97
CONTIG878	14707137_f3_2	13579	27682	279	93
CONTIG88	23925932_c3_4	13580	27683	204	68
CONTIG880	33625666_f2_1	13581	27684	189	63
CONTIG880	10549090_f2_3	13582	27685	318	106
CONTIG881	15635162_f1_1	13583	27686	195	65
CONTIG881	23525300_f3_3	13584	27687	237	79
CONTIG881	163462_c2_4	13585	27688	330	110
CONTIG881	29586000_c3_5	13586	27689	210	70
CONTIG885	21682790_f1_1	13587	27690	198	66
CONTIG888	29457827_f2_1	13588	27691	204	68
CONTIG888	5101562_c1_2	13589	27692	195	65

CONTIG889	21879833_f3_1	13590	27693	198	66
CONTIG890	21484718_f3_3	13591	27694	186	62
CONTIG891	10939180_f1_1	13592	27695	315	105
CONTIG891	817811_f3_2	13593	27696	282	94
CONTIG893	6260187_c3_3	13594	27697	948	316
CONTIG896	24397178_f1_1	13595	27698	297	99
CONTIG896	19728187_f2_2	13596	27699	249	83
CONTIG896	23626551_f3_3	13597	27700	183	61
CONTIG898	24511442_c2_4	13598	27701	645	215
CONTIG90	24094627_f3_1	13599	27702	216	72
CONTIG904	19709637_c1_2	13600	27703	249	83
CONTIG905	14234775_f3_1	13601	27704	744	248
CONTIG906	29335186_c2_2	13602	27705	222	74
CONTIG907	23829387_c3_6	13603	27706	321	107
CONTIG909	10725812_f2_1	13604	27707	207	69
CONTIG909	24335902_f3_2	13605	27708	198	66
CONTIG91	2206258_f3_5	13606	27709	222	74
CONTIG911	23720250_f3_2	13607	27710	198	66
CONTIG913	25431526_c3_3	13608	27711	549	183
CONTIG914	4765700_f1_1	13609	27712	342	114
CONTIG914	24395143_f3_3	13610	27713	399	133
CONTIG915	24298830_f3_2	13611	27714	198	66
CONTIG915	9822530_f3_3	13612	27715	273	91
CONTIG917	183527_f3_1	13613	27716	264	88
CONTIG919	23722812_f1_1	13614	27717	198	66
CONTIG919	15036343_f3_2	13615	27718	183	61
CONTIG92	5907303_f2_2	13616	27719	198	66
CONTIG920	15037577_c1_1	13617	27720	291	97
CONTIG920	25820428_c2_2	13618	27721	252	84
CONTIG923	9964802_c2_3	13619	27722	219	73
CONTIG926	5267180_c3_3	13620	27723	513	171
CONTIG927	23632186_c2_4	13621	27724	189	63
CONTIG928	21520462_c2_1	13622	27725	798	266

CONTIG93	10335468_f3_1	13623	27726	228	76
CONTIG931	26448377_c1_5	13624	27727	279	93
CONTIG932	2788576_f2_1	13625	27728	273	91
CONTIG934	24414075_c3_7	13626	27729	186	62
CONTIG935	4728563_f2_2	13627	27730	186	62
CONTIG935	7073432_c1_4	13628	27731	627	209
CONTIG936	29332681_f2_1	13629	27732	465	155
CONTIG938	5984562_f1_1	13630	27733	288	96
CONTIG938	26459381_c3_5	13631	27734	882	294
CONTIG939	10352000_c3_3	13632	27735	669	223
CONTIG94	14509403_f1_1	13633	27736	213	71
CONTIG940	6407628_c1_2	13634	27737	897	299
CONTIG941	14457625_c3_2	13635	27738	468	156
CONTIG941	34656567_f2_1	13636	27739	198	66
CONTIG945	33437950_f2_3	13637	27740	195	65
CONTIG945	197151_c2_7	13638	27741	312	104
CONTIG946	26803753_c1_2	13639	27742	321	107
CONTIG947	23839387_c2_2	13640	27743	711	237
CONTIG949	4375875_f1_1	13641	27744	222	74
CONTIG95	38425_c2_3	13642	27745	825	275
CONTIG950	13906385_c1_2	13643	27746	213	71
CONTIG951	25501411_f2_1	13644	27747	216	72
CONTIG953	26225450_c3_1	13645	27748	183	61
CONTIG956	442583_f2_1	13646	27749	765	255
CONTIG957	23447305_c1_3	13647	27750	189	63
CONTIG957	5320202_c1_4	13648	27751	225	75
CONTIG960	36072187_c1_4	13649	27752	411	137
CONTIG964	3945127_f1_1	13650	27753	330	110
CONTIG964	29459638_f3_2	13651	27754	351	117
CONTIG964	19688760_c1_3	13652	27755	321	107
CONTIG967	13960092_c1_3	13653	27756	444	148
CONTIG97	35805150_f2_1	13654	27757	255	85
CONTIG970	12266886_f3_2	13655	27758	186	62

CONTIG972	3940760_f2_1	13656	27759	216	72
CONTIG975	33505_c1_1	13657	27760	225	75
CONTIG982	4188812_f2_2	13658	27761	189	63
CONTIG982	4015882_c1_3	13659	27762	234	78
CONTIG982	22455392_c2_5	13660	27763	213	71
CONTIG983	4710886_f1_1	13661	27764	315	105
CONTIG983	24022802_f3_3	13662	27765	201	67
CONTIG984	10345905_f3_1	13663	27766	972	324
CONTIG985	9782958_f3_2	13664	27767	270	90
CONTIG989	22085800_c1_2	13665	27768	189	63
CONTIG991	16969441_f1_1	13666	27769	600	200
CONTIG996	26210131_c3_2	13667	27770	246	82
CONTIG997	11803805_f3_1	13668	27771	213	71
CONTIG999	1255308_c3_3	13669	27772	312	104
b1x18255.y	35348317_f3_1	13670	27773	288	96
b9x13v03.x	14957127_c2_2	13671	27774	552	184
b9x13u01.y	34101662_f2_1	13672	27775	246	82
b9x13t68.x	1208157_f1_2	13673	27776	543	181
b9x13t36.y	881635_f1_1	13674	27777	246	82
b9x13s82.x	4787683_f3_1	13675	27778	189	63
b2x16582.x	33406550_f1_1	13676	27779	294	98
b9x13r20.y	22347163_f3_1	13677	27780	534	178
b9x13q46.y	23866300_f3_1	13678	27781	744	248
b9x13q33.x	4964392_f3_2	13679	27782	267	89
b2x16511.y	11056425_f3_1	13680	27783	354	118
b1x10334.x	36617892_c2_1	13681	27784	207	69
b9x13m42.y	9864092_c3_1	13682	27785	243	81
b1x10357.x	20353500_c1_2	13683	27786	252	84
b9x13k53.y	23625653_c1_1	13684	27787	324	108
b9x13k09.x	22464751_c3_6	13685	27788	438	146
b1x10361.x	4415893_f1_1	13686	27789	471	157
b1x18370.y	23630260_f1_1	13687	27790	477	159
b9x13h46.x	34022550_c1_1	13688	27791	510	170

b2x16278.x	3363200_f3_3	13689	27792	723	241
b2x16264.y	2141053_c3_5	13690	27793	378	126
b9x13g03.x	29468785_f2_1	13691	27794	297	99
b1x13303.x	33229666_f1_1	13692	27795	339	113
b9x13g02.x	30163187_f1_1	13693	27796	477	159
b2x16118.x	24298502_c2_2	13694	27797	198	66
b9x13f89.x	23860912_f2_1	13695	27798	228	76
b9x13f47.y	14922067_f3_3	13696	27799	309	103
b9x13e89.y	12704410_cl_3	13697	27800	417	139
b9x13e70.x	23837513_c2_2	13698	27801	225	75
b9x13e18.y	5281661_c3_5	13699	27802	201	67
b9x13e18.y	35188762_c3_6	13700	27803	222	74
b1x18436.y	1006406_f3_1	13701	27804	201	67
b9x13d35.x	30364566_f1_1	13702	27805	585	195
b9x13d16.y	63488880_f1_1	13703	27806	216	72
b9x13d16.y	22062812_c3_3	13704	27807	528	176
b9x13d08.x	956580_c3_4	13705	27808	255	85
b9x13c92.x	5360383_f1_1	13706	27809	192	64
b2x16057.x	4726536_f2_1	13707	27810	603	201
b9x13c06.y	11915925_f2_2	13708	27811	186	62
b9x13c06.y	30265928_c3_4	13709	27812	183	61
b1x18443.x	22558255_f3_1	13710	27813	492	164
b1x18443.x	35969633_c3_3	13711	27814	243	81
b2x15980.y	33644630_c3_3	13712	27815	564	188
b9x13a50.x	4348957_f2_1	13713	27816	204	68
b9x13872.y	15626282_cl_2	13714	27817	189	63
b9x13854.y	21883437_f1_1	13715	27818	498	166
b9x13854.y	6510906_f2_2	13716	27819	261	87
b1x18485.x	4000338_c3_1	13717	27820	432	144
b9x13665.x	10009626_c3_1	13718	27821	627	209
b9x13527.y	19694066_c2_4	13719	27822	246	82
b2x15766.x	6835838_f3_3	13720	27823	333	111
b2x15766.x	35209750_cl_4	13721	27824	219	73

b2x15766.x	25432825_c3_5	13722	27825	261	87
b9x13491.x	5984467_f1_2	13723	27826	219	73
b9x13491.x	29487557_c3_3	13724	27827	933	311
b2x15753.y	25985317_f2_1	13725	27828	534	178
b9x13380.x	1062693_f1_1	13726	27829	435	145
b9x13319.y	35156537_c1_2	13727	27830	258	86
b2x15753.x	14492337_f2_3	13728	27831	333	111
b9x13249.x	12268763_f1_1	13729	27832	600	200
b9x12z69.x	4456550_f2_1	13730	27833	501	167
b9x12y87.y	31407053_f3_1	13731	27834	492	164
b2x15727.x	4880140_c2_1	13732	27835	210	70
b9x12w88.y	829378_f1_1	13733	27836	195	65
b9x12w88.x	21493761_f2_2	13734	27837	327	109
b9x12w72.x	10350061_c1_4	13735	27838	510	170
b9x12w68.x	24697555_c3_5	13736	27839	387	129
b9x12v46.x	16531686_c2_1	13737	27840	480	160
b2x15689.y	33258342_c2_3	13738	27841	189	63
b9x12v30.x	24318817_c3_2	13739	27842	345	115
b9x12u82.x	32225837_f2_1	13740	27843	243	81
b1x10645.x	4775286_c2_4	13741	27844	204	68
b9x12u61.y	5314677_f3_1	13742	27845	261	87
b1x13827.x	23882951_c3_2	13743	27846	195	65
b9x12u17.y	471040_f2_1	13744	27847	507	169
b9x12t47.y	13023593_f2_1	13745	27848	327	109
b9x12t15.y	34573957_c2_6	13746	27849	237	79
b9x12t15.y	24026578_c2_7	13747	27850	204	68
b9x12q68.y	16408442_f3_2	13748	27851	711	237
b9x12n61.x	3157180_f3_2	13749	27852	588	196
b9x12n61.x	4892127_c3_5	13750	27853	306	102
b9x12n34.y	10600307_f3_1	13751	27854	198	66
b9x15645.y	24016567_f1_1	13752	27855	375	125
b2x15645.y	957827_f2_2	13753	27856	390	130
b2x15645.y	2924177_c2_4	13754	27857	360	120

b2x15632.y	4694377_c1_2	13755	27858	363	121
b2x15632.x	4864211_c2_3	13756	27859	507	169
b9x12665.x	5282802_f1_1	13757	27860	582	194
b9x12665.x	3927008_c2_2	13758	27861	225	75
b2x15443.x	6094632_f1_1	13759	27862	183	61
b2x15443.x	24801342_f2_2	13760	27863	198	66
b2x15443.x	2166042_f3_3	13761	27864	192	64
b9x12h24.x	13880181_f3_1	13762	27865	621	207
b9x12h24.x	25630378_c3_3	13763	27866	327	109
b9x12256.y	21658462_f2_1	13764	27867	231	77
b9x12049.y	23632187_c2_1	13765	27868	690	230
b2x15502.x	4031638_c1_1	13766	27869	582	194
b2x15473.x	25586075_c1_1	13767	27870	339	113
b9x12989.y	806599_c1_2	13768	27871	192	64
b9x12884.x	5979140_c2_3	13769	27872	183	61
b9x12850.y	36537580_f1_1	13770	27873	192	64
b9x12850.y	10945200_f2_3	13771	27874	420	140
b9x12850.y	1225305_c2_6	13772	27875	249	83
b9x12776.y	24020312_c1_4	13773	27876	240	80
b9x12776.y	34429652_c2_5	13774	27877	372	124
b2x12886.x	2437665_c2_3	13775	27878	195	65
b2x12886.x	25428135_c3_4	13776	27879	303	101
b9x12658.y	24801561_f1_1	13777	27880	204	68
b9x12636.y	22296875_c1_2	13778	27881	189	63
b9x12636.y	1174186_c1_3	13779	27882	183	61
b9x12591.x	2394167_f1_1	13780	27883	585	195
b9x12387.y	13944050_f1_1	13781	27884	267	89
b2x12835.y	1289280_f2_1	13782	27885	570	190
b2x12220.x	22267813_c2_2	13783	27886	201	67
b2x12829.x	36382002_f2_1	13784	27887	198	66
b9x11y56.y	14454757_c2_2	13785	27888	474	158
b9x11x80.x	31683200_c1_1	13786	27889	255	85
b1x18647.x	24008386_c1_1	13787	27890	444	148

b9x1u44.x	15051265_f1_1	13788	27891	222	74
b9x1u44.x	15791308_c1_4	13789	27892	285	95
b9x1u44.x	5292132_c1_5	13790	27893	183	61
b9x1u44.x	20045392_c1_6	13791	27894	306	102
b9x1u19.y	4776501_c2_5	13792	27895	237	79
b9x1f77.y	21954530_c2_1	13793	27896	381	127
b2x12792.x	22441402_f2_1	13794	27897	198	66
b2x12792.x	21490875_c1_2	13795	27898	204	68
b9x1s25.x	23469012_c2_1	13796	27899	405	135
b9x1s25.x	23617211_c1_2	13797	27900	189	63
b9x1r08.x	114078_c1_1	13798	27901	195	65
b1x11014.y	4063135_f1_2	13799	27902	204	68
b1x11014.y	8586_f1_1	13800	27903	387	129
b9x1p67.y	937_c2_3	13801	27904	531	177
b9x1p67.y	782807_c3_4	13802	27905	216	72
b9x1m54.x	14563427_f2_1	13803	27906	627	209
b9x1m02.x	3937812_c1_3	13804	27907	186	62
b9x1k38.y	11798151_c3_1	13805	27908	276	92
b2x12587.x	35759750_f3_2	13806	27909	195	65
b2x13483.y	12213275_c1_4	13807	27910	183	61
b2x12566.x	4688812_c3_4	13808	27911	276	92
b9x1j77.y	25516626_c2_4	13809	27912	474	158
b9x1j77.y	13709675_c3_5	13810	27913	207	69
b9x1g23.x	14460137_f2_2	13811	27914	294	98
b9x1f43.x	6817182_c2_5	13812	27915	573	191
b9x1f34.x	22470438_c2_1	13813	27916	570	190
b9x1f26.x	10345443_c2_2	13814	27917	432	144
b2x12437.x	32304200_f3_2	13815	27918	237	79
b9x1e17.x	433332_f2_1	13816	27919	609	203
b1x18781.x	9652_c2_1	13817	27920	399	133
b9x1c47.x	29886501_f3_1	13818	27921	198	66
b9x1c30.y	14644782_c3_2	13819	27922	273	91
b9x1956.x	6412535_f3_3	13820	27923	213	71

b9x11954.y	4006930_cl_5	13821	27924	158
b9x11910.y	15735002_f3_2	13822	27925	71
b9x11910.y	21678402_c2_3	13823	27926	78
b9x11677.x	24413962_c2_3	13824	27927	76
b9x11364.y	10001557_f3_1	13825	27928	96
b9x11160.x	10945950_cl_5	13826	27929	73
b9x11233.y	34199187_cl_3	13827	27930	77
b9x11209.x	390755_f3_2	13828	27931	231
b9x11209.x	35214067_c2_3	13829	27932	309
b9x11203.y	4082031_f2_1	13830	27933	103
b9x11203.x	10977127_c2_2	13831	27934	228
b9x11074.x	26384712_cl_2	13832	27935	62
b9x11137.x	3235386_f3_1	13833	27936	126
b9x11044.y	25875430_c2_6	13834	27937	263
b9x10y60.x	4688952_f3_2	13835	27938	67
b9x10w84.y	1203125_c3_2	13836	27939	154
b9x10v59.x	22848532_c2_2	13837	27940	72
b9x10v30.y	23548425_c3_2	13838	27941	120
b1x18786.x	24414132_cl_2	13839	27942	87
b9x10u31.x	6412687_f3_1	13840	27943	64
b9x10r79.x	15627_f2_1	13841	27944	106
b9x10r79.x	30663212_c2_2	13842	27945	73
b9x10u19.x	4890713_f3_1	13843	27946	290
b2x11969.y	33469040_f3_1	13844	27947	70
b2x11959.y	25413263_c3_2	13845	27948	172
b9x10p88.x	24870777_f3_1	13846	27949	189
b1x18823.x	5275337_cl_1	13847	27950	81
b2x13860.y	22863178_c3_2	13848	27951	63
b9x10j44.x	428192_f1_1	13849	27952	140
b2x11862.y	16925255_f2_1	13850	27953	177
b2x13867.y	6489916_f2_1	13851	27954	66
b9x10g01.y	2000141_f2_1	13852	27955	64
b2x11832.y	3910156_f2_1	13853	27956	172

b2x13879.x	21492000_c3_2	13854	27957	210	70
b9x10168.y	31423312_f1_1	13855	27958	183	61
b2x13887.x	433332_f3_2	13856	27959	603	201
b9x10e19.y	19689442_c2_1	13857	27960	195	65
b2x11681.x	236538_f3_3	13858	27961	756	252
b9x10d47.x	212937_c3_4	13859	27962	207	69
b9x10c06.x	1632782_c2_4	13860	27963	432	144
b9x10b37.y	24228303_f1_1	13861	27964	201	67
b9x10b37.x	5099050_f3_3	13862	27965	303	101
b9x10b27.y	2395762_f2_2	13863	27966	282	94
b9x10b25.x	5975306_f1_1	13864	27967	312	104
b1x18857.y	14196925_c1_2	13865	27968	282	94
b9x10a29.y	20082527_c2_4	13866	27969	336	112
b2x11578.y	16854567_f2_1	13867	27970	462	154
b2x11572.y	9922050_c2_1	13868	27971	492	164
b9x10895.x	20597825_f3_3	13869	27972	384	128
b2x13929.x	9928153_c3_4	13870	27973	444	148
b9x10747.x	4734713_f1_1	13871	27974	213	71
b9x10689.y	6376949_c1_2	13872	27975	180	60
b9x10689.y	13678760_c3_3	13873	27976	492	164
b1x18871.y	7040750_f3_1	13874	27977	294	98
b9x10620.y	396925_c1_2	13875	27978	237	79
b1x11420.y	22394525_f2_1	13876	27979	204	68
b1x11420.y	25572202_f2_3	13877	27980	204	68
b9x10571.y	12695282_f3_2	13878	27981	183	61
b9x10571.y	29510925_c3_3	13879	27982	687	229
b9x10568.x	19956912_c3_3	13880	27983	729	243
b9x10470.y	24431917_f3_1	13881	27984	186	62
b9x10424.y	26455437_c2_3	13882	27985	537	179
b2x11126.x	24431626_f1_1	13883	27986	183	61
b9x10140.y	2756885_c1_3	13884	27987	414	138
b9x10113.y	20348180_f3_3	13885	27988	264	88
b4x10394.x	12678137_c3_1	13886	27989	192	64

b4x10393.x	14100932_c2_2	13887	27990	621	207
b4x10274.y	35238387_c1_2	13888	27991	333	111
b4x10106.x	36132087_c1_4	13889	27992	645	215
b3x19646.y	885386_f2_1	13890	27993	246	82
b3x19646.y	14953427_c2_2	13891	27994	186	62
b3x19605.y	5350325_c2_2	13892	27995	186	62
b3x19517.y	30504813_c3_5	13893	27996	228	76
b2x11002.y	5338561_f3_2	13894	27997	606	202
b3x19470.y	5116406_f1_1	13895	27998	183	61
b3x19283.y	36385062_f1_1	13896	27999	384	128
b3x19243.x	32632974_c1_4	13897	28000	213	71
b3x19234.y	28800030_f3_1	13898	28001	186	62
b1x11554.y	23625305_f3_1	13899	28002	387	129
b1x11554.y	13703450_c1_2	13900	28003	420	140
b3x18982.x	4725030_c1_4	13901	28004	225	75
b3x18807.y	4038442_f3_1	13902	28005	267	89
b3x18737.y	781250_c1_2	13903	28006	657	219
b3x18642.x	29410681_c3_3	13904	28007	411	137
b3x18592.x	2048755_f1_1	13905	28008	405	135
b3x18592.x	4453127_f3_2	13906	28009	192	64
b2x10717.x	23718765_f2_1	13907	28010	489	163
b3x17956.y	21746013_c3_3	13908	28011	501	167
b3x17714.x	26562500_c1_1	13909	28012	324	108
b3x17684.y	15735155_f3_2	13910	28013	183	61
b3x17370.x	4568762_f2_1	13911	28014	441	147
b3x17064.y	4821950_f1_1	13912	28015	459	153
b3x16962.y	23476425_f1_1	13913	28016	207	69
b3x16871.y	3907783_f1_1	13914	28017	486	162
b2x14264.y	1048312_c1_2	13915	28018	207	69
b3x16673.x	291663_f2_1	13916	28019	648	216
b3x16673.x	13939087_f2_2	13917	28020	243	81
b1x19249.x	433332_f1_1	13918	28021	579	193
b1x19249.x	2112877_c2_2	13919	28022	234	78

b2x10230.x	9782967_f3_1	13920	28023	207	69
b3x16529.y	22447260_f3_1	13921	28024	231	77
b3x16483.x	23709678_c3_3	13922	28025	309	103
b1x19259.x	21520002_c3_1	13923	28026	765	255
b3x16120.y	35807758_f1_1	13924	28027	498	166
b3x16113.x	24415637_c2_2	13925	28028	234	78
b3x16093.y	16532836_c1_4	13926	28029	246	82
b3x16089.y	15103550_f1_1	13927	28030	765	255
b3x16083.y	5337801_f1_1	13928	28031	198	66
b3x16069.y	22150053_c2_3	13929	28032	222	74
b3x16067.y	11180135_f1_1	13930	28033	204	68
b3x16067.y	29690641_f2_2	13931	28034	240	80
b3x16062.y	4176290_c1_1	13932	28035	213	71
b3x16061.y	5942261_c1_5	13933	28036	348	116
b3x16058.y	5370182_f2_2	13934	28037	399	133
b3x16054.y	26850392_f2_1	13935	28038	207	69
b3x16050.y	6723214_c1_3	13936	28039	183	61
b3x16050.y	12125043_c2_4	13937	28040	222	74
b3x16048.y	1175375_c2_4	13938	28041	210	70
b1x11921.y	29564002_c1_2	13939	28042	183	61
b3x16046.y	26692801_f1_1	13940	28043	189	63
b3x16043.y	24025288_f2_3	13941	28044	279	93
b3x16043.y	30277288_c2_6	13942	28045	270	90
b3x16042.y	32243965_f3_3	13943	28046	240	80
b3x16041.x	478166_f3_1	13944	28047	189	63
b3x16039.y	23915660_f1_1	13945	28048	258	86
b3x16039.y	480436_c1_3	13946	28049	195	65
b3x16035.y	29334635_f3_4	13947	28050	249	83
b3x16035.y	36598936_c2_6	13948	28051	231	77
b3x16032.y	19631632_f1_1	13949	28052	660	220
b1x11963.y	23603442_f1_1	13950	28053	192	64
b1x11963.y	9853430_f1_2	13951	28054	603	201
b1x11963.y	4766385_c2_5	13952	28055	207	69

b3x16011.y	32610410_f1_1	13953	28056	186	62
b1x11972.x	2193758_c1_2	13954	28057	846	282
b3x16010.y	4193933_f3_2	13955	28058	285	95
b1x11984.y	36525947_f3_3	13956	28059	861	287
b3x16005.y	11062677_c2_4	13957	28060	225	75
b3x16004.y	31698941_f1_1	13958	28061	240	80
b3x16002.y	32518761_f3_4	13959	28062	270	90
b3x15687.x	23486632_c3_2	13964	28067	246	82
b3x15701.x	24422152_c3_2	13963	28066	543	181
b3x15773.y	7157826_c1_2	13962	28065	465	155
b3x15960.y	29296925_c3_2	13961	28064	210	70
b9x13\91.x	14570262_f1_1	13960	28063	258	86
b3x15661.y	191038_f2_1	13966	28069	246	82
b1x19595.y	208325_f2_1	13965	28068	591	197
b3x15457.y	34027307_c3_1	13967	28070	561	187
b1x14536.y	5088533_f1_1	13968	28071	504	168
b3x15367.x	16663391_f3_1	13969	28072	219	73
b3x15361.x	14563885_f3_1	13970	28073	357	119
b3x15328.x	24303812_f1_1	13971	28074	264	88
b1x14543.y	9812625_c2_2	13972	28075	201	67
b1x14543.y	274082_c3_3	13973	28076	312	104
b2x14358.y	10985075_f2_1	13974	28077	231	77
b1x14555.y	5914687_c1_1	13975	28078	261	87
b1x14555.y	26367630_c2_2	13976	28079	255	85
b3x15141.y	2150800_c1_1	13977	28080	189	63
b3x15121.y	3955377_f2_1	13978	28081	201	67
b3x15082.x	29334842_f1_1	13979	28082	210	70
b3x14944.x	23554625_c2_1	13980	28083	522	174
b1x14905.y	21878843_f1_1	13981	28084	504	168
b1x14919.x	2010414_f1_1	13982	28085	186	62
b3x14811.x	21657636_c2_2	13983	28086	204	68
b3x14807.x	22445181_c3_5	13984	28087	510	170
b1x14928.x	6359842_c2_3	13985	28088	183	61

b1x14936.x	13143782_f3_1	13986	28089	570	190
b1x15013.x	13830301_c3_1	13987	28090	189	63
b1x12474.x	3140777_c3_2	13988	28091	195	65
b3x14569.x	861627_c2_1	13989	28092	267	89
b2x13268.x	34117127_c1_1	13990	28093	192	64
b2x13268.x	25823437_c2_2	13991	28094	276	92
b3x14433.y	21538877_c1_3	13992	28095	441	147
b2x14441.y	24406937_f2_2	13993	28096	390	130
b3x14418.y	22837578_f3_4	13994	28097	297	99
b1x12521.y	33382282_c1_2	13995	28098	690	230
b3x14292.y	662887_f1_1	13996	28099	213	71
b1x15077.y	4101562_c2_3	13997	28100	288	96
b3x14239.y	9805406_f1_1	13998	28101	393	131
b1x15145.y	188385_c1_1	13999	28102	645	215
b1x14330.x	4415937_c2_1	14000	28103	360	120
b3x13926.x	14143762_f2_1	14001	28104	204	68
b3x13893.x	22673766_f3_1	14002	28105	351	117
b1x15375.x	585811_f2_1	14003	28106	402	134
b1x15375.x	15762_c3_4	14004	28107	360	120
b3x13751.y	22266893_c1_3	14005	28108	810	270
b3x13728.x	4564752_c2_1	14006	28109	264	88
b1x15451.x	14335937_f2_1	14007	28110	207	69
b3x13525.x	24397802_c2_1	14008	28111	213	71
b3x13430.x	34111378_f3_3	14009	28112	186	62
b3x13315.y	20334687_f1_1	14010	28113	288	96
b3x13305.y	23625187_f2_1	14011	28114	198	66
b3x13305.y	24414633_c3_4	14012	28115	198	66
b3x13296.y	36584432_c2_2	14013	28116	480	160
b2x14580.y	10657512_c2_1	14014	28117	561	187
b1x15611.x	14845125_f3_1	14015	28118	192	64
b2x14584.x	14453557_c2_2	14016	28119	387	129
b3x13229.x	6024000_c2_1	14017	28120	204	68
b3x13227.y	23836406_f1_1	14018	28121	240	80

b3x13227.y	1381932_c3_4	14019	28122	186	62
b1x12619.x	24313408_f2_3	14020	28123	261	87
b1x12619.x	12911410_f3_4	14021	28124	189	63
b3x13156.x	26375187_c3_2	14022	28125	480	160
b3x13155.x	11182316_f1_1	14023	28126	465	155
b3x12876.x	838535_f2_1	14024	28127	633	211
b3x12330.x	23984437_f2_3	14025	28128	300	100
b3x12330.x	34651567_c3_7	14026	28129	345	115
b1x12671.y	14667661_c3_6	14027	28130	207	69
b3x12303.y	19744825_f3_2	14028	28131	558	186
b3x12302.x	23444552_f1_1	14029	28132	810	270
b3x12037.x	22125275_f3_2	14030	28133	753	251
b3x12037.x	36218766_c3_3	14031	28134	216	72
b1x16215.y	19704752_c1_2	14032	28135	204	68
b3x11907.x	35172342_f2_1	14033	28136	186	62
b3x11387.y	10678400_f2_1	14034	28137	183	61
b2x14667.x	24808302_c3_3	14035	28138	519	173
b3x11306.x	26443828_c3_4	14036	28139	186	62
b1x16457.x	13157780_f2_1	14037	28140	399	133
b3x11148.x	34037932_c3_2	14038	28141	192	64
b1x16748.y	34570187_c3_5	14039	28142	183	61
b3x11108.y	2944057_f3_1	14040	28143	462	154
b3x10861.y	14485132_f2_1	14041	28144	210	70
b3x10133.x	2365963_f2_1	14042	28145	210	70
b3x10122.x	961543_c2_4	14043	28146	204	68
b1x16965.y	5110687_c1_2	14044	28147	636	212
b2x19530.y	2925652_c2_2	14045	28148	480	160
b1x16974.y	2832031_f2_1	14046	28149	456	152
b2x19433.x	35203325_f1_2	14047	28150	216	72
b2x14743.x	22711700_c2_2	14048	28151	198	66
b2x14743.x	24335787_c3_3	14049	28152	462	154
b2x19171.y	4860936_c3_1	14050	28153	270	90
b2x14756.y	20080082_c2_2	14051	28154	225	75

b2x19077.y	7126905_f1_2	14052	28155	264	88
b2x19038.x	23475676_f2_1	14053	28156	465	155
b2x18992.y	20113392_f1_1	14054	28157	186	62
b1x17289.y	19923126_f2_1	14055	28158	192	64
b1x17289.y	16578765_c2_2	14056	28159	198	66
b1x17289.y	33314438_c3_3	14057	28160	195	65
b2x18774.y	21486017_f1_1	14058	28161	321	107
b2x18614.y	7156558_f3_1	14059	28162	654	218
b1x12896.y	16900755_f1_1	14060	28163	627	209
b2x18564.y	26842204_f2_1	14061	28164	369	123
b1x12915.y	9845035_f2_1	14062	28165	183	61
b2x18561.y	4901878_f2_1	14063	28166	270	90
b2x18550.y	23865802_c1_3	14064	28167	216	72
b1x7564.y	24339078_f2_1	14065	28168	228	76
b1x7564.y	6831678_f3_2	14066	28169	297	99
b1x7564.y	1990880_f3_3	14067	28170	201	67
b1x7567.y	19970192_f1_1	14068	28171	198	66
b2x18389.x	24851537_f1_1	14069	28172	390	130
b1x7708.y	642665_f3_1	14070	28173	468	156
b2x18370.y	32204787_f1_1	14071	28174	528	176
b2x18261.y	22461532_f1_1	14072	28175	285	95
b1x17784.y	6700_c3_1	14073	28176	210	70
b2x18181.y	32609552_f1_1	14074	28177	576	192
b2x18172.x	22454432_f1_2	14075	28178	429	143
b2x18172.x	14096936_c2_4	14076	28179	279	93
b1x14078.y	127_c2_1	14077	28180	183	61
b1x13049.y	2776442_c3_2	14078	28181	570	190
b2x18152.x	578437_f2_3	14079	28182	192	64
b1x17788.y	32454675_f2_1	14080	28183	714	238
b2x18065.x	11735267_f2_1	14081	28184	219	73
b2x18056.x	33634562_f1_1	14082	28185	516	172
b2x18053.x	16835943_f2_1	14083	28186	276	92
b1x17830.y	33259813_c3_1	14084	28187	306	102

b2x17956.x	30267327_f2_1	14085	28188	61	
b2x17871.y	34181300_f1_1	14086	28189	183	61
b2x17871.y	24414057_c3_2	14087	28190	402	134
b2x17864.x	20595816_c2_1	14088	28191	489	163
b2x14964.y	470641_f3_1	14089	28192	780	260
b2x17609.y	25422252_f1_1	14090	28193	207	69
b2x17954.y	34618753_c3_4	14091	28194	540	180
b1x17976.y	20046901_f1_2	14092	28195	354	118
b1x17976.y	23594000_c1_3	14093	28196	252	84
b2x17388.y	7079206_f2_1	14094	28197	456	152
b2x17371.y	4812501_f2_1	14095	28198	282	94
b2x17371.x	14569682_c3_2	14096	28199	504	168
b2x17301.y	4171903_c2_1	14097	28200	243	81
b2x17276.y	48440902_f2_2	14098	28201	507	169
b2x17229.x	10580253_c2_4	14099	28202	204	68
b2x15106.y	25586442_f3_1	14100	28203	189	63
b2x15106.y	4885965_c2_2	14101	28204	348	116
b2x17138.y	32628776_f2_1	14102	28205	537	179
b2x15171.y	24329705_f2_1	14103	28206	195	65